

# Ivan Liongson

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## Research Interests

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Machine learning for regulatory genomics and systems biology; developing models linking DNA sequence, chromatin context, and gene expression to understand transcriptional regulation and disease mechanisms.

## Education

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### Stanford University, Stanford, CA

- **Master of Science (M.S.) Computer Science**, Artificial Intelligence (AI), Jun 2024
- **Bachelor of Science with Honors (B.S.) Biology**, Computational Biology, Jun 2024
- **Bachelor of Arts (B.A.) East Asian Studies**, Japan, Jun 2024

## Research Experience

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### ML and Bioinformatics Research Assistant | Stanford Bioengineering, Stanford, CA | Jun 2021 – Jun 2023

- Performed DNA/RNA extractions, qPCR assays, and lentiviral infections for large-scale transcription-factor perturbation screens.
- Processed and analyzed high-throughput functional genomics datasets using Python-based analysis pipelines.
- Built machine-learning pipelines for effector-domain activity prediction; contributed to analysis scripts and figure generation for collaborative projects.
- Co-author: DelRosso et al., *Nature* (2023) “Large-scale mapping and mutagenesis of human transcriptional effector domains.”

### Neuroscience Research Assistant | Wu Tsai Neurosciences Institute, Stanford, CA | Dec 2019 – Sep 2020

- Modeled mitochondrial dynamics under stress conditions in neuronal cells to understand energy-regulation failure in neurodegeneration.
- Applied computer-vision segmentation to live-cell imaging data to visualize mitochondrial transport and morphological change.
- Conducted literature synthesis on mitochondrial trafficking and axonal pathology to guide computational experiments.

## Peer-Reviewed Publications

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DelRosso, N., Tycko, J., Suzuki, P., Andrews, C., Aradhana, Mukund, A., **Liongson, I.**, Ludwig, C., Spees, K., Fordyce, P., Bassik, M. C., & Bintu, L. (2023). *Large-scale mapping and mutagenesis of human transcriptional effector domains*. *Nature*.

## Presentations & Posters

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**Biology Achauer Honors Research Symposium, Stanford University — May 2023**

**Stanford Symposium of Undergraduate Research & Public Service (ASURPS) — Apr 2023**

## Professional & Technical Experience

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### Software Engineer AI Training Consultant | Outlier AI | Oakland, CA (Remote) | Feb 2024 – Present

- Authored and reviewed test cases to verify Python and C++ solutions generated by large language models.
- Evaluated hundreds of model outputs, providing detailed analyses of logic, efficiency, and security to improve training datasets.
- Helped develop internal evaluation criteria and peer-review guidelines for assessing AI-generated Python and C++ solutions across multiple domains.

## Selected Projects

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### Deep Learning Modeling of Transcription Factors (Honors Thesis Work) | 2023

- Constructed CNN architectures to predict activation and repression from sequence motifs and disorder scores.
- Used Optuna for hyperparameter optimization and Weights & Biases for experiment tracking and visualization.
- Maintained code repository and documentation on GitLab for collaborative use within the lab.

### Computational Analysis of Japanese and Chinese Character Readings (Capstone, iOS App) | 2023 – 2025

- Developed a Python pipeline to map phonetic correspondences between Japanese and Mandarin characters.
- Applied corpus statistics and rule-based transformations to identify cross-language regularities.
- Extended the work into *Hikaku*, an iOS application for cross-lingual character comparison, demonstrating computational breadth and independent project design.

### Cloud Computing for Healthcare (Course Project) | 2023

- Designed distributed microservice architecture on AWS and GCP for processing large biomedical datasets.

## Honors & Awards

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**Honors in Biology — Stanford University (2023)**

**VPUE Major Grant — Stanford University (2022)**

**Bioengineering REU Fellowship — Stanford Bioengineering (2021)**

**NeURO Fellowship — Stanford Wu Tsai Neurosciences (2020)**

## Technical Skills

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**Machine Learning & Data Science:** PyTorch, Keras, TensorFlow, Scikit-learn, Optuna, Weights & Biases, Pandas, NumPy, Matplotlib

**Computational Biology:** Biopython, Sequence/Structure Modeling, Genomic Data Integration, Statistical Genomics Analysis

**Programming Languages:** Python, C++, C, Java, SQL

**Systems & Cloud:** AWS, Google Cloud Platform, Kubernetes

**Laboratory Techniques:** PCR/qPCR, DNA/RNA Extraction, Cell Culture (BSL-2), Lentiviral Transduction