Ivan Liongson

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Research Interests

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

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

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

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

Biology Achauer Honors Research Symposium, Stanford University — May 2023
Stanford Symposium of Undergraduate Research & Public Service (ASURPS) — Apr 2023

Professional & Technical Experience

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

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

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

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