Justice (Hsiu-Yi) Lu

PhD. Candidate, Duke University

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Summary

I am passionate about the intersection of computation and biology. I have a broad interest in leveraging data science to solve complex biological questions, with experience in multi-omics analysis, structural biology, and protein engineering. My work spans building tools to study gene regulation and developing machine learning models to predict receptor-ligand interactions — all with a focus on applying computational methods to real biological systems.

Skills

Computer Programming Language: Python, R, Bash, Git
Bioinformatics: omics analysis (single-cell/bulk RNA-seq, proteomics), protein modeling
ML & Data Science: PyTorch, scikit-learn, data visualization, CNNs, regression/classification

Education

Duke University (Expected graduation, Fall 2025)   2019 - Present
Ph.D. in Molecular Genetics and Microbiology (Advisor: Hiroaki Matsunami)
- IBIEM Computational Biology Fellow | Taiwan-Duke Fellowship Recipient

Purdue University, B.S in Biological Science   2013 - 2016

Research Experience

Graduate Student Researcher, Duke University, Hiroaki Matsunami Lab   2020 - Present
- Developed single-cell, bulk RNAseq and proteomic analysis pipeline and identified gene candidates to enhance olfactory receptor cell surface expression for *in vitro* genetic screen.
- Led and developed ML models (CNNs) to predict receptor-ligand binding from protein structures.
- Built geLine, a web tool for gene co-expression analysis and maturation trajectory tracing.
- Mentored trainees for independent computational/experimental projects.

ML Data Science Intern, Kriya Therapeutics   2023
- Engineered scalable ML pipelines for high-throughput drug target prediction, achieving 10× data throughput.
- Optimized data preprocessing and model training workflows using Python, pandas, scikit-learn, and cloud computing resources.
- Collaborated with bench science teams to integrate transcriptomic features into predictive models.

Research Technician II, Duke University, John Rawls Lab   2017 - 2019
- Demonstrated host-microbial protective response from zebrafish gut against pathogenic bacteria in vivo.
- Conducted genetic screen to identify novel regulators of lipid metabolism and adipose tissue morphogenesis in zebrafish. Identified genes may represent new therapeutic targets for human diabetes, obesity and associated disorder through control of distinct lipid metabolic processes.

Selected Publications (* First author)

- Identifying Key Regulators in Odorant Receptor Trafficking.
  Lu, HY*. & Matsunami, H. **Journal of Neuroscience** (in revision)
- Physiology of olfactory sense.
  Lu, HY*., Meesa, P. & Matsunami, H., **Digital Technologies in Olfaction, 7-14** (2025)
- Role of iRhom2 in Olfactory Sensory Neurons: Implications for Odorant Receptor Regulation.
  Azzopardi, S*., **Lu, HY*.**, Monette, S., Rabinowitsch, A., Salmon, J., Matsunami, H., & Blobel, C. **IJMS** (2024)
- Sex steroid hormones synthesis, metabolism and the effects on the mammalian olfactory system.
  Abaffy, T., **Lu, HY.**, & Matsunami, H. **Cell and tissue research** (2023).
- An odorant receptor that senses four classes of musk compounds
  Yoshikawa, K., Deguchi, J., Jieying, H., **Lu, HY**., & Matsunami, H. **Current Biology** (2022).
- Enteroendocrine cells sense bacterial tryptophan catabolites to activate enteric and vagal neuronal pathways.
  Ye L, Bae M, Cassilly CD, Jabba SV, Thorpe DW, Martin AM, **Lu HY.**, … & Rawls JF. **Cell Host Microbe** (2021).