Yue Wu

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Project Display Page: https://yuewu710.github.io/

EDUCATION

Northwestern University Evanston, IL *Jun 2025 – Jun 2026 (Expected)*
- **Major:** Quantitative and Systems Biology (M.S.) **GPA:** 4.0

University of California, Santa Barbara Santa Barbara, CA *Sep 2021 – June 2025*
- **Major:** Biology (B.A.), **Honors College** **GPA:** 3.77 (Junior–Senior GPA: 3.88)
- **Graduate-Level Coursework** (as an undergradruate)**:** BioDynamics (A+), Model-Guided BioSystems (A+), Gene Therapy (A+), SystemsBio (A), Qualitative Experiments (A), Biomolecular Methods (A), Omics and Biotech (A), and 2 more

Academic Background: Systems and Synthetic Biology, Applied Math and Dynamics Modeling, Programming and Machine Learning, Probability and Statistics, Molecular and Omics Biology, Organic Chemistry

RESEARCH INTERESTS

With training from both **molecular experiments** and **mathematical computation**, I study **biology as a complex system** and apply novel technologies such as **control theory**, **optogenetics**, and **representation learning** to understand how cells make dynamic decisions in **development**, **aging**, and **rejuvenation**.

CONFERENCES

Wu, Y., Dickson, E., Wilson, M. **Cellular Reporters for Drug Screening in Reprogramming-induced Rejuvenation**, and **Decoding ISR Dynamics to Inform Effective Cancer Treatment** (*Co-author Poster*), *14th Annual Southern California Systems Bio Symposium*, UC Irvine*, May 2025*

Wu, Y. **Applying Waddington Landscape to Epigenetic Rejuvenation and Theory of Aging,** *Mechanism of Aging Symposium*, Cold Spring Harbor Laboratory*, Sep 2024*

Dickson, E., Hao, E., Wu, Y., Wilson, M. **Dynamical Profiling of Cancer Cell Stress Signal Processing Through Optical PKR Activation**, *AIChE Optogenetic Conference*, Boston University*, Sep. 2024*

Wu. Y., Dickson, E., Wilson, M. **Discover Small Molecules for Reprogramming-Induced Rejuvenation**, *Oral Presentation*, **Light-Controlled Precise Temporal Activation of Yamanaka Factors for Optimal Anti-Aging Scheme Determination** *Poster*, *College of Creative Studies Research and Creative Activities Conferences*, UC Santa Barbara*, Nov 2023 & 2024*

RESEARCH EXPERIENCE

#ControlTheory #CellFateEngineering #VelocityField

Xiaojie Qiu Lab| Dept of Genetics, Stanford University *Aug 2025 – Present*
Independent Researcher
Project: Applying Control Theory to Generate Minimal Fate-Driving Genetic Intervention
- Developed optimal control framework to traverse cells from source to target fates through biologically feasible, minimal-dose intervention paths on Jacobian reconstructed RNA velocity cell fate landscape
- Applied to hematopoietic differentiation dataset, where the controller identified biologically-meaningful minimal gene sets (e.g., upregulation of *GFI1* and *MYCN* for Human Stem Cell to Erythroid, and inhibition of *ALAS2* only for Erythroid to Megakaryocyte) and generated precise timing windows with respective gene expression strength
- Redesigned trajectory optimization using iterative Linear Quadratic Regulator (iLQR) guided by Dynamo-computed Least Action Path references, eliminating suboptimal wandering trajectories while minimizing gene perturbation doses

#RepresentationLearning #GeneRegulatoryNetwork #VirtualPerturbation

Rosemary Braun Lab| Dept of Molecular Biosciences, Northwestern University *Jun 2025 – Present*
Independent Researcher
Project: Inferring Causal Cell Fate Drivers Through Network Modeling and Latent-Space Analysis

- Constructed de novo causal gene regulatory network using information theory-based Aracne algorithm and updated its direction and edge weight by linear regression from bulk RNA-seq datasets derived from ten single-gene RNAi knock-down (KD) experiments; applied network controllability analysis to discover *FOXM1* and *MYBL2* as key proliferating regulator
- Developed variational autoencoder (VAE) framework to learn low-dimensional latent manifolds from single-cell data, successfully prioritizing known master regulators (*JUNB*, *ZNF750*, *CEBPA/B*, *KLF4*) along differentiation trajectories
- Applied VAE to cluster ~10k genes from single-cell RNA-seq data into 11 distinct function-based clusters in an unsupervised manner; recovered topological patterns of cell types involved in epithelial cell differentiation
- Integrated VAE-derived trajectory markers and Geneformer perturbation predictions into de novo gene regulatory network model, with 70.4% of inferred edges matching curated interactions in KEGG, BioCarta, and Reactome

#SynBio #Optogenetics #Rejuvenation #CellularStress #Senescence

Max Wilson Lab| Dept of MCDB, UC Santa Barbara *Dec 2022 – May 2025*

Independent Researcher

Project I: Optogenetic & Cellular Reporter Systems for Reprogramming-Induced Rejuvenation (RIP)

- Constructed OSK (Oct4, Sox2, Klf4)-inducible human fibroblast cell lines; validated reprogramming functionality through immunofluorescence staining
- Engineered optogenetically controlled HEK cell lines with RedOn/GreenOff and BlueOn (Opto-Tet) systems, achieving 3.25-fold and 11.6-fold increases in OSK expression after 15 minutes and 12 hours of blue light stimulation, respectively
- Designed and built eight OSK-responsive fluorescent cellular reporters to screen for OSK-activatable anti-aging drugs; performed time-lapse microscopy, observing 1.3-fold and 1.75-fold increases in reporter signal for Oct4 and Sox2 induction respectively, requiring further optimization

Research Assistant

Project II: Engineering & Quantifying Cellular Stress Responses and Senescence

- Performed timepoint-specific β-galactosidase senescence assays on chronic-stressed cells under graded stress induction; developed a CellPose 3.0-based pipeline to quantify senescence levels, distinguishing low-stress-induced senescence from high-stress-induced apoptosis
- Engineered multiple cell lines to monitor or induce stress signaling dynamics, including CHOP reporter regulated by trimethoprim-controlled fluorescent signal accumulation, and opto-Dele1 constructs for blue light-induced mitochondrial stress; confirmed second-scale mitochondrial targeting via fluorescence microscopy
- Cloned and transduced dimerizer-controlled systems into chronic stress models; prepared synthetic reporter libraries and sequencing for sonogenetic screening; cloned and purified 3 synthetic Wnt ligand variants to investigate cell fate decisions

#MathematicalModeling #SingleCellTranscriptomics #3DCellFateMapping

Independent Research Projects | UC Santa Barbara

Project I: Mathematical Modeling of Cell Fate Decision *May 2025 – Jun 2025*

- Generated a ranked list of candidate senescence driver genes from published human transcriptome data, using the GeneSurrounder network analysis algorithm; identified the integrated stress response (ISR) pathway as a key contributor
- Constructed minimal ODE model of ISR signaling pathway incorporating eIF2α phosphorylation, ATF4, CHOP, GADD34, p21, and DR5 dynamics to simulate stress-induced cell fate decisions (hormesis, senescence, apoptosis)
- Generated 3D cell fate landscape showing how stress intensity, duration, and timing determine outcomes; model recapitulated threshold-based transitions between adaptive response and terminal fates, aligning with wet-lab data

Project II: Theoretical Developmental Biology with Computation *Mar 2024 – Apr 2024*

- Constructed a 3D Waddington Landscape by decomposing RNA velocity fields from published single-cell RNA-seq and ATAC-seq datasets of hematopoietic progenitor stem cells, revealing 3D differentiation trajectories

SKILLS

Wet Lab: Fluorescence-activated cell sorting (FACS), Electron microscopy, Resazurin-based cell viability assays, Beta-gal cellular senescence assay, Immunofluorescent staining, Transduction, Transfection, Tissue culture, Protein purification, Molecular cloning, Plasmid design

Dry Lab: Representation learning, Gene network analysis, Mathematical modeling of biological dynamics, Single-cell / bulk RNA sequencing analysis, Microscopy image signal quantification, Cell segmentation model training, Programming opto-plate patterning for optogenetic experiments

Communication: native Chinese, near-native English, and advanced German