Daniel Y. Zhu



April 14th, 1997



danielyumengzhu@gmail.com zhudy@mit.edu



(307)-761-1465



195 Binney St., Cambridge, MA

Education ——

PhD in Biological Engineering: Massachusetts Institute of Technology, Lauffenburger lab | 2020-now GPA: 4.9/5.0

BSE in Electrical Engineering: University of Wyoming | 2015-2020 GPA: 3.92/4.00, Magna Cum Laude

BS in Molecular Biology: University of Wyoming | 2015-2020 GPA: 3.95/4.00, Magna Cum Laude

Minor in Honors Program: University of Wyoming | 2015-2020

Skills ——

Computational Skills:

Highly Proficient: Python, Machine Learning (PyTorch, Tensorflow, Keras), Data Integration, Comparative Analysis, Data Representation (Matplotlib, Plotly, Seaborn) Proficient: MATLAB, C/C++, R

Microsoft Office:

Proficient: Excel, PowerPoint, Word,

Publisher, Visio

Electronic/Software Platforming: Highly Experienced: Arduino

Wet Laboratory Skills:

Highly Experienced: Pipetting, PCR/RT-PCR, Gel Electrophoresis, Western Blot, Wide-Field Light Microscopy, DNA/RNA Isolation/Purification, Microfluidic Fabrication

Experienced: DNA Transformation, Conjugation, Immunoprecipitation, Confocal Microscopy, ELISA, Flow Cytometry, Mammalian Tissue Culture

Other:

Proficient: LaTeX, Adobe Illustrator Experienced: ImageJ, Graphpad Prism

Research Experience

Jan'17-'18

Investigation of Polar-Localizing Proteins and Their Role in Chromosomal Segregation in *Agrobacterium* University of Wyoming Bowman lab, department of Molecular Biology.

· Conducted regular DNA transformations, amplifications and purifications for gene insertion into a non-native bacterial host.

Feb'19-Auq'20 Characterizing the Relationship Between Microtubule (MT) Dynamics and Growing End Density University of Wyoming

Gatlin lab, department of Molecular Biology.

- Developed a MATLAB program to quickly quantify the relationship between growing end velocity and density.
- Simulated intracellular MT growth using *X.laevis* egg extract and biochemical perturbations, tracked growing ends with software and confocal microscopy in photolithographically manipulated hydrogel structures.

May-Aug'19

The Effect of Neuronal Compartmentalization on Exosome Profiles and Neurodegenerative Disease Montana State University McCalla lab, department of Chemical and Biological Engineering as

temporary researcher (MT INBRE Summer Program).

· Utilized and refined a microfluidic device-based (PDMS hydrogel) platform for the growth of neurons, extracted exosomes and isolated miRNA to analyze concentration.

Sep'20-now

Unsupervised Domain Adaptation for the Cross-Species Translation of Transcriptomic Insights.

Lauffenburger lab, department of Biological Engineering.

- Developed a simulation platform through the use of generative deep learning models (VAE, GAN and an inferential Gaussian Process model) capable of faithfully generating synthetic samples with thousands of features.
- Developed a module to automatically parse large transcriptomic datasets to find orthologous genes and filter the original dataset accordingly.
- Aided in development of a multi-output Gaussian Process to identify features that can be used to regress on clinical outcome across disparate domains.

MIT

Feb'21-now

Identification of the Serological Correlates of Protection Against COVID-19

Collaboration with Alter lab, Ragon Institute of MGH, MIT and Harvard.

- Defined the vaccine-induced determinants of protection against SARS-CoV-2 infection in a non-human primate dose-down study of the Janssen Ad26.CoV2.S vaccine.
- Characterized B cell and T cell responders and inter-group immunological differences in a SARS-CoV-2 household study.
- Characterized humoral profiles of immunosuppressed patients following vaccination with Pfizer mRNA BNT162b2 containing the Delta variant.

Aug'21-now

Computational Methods for Analyzing Spatial Transcriptomic Data

Multi-lab collaborative efforts

- Developing methods for decomposition, representation learning, and cell-cell communication prediction to analyze spatial transcriptomic data and contextualize findings.
- Work on a generalized computational platform to perform multiple different analyses on spatial omics data with original code as well as existing resources, including 3D visualization, segmentation, cell-cell communication and identification of spatial domains.

Daniel Y. Zhu



April 14th, 1997



danielyumengzhu@gmail.com zhudy@mit.edu



(307)-761-1465



3828 Little Moon Trail, Laramie, WY 82070

Relevant Courses

Undergraduate-level: Biochemistry, General Microbiology, Cell Biology, Immunology, Organic Chemistry, Electronics, Bioinstrumentation, Biomedical Signal Processing

Graduate-level:

Advanced Image Processing, Object and Pattern Recognition, Neural Networks and Artificial Intelligence, Principles of Molecular Bioengineering, Analysis of Biological Networks, Biomaterials, Hallmarks of Cancer

Extracurricular —

MIT Biological Engineering Board: September 2020-now

- Welcoming Chair for 2020-2021
- Community Service Chair for 2021-2022

Tau Beta Pi, the Engineering Honor Society: November 2017-now

- Recording Secretary for 2019-20

Institute of Electrical and Electronics Engineers (IEEE): 2015-now

- President for 2019-20

Mortar Board, the Collegiate Senior Honor Society: April 2019-now

- Points Committee

Circle K International:

August 2015-August 2016

- Recording Secretary for 2015-16

References

Available Upon Request.

Work Experience

May'18-Jun'19RnD Intern for the ESP4T Program

University of Wyoming

Department of Electrical and Computer Engineering

- Using C/C++ and electronic components, created math and science modules for use as teaching aides.
- Hosted workshops teaching people to work with Arduino and Raspberry Pi, especially teachers and underrepresented aroups in STEM.
- Demonstrated Arduino and Raspberry Pi modules to interested audiences.

Publications

Geisterfer, Z. M., Zhu, D. Y., Mitchison, T. J., Oakey, J., Gatlin, J. C. (2020). Microtubule growth rates are sensitive to global and local changes in microtubule plus-end density. Current Biology.

Chen, R., Gorman, M., Zhu, D., Diamond, M. et al. (2021). Reduced antibody activity against SARS-CoV-2 B.1.617.2 Delta virus in serum of mRNA-vaccinated patients receiving TNF- α inhibitors. *Med*.

Zhu, D. Y.*, Gorman, M. J.*, Lauffenburger, D. A., Barouch, D. H., Alter, G. et al. (2021). Defining the determinants of protection against SARS-CoV2 infection and viral control in a dose-down Ad26.CoV2.S vaccine study in non-human primates. PLOS Biology.

Posters

Zhu, D.*, Kang, B.*, Souillard-Mandar, W.*, Chung, H., Chen, F. (August 2019). Deep Generative Modeling of Transcription Factor-Gene Expression Relationships. Presented at NeurIPS Learning Meaningful Representations of Life 2021.

Honors and Awards

Feb'15	Trustees' Scholars Award Full-ride scholarship to the University of Wyoming
May'19	Recipient of the Tau Beta Pi scholarship Stabile Award no. 700
Sep'19	Recipient of University of Wyoming INBRE Undergraduate Research Fellowship
May'20	Recipient of the University of Wyoming Department of Electrical Engineering Honor Book Awarded to the department's outstanding graduating senior
	President's List (5 semesters), Dean's List (5 semesters)

President's List: 4.0 GPA, Dean's List: 3.4-3.99 GPA

Other Projects

Motion Pattern Recognition for Trunk Exoskeleton:

Sep'19-May'20

- Used CAD software to design printed circuit boards to mount sensors onto.
- Designed a neural network classifier to discriminate between various physical motions.
- Used Simulink to interface between each sensor and the computer.

A Computational Platform for Genetic Matching

Jun'20-Jul'20

- Designed a Python program to find closely aligning sequences to gene(s) of interest via remote NCBI BLAST.
- · Applied said program to search for simpler Type I-resembling CRISPR systems.