

KATIE HUANG

Elmhurst, NY | katie.huang830@gmail.com | www.linkedin.com/in/KatieHuang20 | https://kthuang20.github.io/Katie_Portfolio

Education

University of Massachusetts Lowell – Lowell, MA

Dec. 2024

Master of Science in Biomedical Engineering and Biotechnology

Cumulative GPA: 4.00/4.00

Awards: 2024 Student Research and Community Engagement Symposium Winner

Poster Presentations: RECOMB 2024, ISMB 2024

[\(Overview of project\)](#)

Relevant Coursework: Data Science for Biologists, Probability & Math Stats, Genomics, Cancer Genomics, ML and AI in Living Organisms

University of Massachusetts Lowell – Lowell, MA

Dec. 2023

Bachelor of Science in Biomedical Engineering

Cumulative GPA: 3.92/4.00

Chancellor's List: Fall 2023; Dean's List: Fall 2020, Spring 2021, Fall 2021, Spring 2022, & Fall 2022

Clubs and Activities: Co-president of UML Badminton Club (2023), STAARS mentor, member of UML Table Tennis Club

Technical Skills

Programming Languages: Python, command line (bash, terminal)

Data Analysis & Visualization: pandas, numpy, matplotlib, seaborn, scikit-learn, statsmodels, scipy, plotly

Development Tools: git, GitHub, conda, streamlit, JupyterLab

Professional Experience

Adjunct Faculty, Data Scientists for Biologists with Lab

Nov. 2024 – Dec. 2024

Department of Biological Sciences, University of Massachusetts Lowell – Lowell, MA

- Empowered students to apply linear models (e.g., correlation coefficient, r-squared) to real-world problems using statsmodels
- Fostered critical thinking and collaboration through group projects, peer review, and hands-on coding exercises
- Built student confidence in computational skills, including Python programming and basic command line skills
- Delivered prompt, detailed feedback to support individual learning and enhance technical understanding

Graduate Biomedical Data Science Researcher

Sept. 2023 – Dec. 2024

Computational Disease Biology Lab, University of Massachusetts Lowell – Lowell, MA

- Built a logistic regression model to predict new treatments for existing drugs by analyzing how similar their molecular effects are
- Validated the hypothesis that drugs with shared indications induce similar gene expression changes
- Developed and implemented a predictive framework across three diverse cancer cell lines, achieving an AUC of 0.708 in predicting clinical trial outcomes
- Mentored a junior researcher, guiding her through project development and empowering her to build her own data dashboard

Data Science Projects

Accelerating Targeted Drug Discovery Against Antibiotic Resistance Using CNNs

- Developed a CNN to predict the efficacy of drug candidates against β -lactamase using the ChEMBL database, achieving 98% precision, accuracy, recall, and 100% AUC on the testing dataset
- Converted canonical SMILES into 2D images, allowing the CNN to automatically identify key molecular features, eliminating the need for manual feature engineering and drastically reducing dataset preparation time
- Demonstrated the potential of CNNs for predicting antibiotic resistance treatment, showing promise for accelerating drug discovery and reducing the workload on traditional methods

Exploring the Genetic Effects of Wnt Pathway on Pancreatic Adenocarcinoma

- Analyzed TCGA data to examine Wnt pathway's role in pancreatic cancer
- Discovered recurring mutation patterns and potential tumor-suppressing activity
- Identified key targets for further biological investigation, providing insights for future research