

# KATIE HUANG

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## 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, matplotlib, seaborn, scikit-learn, statsmodels, scipy, plotly

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

## Professional Experience

### Adjunct Faculty

Nov. 2024 – Dec. 2024

Department of Public Health, 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 Researcher

Sept. 2023 – Dec. 2024

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

- Developed an ensemble logistic regression model to predict novel treatments for existing drugs by assessing similarity in drug molecular effects
- Summarized statistical and visualize analyses, confirming hypothesis that drugs with shared treatments exhibit similar gene expression changes
- Co-mentored a junior researcher, fostering independence on a self-directed project by providing support, resources, and collaboration
- Maintained thorough documentation of analyses in Jupyter notebooks and continually optimized algorithms

## Data Science Projects

Accelerating Targeted Drug Discovery Against Antibiotic Resistance Using CNNs

[\(link to Google Colab notebook\)](#)

- Leveraged a Convolutional Neural Network (CNN) to predict the efficacy of potential drug candidates against  $\beta$ -lactamase using the ChEMBL database, achieving over 90% accuracy, precision, and recall
- Converted canonical SMILES of compounds into 2D images using RDKit, allowing the CNN to automatically identify key molecular features for inhibiting  $\beta$ -lactamase, thus eliminating the need for manual feature engineering
- Demonstrated the potential of using compound chemical structures for predicting antibiotic resistance prevention, highlighting CNNs' promise in accelerating the discovery of  $\beta$ -lactamase inhibitors and reducing the workload for data preparation

Exploring the Genetic Effects of Wnt Pathway on Pancreatic Adenocarcinoma

[\(link to Google Colab notebook\)](#)

- Utilized pandas and scipy to analyze TCGA Pancreatic Adenocarcinoma data, examining mRNA expression, methylation levels, and mutation profiles in 184 tumor samples
- Identified top 3 mutated genes in the Wnt pathway, determining their mutation types and association with patient survival, revealing potential tumor suppressor activity
- Utilized plotly and dash-bio to create visualizations comparing gene expression levels between tumor and non-tumor patients, highlighting significant findings supported by literature