

# KATIE HUANG

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[https://kthuang20.github.io/Katie\\_Portfolio/](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

Relevant Coursework: ML and AI in Living Organisms, Cancer Genomics, Data Science for Biologists, Probability and Mathematical Statistics I

### 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

## Skills

Programming Languages: Python, bash

Data Analysis & Visualization: JupyterLab, pandas, matplotlib, scikit-learn, statsmodels, scipy, plotly, dash-bio

Development Tools: conda, GIT, streamlit

## Professional Experience

### Graduate Research Assistant

Sept. 2023 – Present

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

- Developing an ensemble logistic regression model to predict novel treatments for existing drugs by assessing on similarities mRNA expression profiles
- Summarized statistical and visually analyses, confirming hypothesis that drugs with shared treatments exhibit similar changes on gene expression
- Co-mentoring a junior researcher, fostering independence on a self-directed project by providing support, resources, and collaboration
- Communicate technical findings effectively to a multidisciplinary team during lab meetings, using accessible language
- Maintain thorough documentation of analyses in Jupyter notebooks and continually optimize 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