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

Skills

Programming Languages: Python, command line (bash, zsh)
Data Analysis & Visualization: pandas, matplotlib, seaborn, scikit-learn, statsmodels, scipy, plotly, dash-bio
Development Tools: GIT, GitHub, conda, streamlit, JupyterLab

Professional Experience

Graduate Research Assistant   **Sept. 2023 – Present**
Computational Disease Biology Lab, University of Massachusetts Lowell – Lowell, MA   *(Overview of project)*
  • 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
  • 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 β-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 β-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 β-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

Conference Presentations

Predicting New Indications of Known Drugs Based on Spearman Correlation Between Gene Signatures
  • Presented by Katie Huang at 28th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2024), Cambridge, MA, May 2024.
  • Presented by Katie Huang at 2024 International Conference on Intelligent Systems for Molecular Biology (ISMB 2024), Montreal, Quebec, Canada, July 2024.