

Wenya Chen

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EDUCATION

University of Washington

Major: Data Science in Chemical Engineering (MS)

GPA: 3.6/4.0

December 2021

Indiana University of Bloomington

Major: Biochemistry, Bachelor of Science

Cumulative GPA: 3.4/4.0

May 2020

COURSES & PROJECTS

- **Breast Cancer Predictive Analysis:** Predicted malignancy of breast tumors given details breast cancer cells using data from Kaggle. Employed various feature selection strategies to reduce the number of features and used popular Machine Learning classifiers with different model selection strategies to achieve approximately 92% accuracy
- **Numerical Investigation of the Airflow in Face Masks Used for Protection Against COVID-19 Virus:** Model 2D-flow simulation and 3D airflow-simulations by using finite difference approach (Jacobi Method) to give an approximate solution of the Navier Stoke Equation
- **Speed Dating** Modelled data to predict outcomes of speed dating events and analyzed the self-perception of participants. Identified and quantified characteristics of participants that lead to successful dates

PUBLICATION

- Gabale U, Peña Palomino PA, Kim H, Chen, W., Ressl, S. (2020) New functional identity of the essential inner membrane protein YejM: the cardiolipin translocator is also a metalloenzyme. *Manuscript under revision; preprint available on BioRxiv: <https://doi.org/10.1101/2020.02.13.947838>.*
- Gabale, U., Peña Palomino, P.A., Kim, H. Chen, W., Ressl, S. The essential inner membrane protein YejM is a metalloenzyme. *Nature, Sci Rep* **10**, 17794 (2020). <https://doi.org/10.1038/s41598-020-73660-6>
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TECHNICAL SKILLS

- Coding/Tools: Proficient in Python, R, TensorFlow, Keras, Java, JavaScript, SQL, D3.js, Vega/Vega-Lite, and Tableau
- Skill set: Algorithms, Machine Learning, Deep Learning, Hypothesis Test, Z Test, T Test, Chi Squared Test

PROFESSIONAL EXPERIENCE

Indiana University Molecular and Cellular Biochemistry Department

Bloomington, Indiana

January 2017 – May 2020

Research Assistant in Ressl Lab

- Used algorithms including AlphaFold to predict the YejM protein structure from the primary sequence given as well as the primary sequence with mutants
- Solved three-dimensional structures of the soluble domain of a Gram-negative bacterial cardiolipin translocator membrane protein, YejM, and its mutants by using XDS, HKL2000, Phenix, and CCP4 Python-based program suites
- Optimized algorithms to compare the similarities of two YejM periplasmic domain homologues and the hydrolase fold enzymes like arylsulfatases and alkaline phosphatase

Lannett Company, Inc, Seymour, Indiana

June 2019 – August 2019

Data Analytic Intern

- Performed complex data analysis of HPLC chromatograms and prepared visualization of HPLC chromatogram by using Tableau and Vega-Lite
- Performed Assay and Impurities/Degradants tests, Uniformity of Dosage tests, Acid Resistance tests, and Dissolution tests for omeprazole, atorvastatin and pantoprazole, analyzed HPLC chromatograms