

HARRISON WANG

R&D DATA SCIENTIST

✉ harrison.c.wang@gmail.com
🌐 <https://harrisonized.github.io/>
in <https://www.linkedin.com/in/harrisonized/>
🐙 <https://github.com/harrisonized>

PROGRAMMING: Python, SQL, Datalog, Matlab

DATABASES & WEB FRAMEWORKS: Postgresql, Datomic, MongoDB, Flask, Django

CLOUD COMPUTING & DASHBOARDING: AWS, EC2, S3, Sagemaker, Redshift, Athena, Quicksight, Tableau, Power BI

TOOLS & LIBRARIES: Pandas, Numpy, Matplotlib, Plotly, Sklearn, Statsmodels, BeautifulSoup, Selenium

MACHINE LEARNING: Regression, Classification, Clustering, Time Series Analysis, Natural Language Processing

EXPERIENCE

UNIVERSITY OF PENNSYLVANIA

Doctoral Candidate

Aug. 2022 to Current

Ph.D. Student in the NIH-Penn Immunology Partnership Program

- First rotation in Michela Locci's lab, exploring the role Activin A in rheumatoid arthritis

THERMO FISHER SCIENTIFIC

Research and Development Data Scientist

South San Francisco
Feb. 2021 to Aug. 2022

- Built a **scalable, end-to-end ETL process** to achieve **real-time monitoring** of **SARS-CoV-2 RT-PCR** test data from labs and universities using **Amazon AWS** and **Power BI**. Listed as third author on a **symposium abstract** based on this work
- **Lead the development** of the **data pipeline**. Heavily **refactored** and **optimized** the existing data pipeline for **scalability** through clever use of **parallelization** and **batch processing**, cutting the time it takes to transform 2000 csv files from 2 hours to 3 minutes. Add new **KPIs** and support **backward compatibility**
- **Analyzed** performance of sample retests using **Python** and **SQL**, enabling stakeholders to understand the limit-of-detection of our **SARS-CoV-2 RT-PCR** tests
- Designed dashboards in **Amazon Quicksight** and **Power BI** to monitor data ingestion and filtering, eliminating up-front time in scoping projects for data projects
- Created new **Plotly interactive visualization** for 96- and 384-well plates, enabling the Data Science team to rapidly **identify anomalies** in new data
- Saved a legacy **Matlab** codebase from disrepair through heavy **refactoring**

INVITAE

Bioinformatics Data Scientist

San Francisco
Jan. 2020 to Sept. 2020

- Discovered the **root cause** for a high-visibility, time-sensitive issue on a new assay that resulted in batch failures impacting 500+ samples
- Analyzed **trends** using **Python** and **SQL** to **monitor next-generation sequencing (NGS)** production-line data for anomalies
- Efficiently diagnosed **customer issues** by writing a **Python script** to **automate** generation of standardized **visualizations** and **statistics**
- Wrote maintainable **Datalog** and **SQL** queries for **Flask** app used to migrate data from **Datomic** to **Amazon Redshift** for consumption by **Tableau**
- Built an 8-page **Tableau dashboard** to enable our operations team to carefully monitor a new product launch

BIOVERATIV, FORMERLY TRUE NORTH THERAPEUTICS

Research Associate 2

South San Francisco
Jan. 2017 to Mar. 2019

- Led **protein-engineering project** on of lead antibody drug (BIVV009). Handled all **cloning and expression** of antibody variants and most of protein purification for the lab. **Collected binding and efficacy (KD and IC50) data** and performed **regression analysis**, revealing a log-linear relationship between KD and IC50. This enabled us to select which variants to use in downstream experiments.
- Led **research project** to make a protein complex of BIVV009 and its target (C1s of the complement immune system) for crystallography study.
- Wrote **Python script** to automate design of short DNA oligos, reducing a task that normally took 2 hours/week of manual labor to a 3 minute script.
- Wet lab: tissue culture, protein expression and purification, ELISAs, affinity and kinetics characterization, crystallography

GENE YEO LAB, UCSD

Staff Research Associate 1

La Jolla
May 2013 to Nov. 2016

- Developed **standardized protocols** to create tagged cell lines for **next-generation sequencing** (ENCODE)
- Co-authored a **Neuron paper** that included my experiments on elucidating the mechanism for how a mutation in an RNA-binding protein can cause ALS
- Co-authored a **Cell paper** that included my experiments on using a new genome-editing technology (CRISPR/Cas9) to track RNA in live cells
- Wet lab: **fluorescent cell imaging**, **next-generation sequencing**, high-throughput sequencing, CRISPR-Cas9, **qPCR**

FEATURED PROJECT

CLIMBING LOG WEB APPLICATION

Live app at: <https://harrisonized-climbing-app.herokuapp.com>

Blog post at: <https://harrisonized.github.io/2020/11/05/climbing-dashboard.html>

Built a **Flask app** to function as a **live dashboard** that keeps track of my climbing records. On the back-end, executes **SQL queries** to extract data from **Heroku Postgres**, transform the data, and generate **Plotly interactive visualizations**. On the front-end, displays the **visualizations** in logically organized web pages. Visualizations are **cached** to streamline data access and improve user experience. Users can **upload custom data** to generate their own figures.

EDUCATION

Metis Data Science Bootcamp

Apr. 2019 to June 2019

University of California, San Diego

2015

Double Major: B.S. Physics, B.S. Physiology & Neuroscience