

HARRISON WANG

PH.D. CANDIDATE

✉ harrison.c.wang@gmail.com

🌐 <https://harrisonized.github.io>

in <https://www.linkedin.com/in/harrisonized/>

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PROGRAMMING: Python, R, SQL, Matlab, Datalog

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

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

WET LAB: Cloning, Site-Directed Mutagenesis, Tissue Culture, Western Blot, qPCR, Confocal Microscopy, Flow Cytometry, CRISPR/Cas9, Next-Generation Sequencing, ELISA, Protein Expression, Protein Purification, Biolayer Interferometry, Assay Development, Mouse IP Injections, Mouse Anesthesia and Euthanasia

EXPERIENCE

UNIVERSITY OF PENNSYLVANIA

Ph.D. Candidate

Aug. 2022 to Current

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

- Second (current) rotation in Montserrat Anguera's lab, studying how X-inactivation contributes to female bias for autoimmune diseases. Used R to productionize an RNA-seq data analysis pipeline to identify and evaluate escape genes. Currently building a Python image processing pipeline for quantifying Xist puncta in RNA FISH images for the quantification of activated T cells obtained from MRL/lpr mice, a mouse model of lupus.
Wet lab: RNA FISH and H3K27me3 immunofluorescence
Dry lab: R, Python
- First rotation in Michela Locci's lab, exploring the role Activin A in rheumatoid arthritis. Completed a short rotation project on the effect of an anti-Activin A antibody on the disease progression of collagen-induced arthritis. Built a custom Python plot to show average disease severity scores for each toe and paw on the mouse.
Wet lab: cell-based activity assay, ELISA, tissue culture, mouse IP and tail dermal injections, anesthesia, euthanasia, flow cytometry
Dry lab: Graphpad, Flowjo, Python

THERMO-FISHER SCIENTIFIC

R&D Data Scientist

South San Francisco, CA

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 co-author on a **symposium abstract** based on this work
- Led the development of the **data pipeline**. Heavily **refactored** and **optimized** the existing data pipeline for **scalability** through clever use of **parallelization** and **batch processing**, reducing the runtime by 40x. Added new KPIs and support for 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 an **Amazon Quicksight** dashboard to monitor data ingestion and filtering, eliminating up-front time for scoping new projects
- Created new **Plotly interactive visualizations** for 96- and 384-well plates, enabling the Data Science team to rapidly **detect anomalies**
- Rescued a legacy **Matlab** codebase from disrepair through heavy **refactoring**

INVITAE

Operations Data Scientist

San Francisco, CA

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 2000+ patients
- 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** apps 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

BIOERATIV, FORMERLY TRUE NORTH THERAPEUTICS

Research Associate 2

South San Francisco, CA

Jan. 2017 to Mar. 2019

- Led **protein-engineering project** of lead antibody drug (TNT009). Handled all **cloning and expression** of antibody variants and most **protein purification** for the lab. Collected **binding and efficacy (KD and IC50) data** using **biolayer interferometry** and **ELISAs**. Performed **regression analysis**, revealing a log-linear relationship between KD and IC50, enabling our team to select variants to use in downstream experiments.
- Led **research project** to make a protein complex of TNT009 and its target (complement C1s) for crystallography study
- Developed **ELISAs**, **hemolysis assays**, and **flow cytometry assays** to measure classical and alternative complement activation
- Wrote **Python** script to automate design of short DNA oligos, reducing a 2 hours/week task to a 3 minute script.

Wet lab: tissue culture, protein expression, protein purification, column chromatography, ELISA, biolayer-interferometry kinetics assays

GENE YEO LAB, UCSD

Staff Research Associate 1

La Jolla, CA

Aug. 2015 to Nov. 2016

- Used **CRISPR/Cas9** to create, validate, and maintain 36 stable HEK293XT cell lines with end-tagged RNA-Binding Proteins (RBPs) for CLIP-seq as an extension of the Encyclopedia of DNA Elements (ENCODE) project
- Constructed and tested catalytically dead Cas9 (dCas9) fused to split proteins (GFP, Venus, thymidine kinase) as tools to detect RNA abundance in cultured HEK293XT and U2OS cells. Performed **flow cytometry** and **Western blot** to quantify results.
- Designed and **Gibson assembled** plasmids encoding human codon-optimized Cas-protein orthologs
- **Co-authored a Cell paper** on using CRISPR/Cas9 to track RNA in live cells

Wet lab: cloning, next-generation sequencing, high-throughput sequencing, CRISPR-Cas9, flow cytometry

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EXPERIENCE (CONTINUED)

GENE YEO LAB, UCSD

Undergraduate Research Assistant

La Jolla, CA
May 2013 to Aug. 2015

- Optimized **fluorescence-coupled activity assay** to measure D- and L-serine levels with up to 5 nM sensitivity on in-vitro synthesized DAO and in-vivo DAO-overexpression HEK293 cell lines
- Used **Flp-In system** to create, validate, and maintain stable D-amino Acid Oxidase (DAO) overexpression HEK293 cell lines
- Took high-resolution **confocal microscopy** images of stained iPSC-derived motor neurons
- Validated via **qPCR** splicing changes of 36 genes related to familial amyotrophic lateral sclerosis (fALS) found via RNA-seq
- **Co-authored a Neuron paper** that included my experiments on investigating the mechanism for how a mutation in an RNA-binding protein (hnRNPA2B1) can cause ALS

Wet lab: cloning, tissue-culture, qPCR, Western blot, confocal microscopy, fluorescent cell imaging, assay development

TEACHING EXPERIENCE

OFFICE OF ACADEMIC SUPPORT AND INSTRUCTIONAL SERVICES, UCSD

Physics Tutor

La Jolla, CA
Apr. 2013 to Mar. 2015

- Independently led 2-hour workshops of 10 to 20 students twice a week
- Created 18 original physics lectures with 4 practice problems each
- Fostered a collaborative learning environment free of discrimination and judgment

PUBLICATIONS AND POSTERS

EPIDEMIOLOGICAL AND BIOLOGICAL ASSOCIATIONS OF SARS-COV-2 VARIANTS BASED ON REAL-WORLD OBSERVATIONAL DATA

Nov.
2021

Imran Mujawar, Mani Manivannan, **Harrison Wang**, David Woo, Li Chan, Eduardo Sanchez, Teddy Proctor, Jared Auclair, Manoj Gandhi

Conference Poster for Labroots Coronavirus Conference Virtual Event Series on May 4, 2022

Conference Link: <https://www.labroots.com/trending/coronavirus/22926/advances-coronavirus-research-2022-ongoing-labroots-virtual-event-series-2>

Official Release: <https://assets.thermofisher.com/TFS-Assets/GSD/posters/epidemiological-and-biological-associations-of-sars-cov-2-variants-poster.pdf>

Copy: <https://harrisonized.github.io/publications/epidemiological-and-biological-associations-of-sars-cov-2-variants-poster.pdf>

ELIMINATION OF TOXIC MICROSATELLITE REPEAT EXPANSION RNA BY RNA-TARGETING CAS9

Aug. 2017

David A. Nelles, Elaine Pirie, Steven M. Blue, Ryan J. Marina, **Harrison Wang**, Isaac A. Chaim, James D. Thomas, Nigel Zhang, Vu Nguyen, Stefan Aigner, Sebastian Markmiller, Guangbin Xia, Kevin D. Corbett, Maurice S. Swanson, and Gene W. Yeo. **Cell**. 2017 Aug 24;170(5):899-912.e10. doi:

[10.1016/j.cell.2017.07.010](https://doi.org/10.1016/j.cell.2017.07.010). Epub 2017 Aug 10. PMID: 28803727; PMCID: [PMC5873302](https://pubmed.ncbi.nlm.nih.gov/28803727/).

PROTEIN-RNA NETWORKS REGULATED BY NORMAL AND ALS-ASSOCIATED MUTANT HNRNPA2B1 IN THE NERVOUS SYSTEM

Oct.
2016

Fernando J. Martinez, Gabriel A. Pratt, Eric Van Nostrand, Ron Batra, Stephanie C., Huelga, Katannya Kapeli, Peter Freese, Seung J. Chun, Karen Ling, Chelsea Gelboin-Burkhart, Layla Fijany, **Harrison Wang**, Julia K. Nussbacher, Hong-joo Kim, Rea Lardelli, Balaji Sundararaman, John P. Donohue, Jens Lykke-

Andersen, Frank Bennett, Manuel Ares Jr., Christopher B. Burge, J. Paul Taylor, Frank Rigo, Gene W. Yeo. **Neuron**. 2016 Nov 23;92(4):780-795. doi:

[10.1016/j.neuron.2016.09.050](https://doi.org/10.1016/j.neuron.2016.09.050). Epub 2016 Oct 20. PMID: 27773581; PMCID: [PMC5123850](https://pubmed.ncbi.nlm.nih.gov/27773581/).

EDUCATION

Metis Data Science Bootcamp

2019

University of California, San Diego

2015

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