

SKILLS

Data Science & Programming

- Python (Numpy, Pandas, Scikit-learn), SQL, Linux, R, Data Visualization, Git
- Machine Learning (Natural Language Processing, Time Series), Spark (Mapreduce, ML)
- Deep Learning (Tensorflow, Keras, Neural Network)

Bioinformatic Pipeline and Bio Assay Development

- **Next Generation Sequencing (NGS) and transcriptomic proficiency**
 - FASTQ meta-analysis on NCBI TNBCs with BWA, RSEM, STAR, Samtools
 - Nanostring analysis for p53 target mRNA expression level in breast cancer cells
- **Molecular Assay Development**
 - High-throughput screening platform for mutant p53 reactivating compounds
 - yeast screening platform
 - mammalian cells based screening platform
 - **CRISPR-mediated gene editing:** Rapid knockout and tagging tools
- **Proteomic Analysis:** Western Blot, Stable Isotope Labeling (SILAC), LC-Mass Spectrometry
- **Biomarker Analysis:** Multicolor flow cytometry (BD FACSDIVA), ELISA

Project Management

- Provided training and mentorship for new hires
 - Responsible for project timelines and excellent communication with stakeholders in R&D Assay Development, Clinical Diagnostics, Assay Validation, and Quality Assurance teams
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EXPERIENCE

Bioinformatic Scientist III

Ambry Genetics

Dec 2019 - Present

- Evaluate **Liquid Biopsy** probe coverage, panel uniformity, sensitivity and specificity
- Provide data insight for research, development, and validation for HGMDNext panel (4500 genes)
- Assess and validate pipeline performance on oncology panels, including **CancerNext** (majority of the sample volume) and Somatic panels
- Provide insight to reduce CNV calling QC failure and FP rate during a capture chemistry change
- Contribute to NGS bait-capture automation and library prep project: Tecan-robot DNA M200 workflow
- Provide weekly CNV calling statistics and ensure CNV calling quality
- Establish quality variant calling by statistics threshold to reduce lab Sanger workload
- Provide pipeline maintenance, troubleshooting, and identify solutions
- Generate critical data for variant assessment: SNV, indel, CNV, complex rearrangement, processed pseudogenes

Data Science Fellowship

The Data Incubator

June 2019 - Sept 2019

- Identified degree of connection, page rank, and best friends in "New York Social Diary" archive using Beautiful Soup, **Pandas**, Regex, Web-scraping, and NetworkX
- Analyzed New York restaurant inspection data with **SQL**: table joining, aggregation, and clean up
- Predicted Yelp star ratings based on venue features through **Machine Learning** models
- Utilized Vectorizers for **Natural Language Processing** on Yelp review text to predict star ratings

Postdoctoral Researcher

UC Irvine

Jan 2014 - Dec 2019

- Developed **CRISPR gene editing** (tagging and knockout) and viral derived vectors to investigate PP2A L309 methylation during SAM-checkpoint activation
- Purified HBTH-tagged PP2A (SILAC) for LC-MS and used Python for proteomic analysis. Resulted in identifying PP2A interaction map during methionine stress
- Characterized spliceosome activity with reporter and minigene assay in cells under methionine stress

Actavalon Inc.

Jan 2014 - Jan 2015

- Developed bio-screening platform in mammalian cells for p53 reactivating compounds, resulted in a publication in **Nature Communication**
- Characterized, optimized, and increased efficacy of lead compounds for mutant p53 activation

EDUCATION

University of California, Irvine

Sept 2007 - Jan 2014

Ph.D. Biological Sciences

- Identified metabolic checkpoint responses with virus-mediated gene expression and knockdown, resulted in discovery of p38 and MK2 induced cell cycle arrest during methionine stress

Georgia Institute of Technology

M.S. OMSCS with Machine Learning Specialization

Since Sept 2020

AWARDS & PUBLICATIONS - <https://tinyurl.com/33r2yc2j>

Journal of lipid research | Lipid remodeling in response to methionine stress in MDA-MBA-468 triple-negative breast cancer cells

2021

Data Science Fellowship | The Data Incubator - San Francisco

2019

Journal of Biological Chemistry | Microhomology based CRISPR tagging tools for protein tracking, purification, and depletion

2019

Methionine Dependence of Cancer and Aging | Isolation and characterization of methionine-independent clones from methionine-dependent cancer cells

2019

U.S. Patent | Chembridge Small Molecules that could enhance p53 activity

2015

Journal of Cell Science | SAM limitation induces p38 mitogen-activated protein kinase and triggers cell cycle arrest in G1

2014

Nature Communication | Computational identification of a transiently open L1/S3 pocket for reactivation of mutant p53

2013

Cell Cycle | Downregulation of Cdc6 and pre-replication complexes in response to methionine stress in breast cancer cells

2012

Predoctoral Fellowship | California Institute for Regenerative Medicine

2012

Journal of Biological Chemistry | Transforming growth factor β up-regulates cysteine-rich protein 2 in vascular smooth muscle cells via activating transcription factor 2

2008

Genes to Cells | Identification of a putative human mitochondrial thymidine monophosphate kinase associated with monocytic/macrophage terminal differentiation

2008

REFERENCES

Upon request