
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)

Bio Expertise

- **Next Generation Sequencing (NGS) and transcriptomic proficiency**
 - FASTQ meta-analysis on NCBI TNBCs with BWA, RSEM, STAR, Samtools
 - RNA splicing analysis on SAM depleted cells with HiSAT2, rMATS
 - Nanostring analysis for p53 target mRNA expression level in breast cancer cells
 - Target validation with nucleic acid isolation, qPCR, RT-PCR
- **Bioassay Development**
 - High-throughput screening platform for mutant p53 reactivating compounds
 - CRISPR-mediated gene editing: Gene knockout and Gene knock-in
- **Proteomic Analysis:** Western Blot, Stable Isotope Labeling (SILAC) LC-Mass Spectrometry
- **Biomarker Analysis:** Multicolor flow cytometry (BD FACSDIVA), ELISA
- **Mice handling, PBMC, and Stem Cell** culture experience
- **Regulatory Affairs Certificate:** UCSD, in progress

Management, Troubleshooting, and Communication

- Mentored 6+ graduate students and research associates to help them achieve their project goals

EXPERIENCE

Data Science Fellowship

The Data Incubator

June 2019 - Present

- Used Beautiful Soup, **Pandas**, Regex, Web-scraping, and NetworkX to identify degree of connection, page rank, and best friends in "New York Social Diary" archive
- Used **SQL** to query, aggregate, and analyze New York restaurant inspection data
- Used **Machine Learning** models to predict Yelp star ratings
- Used Count and Tfidf Vectorizer for **Natural Language Processing** on Yelp reviews for star ratings
- Used **Spark** to compute and predict user question tags from body texts on Stack Exchange
- Used Fully Connected **Neural Network**, CNN, RNN, and Learning Transfer to predict image classes in CIFAR-10 image dataset

Postdoctoral Researcher

UC Irvine

Jan 2014 - Present

- Used CRISPR gene editing (gene 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**
- Characterized, optimized, and increased efficacy of lead compounds for mutant p53 activation

EDUCATION

- 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
- Measured and quantified S-adenosylmethionine in mammalian cells with HPLC

AWARDS & PUBLICATIONS

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

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