

SKILLS

Data Science & Programming

- Adept in Python (NumPy, Pandas, Scikit-learn), SQL, R, Data Visualization (Plotnine, Seaborn, Plotly), Databrick workflow, and GitHub
- Proficient in statistical Machine Learning and Big Data analysis using Spark (PySpark)
- Skilled in using the PyTorch API for deep learning with in-depth mastery of loss and activation functions, and regularization techniques
- Enthusiastic about Nextflow for achieving consistent results and efficient pipeline execution

Multi-Omic Data, Experimental Design, and Bioinformatics Expertise

- Experienced in transcriptomic and genomic data
 - Knowledge of germline, somatic, RNA-seq, and WES NGS workflows and pipelines
- Expertise in molecular assay development and proteomic assays
 - High-throughput screening platform for mutant p53 reactivating compounds
 - CRISPR-mediated gene editing: Rapid knockout and tagging tools
 - LC-Mass Spectrometry, HPLC, multicolor flow cytometry, ELISA
- Conversant in scRNA-seq, Methyl-seq, and spatial genomic analysis
- Broad domain knowledge in Cancer Metabolism. Navigator of the intricate pathways of Cell Cycle regulation. Explorer of Stem Cell Biology. CRISPR expert in the vast ocean of gene editing

Project Management

- Skilled in using JIRA, GitHub, Databrick, and Confluence for project organization, repository management, and documentation
- Supportive team player and mentor to junior scientists
- Responsible for cross-departmental communication with stakeholders in R&D, clinical diagnostics, assay validation, clinical super lab, grantee collaborators

EXPERIENCE

DATA SCIENTIST III

Sapient Bioanalytics

Oct 2023 - present

- **Led the analysis on population-scale biomarker identification** and risk score machine learning for preeclampsia, stillbirth, small for gestational age, and preterm birth across five global locations as part of the Gates Foundation's MOMI project.
- **Spearheaded capacity-building initiatives in developing countries**, organizing workshops on metabolomics data analysis and offering personalized support to empower global researchers and healthcare professionals.
- **Collaborated with cross-functional teams** at Sapient Bioanalytics, including mass spectrometry, computational chemistry, and principal scientists from the MOMI sites, managing and cleaning data from 50,000 samples, each with over 40,000 metabolomic features, making it the largest metabolomics study to date.
- **Developed and Optimized a Three-Stage Analytical Pipeline:**
 1. **Data Cleaning and Stratification:** Streamlined the process for handling large-scale datasets, ensuring the integrity and quality of the data for subsequent analysis.
 2. **Feature Engineering and Regression Analysis with PySpark:** Leveraged advanced machine learning techniques within PySpark to extract meaningful features and develop predictive models, enabling scalable and efficient processing of vast datasets.
 3. **Data Visualization and Pathway Enrichment Analysis:** Employed sophisticated data visualization tools and conducted pathway enrichment analysis to reveal significant biological pathways, providing deeper insights into the data's biological relevance.

4. **Metabolic Risk Score Development with XGBoost:** Applied cutting-edge machine learning and AI techniques using XGBoost to develop a metabolic risk scoring system. This AI-driven model predicted maternal and infant health outcomes with high accuracy, offering actionable insights for clinical interventions.

BIOINFORMATIC SCIENTIST III

Ambry Genetics

Dec 2019 - Oct 2023

- Analyzed NGS panel probe coverage, sequencing run consistency, coverage uniformity, detection sensitivity and specificity for improved results.
- Evaluated and validated pipeline performance for oncology panels, including high-volume CancerNext, RNA, Exome, and Somatic panels.
- Advised on reducing CNV calling QC failures and false positive rates during a chemistry transition.
- Established sample DNA concentration thresholds using Logistic Regression for the bait-capture automation project, involving the Tecan-robot DNA M200 workflow.
- Maintained weekly CNV calling statistics, ensuring high-quality CNV calling.
- Set statistical thresholds on allele frequency for reducing laboratory Sanger workload.
- Produced crucial data for variant assessment, including SNV, indel, CNV, Mobile Elements, and processed pseudogenes.
- Key contributor in the BIMM project to visualize and monitor KPIs across all Ambry panels.
- Employed GradientBoostingRegressor for estimating the number of CNVs per sample and determining feature importance (including sequencing, coverage, and augmented metrics) in high false positive CNV investigations.

Data Science Fellowship

The Data Incubator

Jun 2019 - Sep 2019

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. Followed by proteomic analysis and resulted in identifying PP2A interaction map during methionine stress
- Developed bio-screening platform in mammalian cells for p53 reactivating compounds, resulted in a publication in **Nature Communication**
- Analyzed RNA-seq data for hypothesis testing and discovered actionable targets for investigating SAM-checkpoint

EDUCATION

University of California, Berkeley

M.S. Master of Information and Data Science

In progress

University of California, Irvine

Ph.D. Biological Sciences

Sep 2007 - Jan 2014

California Institute for Regenerative Medicine (CIRM) fellowship

2009 - 2011

AWARDS & PUBLICATIONS

Submitted | Nutrient control of splice site selection contributes to methionine dependence of cancer 2023

Submitted | Sphingosine and anti-neoplastic sphingosine analogs activate PP2A and inhibit nuclear import in parallel by engaging PPP2R1A and importins 2023

Cell Chemical Biology Discovery of compounds that reactivate p53 mutants in vitro and in vivo	2022
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
Methods Mol. Biol. 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
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