

DANNY ANTAKI

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Experience

Twist Bioscience

Senior Bioinformatics Scientist

Oct. '22 – Present

- Led development of an RNA-seq pipeline on a cloud-based platform, which was later deployed to production.
- Co-managed a wet-lab scientist to develop and optimize protocols for a new NGS library prep product line.
- Worked closely with data science team to improve existing ML scoring models for syn-bio gene products.

Bioinformatics Scientist

Feb. '21 – Oct. '22

- Built an ETL pipeline to capture and store daily updates of gene manufacturing outcomes predicted by machine learning.
- Played key role in the design and execution of new experiments aimed at improving MRD targeted enrichment panels, leveraging insights gained from mining internal databases.
- Improved and streamlined pipeline for design of synthetic Cot-1 blockers.

Gleeson Lab for Pediatric Brain Disease

Postdoctoral Researcher

Sep. '18 – Feb. '21

- Laid groundwork for image-based AI model for somatic variant detection ([Nature Biotechnology](#)).
- Analyzed deeply sequenced whole genomes for somatic variation analysis in postmortem human brain ([Nature](#)) and in sperm ([Cell](#), [Nature Medicine](#))
- Spearheaded study integrating rare variants and polygenic risk scores in an Autism cohort of more than 37,000 individuals ([Nature Genetics](#))

Education

UCSD

PhD, Biomedical Sciences

Sep. '13 – Sep. '18

Advisor: Jonathan Sebat

Thesis: *Disparity between Maternal and Paternal Contributions to Inherited Risk for Autism*

- Led groundbreaking discovery that noncoding deletions inherited from fathers contribute risk for Autism ([Science](#))
- Designed a novel ML tool for structural variation genotyping ([Bioinformatics](#), [GitHub](#))

Purdue University

BS, General Biology – Dean's List & Honor's Biology

Jan. '09 – May '13

Skills

Python – pandas, pyspark, mlflow, sklearn, keras, matplotlib, seaborn, scipy, pysam, pybedtools

Bioinformatics Tools – samtools, bcftools, bedtools, GATK, Picard, VEP, Plink

Bioinformatics Analysis – Structural variation, RNA-seq, Somatic variants, Long Reads, Microarrays

Platforms - AWS, Databricks, Snowflake, Seven Bridges Genomics, Jira, Confluence, Trello

Languages - R, Perl, SQL, Bash