DANNY ANTAKI

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Experience

Twist Bioscience

Senior Bioinformatics Scientist Oct. '22 – Present

- Spearheaded development of an RNA-seq pipeline on a cloud-based platform and worked with multiple teams to deploy it to production, after which it was used to analyze all internal and customer facing RNA-seq runs.
- Designed experiments and closely collaborated with wet-lab scientists to develop protocols for NGS library prep products, resulting in the release of a new RNA-seq library prep kit.
- Played a pivotal role in improving existing ML scoring models for synthetic gene products by contributing expertise in structural variation, which improved performance by 5%.

Bioinformatics Scientist Feb. '21 – Oct. '22

- Built a ML classifier to predict gene manufacturing outcomes and automated a daily task that stores outcomes in a database, generating real-time predictions and future training data.
- Played a key role in identifying and resolving problematic features of minimal residual disease panels by mining internal databases and applying statistical inference, ultimately allowing manufacturing of this product line to proceed.
- Improved design algorithm for synthetic Cot-1 blockers reducing material cost by 50-75% while increasing performance by 5-10%.

Gleeson Lab for Pediatric Brain Disease (UCSD)

Postdoctoral Researcher Sep. '18 – Feb. '21

- Developed visualization code for image-based AI somatic variant caller, doubling the validation rate over previous methods. (Nature Biotechnology)
- Analyzed deeply sequenced whole genomes for somatic variation analysis in postmortem human brain (Nature) and in sperm (Cell, Nature Medicine), discovering recurrence risk for autism in ¼ men.

Education

UCSD Sep. '13 – Sep. '18

PhD, Biomedical Sciences Advisor: Jonathan Sebat

- Led analysis integrating rare variants and polygenic risk in over 37,000 individuals, leading to the discovery that noncoding deletions inherited from fathers contribute risk for Autism, increasing diagnostic yield by 2% (Science, Nature Genetics)
- Designed a novel ML tool for structural variation genotyping, reducing the false discovery rate from 20% to below 1%. (Bioinformatics, GitHub)

Purdue University Jan. '09 – May '13

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

Skills

Python	pandas, pyspark, mlflow, sklearn, keras, matplotlib, seaborn, scipy, pysam, pybedtools
Bioinformatics Tools	samtools, bcftools, bedtools, GATK, Picard, VEP, Plink, STAR, STAR-Fusion, QTL2
Platforms	AWS, Databricks, Snowflake, Seven Bridges Genomics, Jira, Confluence, Trello
Languages	R, Perl, SQL, Bash

Leadership

Mentored and supervised over 10 trainees (2013-2021) and currently co-manage a wet-lab scientist.