

Nima Mousavi

nima.mousavi.ee@gmail.com | nmmsv.com

EXPERIENCE

10X GENOMICS | COMPUTATIONAL BIOLOGIST

Aug 2024 – May 2025 | Senior Computational Biologist

Sep 2021 – Aug 2024 | Computational Biologist II

Jun 2020 – Sep 2020 | Computational Biology Intern

- Developed several pipeline stages, both customer-facing and internal, across multiple 10X Genomics Single Cell pipelines (Flex and Universal Gene Expression, Immune Profiling, CRISPR, and Antigen Capture) using Rust, Python, and Martian pipeline development language.
- Using test-driven programming and performing code review to maintain reliability and reproducibility in the pipeline.
- Performed data analysis and visualization using Polars, Pandas, matplotlib, and seaborn in Jupyter notebooks to evaluate the assay and presented the results to the lab team in the product development process.
- Designed and validated probes to support the Flex (probe-based) gene expression assay team.
- Improved the customer-facing web summary using Java Script and Rust to create and present new metrics and figures.
- Contributed to the sustaining pipeline development and collaborated closely with the customer support team to resolve pipeline issues.
- Led and supported initiatives spanning early feasibility and risk mitigation through product development and launch.

UC SAN DIEGO | GENOME-WIDE LANDSCAPE OF TANDEM REPEATS (PHD THESIS)

Sep 2015 – Sep 2021 | San Diego, CA

- Created a novel software for genome-wide profiling and genotyping of germline short tandem repeats from aligned short-read sequencing data. Using maximum likelihood, C++, and Python.
- Engineered an open-source toolkit for genome-wide analysis of tandem repeats (TRTools) using Python.
- Presented our findings in major human genetics journals (NAR, Nature, and Bioinformatics) and conferences (ASHG 2018, ISMB 2018, and ASHG 2020).

DYNO THERAPEUTICS | DATA SCIENCE INTERN

Mar 2021 – Jun 2021 | Remote

- Analyzed data using Pandas library and created methods to evaluate AAV capsids for gene therapy.
- Investigated capsid performance using short and long-read sequencing data.

ILLUMINA | ONCOLOGY BIOINFORMATICS INTERN

Jun 2018 – Sep 2018 | San Diego, CA

- Implemented algorithmic improvements to increase the accuracy of a somatic variant caller to meet pipeline requirements, presented findings to technical and marketing teams.
- Utilized object-oriented design and GitHub code review to facilitate test-driven C# development. Performed rigorous benchmarking in High-Performance Computing (HPC) environment.

EDUCATION

UC SAN DIEGO

PHD, ELECTRICAL AND

COMPUTER ENGINEERING

2015 - 2021 | San Diego, CA

SKILLS

PROGRAMMING

3+ years:

Python • Rust • Martian •

C/C++

Familiar:

JavaScript • R • C#

SINGLE CELL

- 10X Genomics Flex (probe based) Gene Expression
- 10X Genomics Universal (3' and 5') Gene Expression
- 10X Genomics CRISPR Analysis
- 10X Genomics Immune Profiling

TECHNOLOGY

Git/Github • HPC • Linux •
Polars • Pandas • Numpy •
Seaborn • Matplotlib

PUBLICATIONS

- Mousavi et al., "Profiling the genome-wide landscape of tandem repeat expansions", NAR (2019) doi
- Mitra et al., "Patterns of de novo tandem repeat mutations and their role in autism", Nature (2021) doi
- Mousavi et al., "TRTools: a toolkit for genome-wide analysis of tandem repeats", Bioinformatics (2020) doi

LINKS

Github:// nmmsv10x

Github:// nmmsv

LinkedIn:// nmmsv