nima.mousavi.ee@gmail.com | Oakland, CA

# **Senior/Staff Bioinformatics Engineer**

Architecting Pipelines & Tools | Data Analysis & Modeling | Cross-functional Collaboration | Mentorship & Technical Leadership Scientific Research | Product / Platform Development | NGS (short and long-read) Data Analysis | Reproducible Genomic Pipelines

Innovative and detail-oriented Computational Biologist with a PhD in Electrical and Computer Engineering and a focus on genomic data analysis, single-cell pipelines, and bioinformatics tool development. Experienced in building scalable, high-performance computational workflows, statistical models, and software solutions that support R&D and enable robust genomic research. Proven success in cross-functional biotech environments, supporting assay development and platform innovation.

## **Core Competencies**

- **Programming Languages**: Python, Rust, C++, C#, Bash, Martian
- Bioinformatics Tools: Cellranger, IGV, SAMTools, BLAST
- Data Analysis and Visualization: Polars, Pandas, NumPy, Seaborn, Matplotlib, Scikit-learn
- Environments: Linux, Git, HPC clusters, Docker
- Concepts: Statistical modeling, deep learning fundamentals, object-oriented design

# Career Experience

# Senior Computational Biologist/Computational Biologist II | 10X Genomics - Pleasanton, CA | Sep 2021 - May 2025

Served as a pivotal link between software engineering and experimental science, transforming complex research needs into scalable, production-grade computational solutions implemented in Cellranger, accelerating the development and commercialization of advanced single-cell assays.

#### **Product & Pipeline Development**

- Developed and optimized multi-stage computational pipelines in Cellranger software for antigen capture, immune profiling, and CRISPR screening assays using Rust, Python, and Martian.
- Enabled scalable and reproducible single-cell and perturbation data analysis supporting R&D assay teams.
- Designed data processing workflows that significantly improved performance and maintainability of production pipelines.

### **Cross-functional Collaboration & Support**

- Acted as key computational partner to assay development scientists, translating research needs into robust software tools and analytical workflows.
- Leveraged a functional understanding of cell biology and immunology and provided ongoing computational biology support, data interpretation, and rapid iteration to experimental development teams.
- Collaborated closely with the customer support team to resolve pipeline issues reported by users.

#### **Key Achievements**

- Presented a poster on antigen capture assay in a regional 10X Genomics user group meeting as a representative from the R&D team.
- Delivered production-grade pipelines that accelerated time-to-market for new 10X Genomics products.
- Improved software performance and accuracy for gene expression and immune profiling applications.

#### <u>Data Science Intern</u> | Dyno Therapeutics - Boston, MA | Mar 2021 - Jun 2021

Contributed to gene therapy R&D by engineering bioinformatics workflows that provided performance metrics and selection insights for AAV capsid variants.

# **AAV Capsid Analysis**

- Designed and implemented methods for evaluating AAV capsid variants using sequencing datasets.
- Developed custom analysis workflows leveraging both short-read and long-read genomic data.
- Informed capsid engineering and selection strategies through quantitative performance metrics.

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## Computational Biology Intern | 10X Genomics - Pleasanton, CA | Jun 2020 - Sep 2020

Built foundational components for immune profiling pipelines that enhanced modularity and scalability, enabling rapid iteration in early-stage product development.

# **Pipeline Engineering**

- Contributed core modules to the single-cell immune profiling of Cellranger pipeline in Rust and Python.
- Developed reusable and testable components to support rapid prototyping and production scaling.

## Oncology Bioinformatics Intern | Illumina - San Diego, CA | Jun 2018 - Sep 2018

Advanced the precision of somatic variant detection in oncology by optimizing algorithmic performance and implementing rigorous software engineering practices.

# Variant Calling & Algorithm Optimization

- Improved somatic variant calling algorithms to meet strict clinical and research pipeline criteria.
- Implemented test-driven C# code modules and participated in GitHub-based code review.
- Performed large-scale benchmarking in an HPC environment to validate improvements.

## **Stakeholder Engagement**

• Presented results and technical specifications to internal engineering and marketing teams, aligning product and technical goals.

# Research Projects & Open-Source Contributions

## PhD Research Project | GangSTR | UC San Diego | 2017 - 2021

Pioneered a high-impact bioinformatics tool for genome-wide analysis of STR expansions.

- Developed a novel tool for genome-wide profiling and genotyping of STR expansions using short-read sequencing data.
- Engineered a maximum likelihood model in C++ after Python prototyping; validated with simulation and experimental methods.
- Presented at ASHG and ISMB; recognized in the top <u>10%</u> of ASHG 2020 abstracts (Reviewers' Choice Award).

## **Toolkit Development | TRTools | UC San Diego | 2020**

Contributed a harmonized toolkit to the genomics community for tandem repeat variation analysis.

- Created a suite of tools for harmonizing and analyzing tandem repeat genotyping datasets.
- Released as a widely used open-source Python package supporting multiple variant callers.

#### Modular IoT Middleware Project | Context Engine | UC San Diego | 2016

Led development of an IoT middleware framework integrating local sensing, embedded systems, and cloud analytics.

- Designed and integrated a modular IoT system for local sensing, machine learning, and cloud communication.
- Led system integration and embedded interfacing, culminating in a live demo and poster session.

# Academic Experience

#### **Teaching Assistant** | UC San Diego & Sharif University | 2014 - 2018

• Designed lab materials, graded coursework, and mentored students across Digital Systems, Bioinformatics, and Electrical Engineering courses.

## Education and Professional Development

PhD, Electrical & Computer Engineering (Concentration: Bioinformatics & Human Genetics) University of California, San Diego

Advisor: Prof. Melissa Gymrek

Master's degree, Electrical and Computer Engineering, UC San Diego, Jacobs School of Engineering

BSc, Electrical Engineering - Digital Systems, Sharif University of Technology, Tehran, Iran