

Nima Mousavi

<http://nmmsv.com> — nima.mousavi.ee@gmail.com — Oakland, CA 94618

SKILLS

- Extensive experience with *10X Genomics single-cell pipelines* and familiar AAV Capsid design for gene therapy.
- Solid research and implementation experience in method development and NGS data processing using *short-read genomic sequencing* and *single-cell transcriptomic data*.
- Strong background in software development using object-oriented *C++*, *Python* and *Rust*.
- Experienced in Python data science and scientific computing packages such as *pandas*, *numpy*, and *seaborn*.
- Deep mathematical and probabilistic knowledge and experienced in theoretical problem analysis and statistical methods. Familiar with Deep Learning.
- Extensive experience in *High-Performance Computing (HPC)*, *Linux* environment, and *Git* version control.
- Excellent teamwork and communication skills, shown as constructive cooperation with colleagues in interdisciplinary teams.

EXPERIENCE

Computational Biologist II, 10X Genomics, Pleasanton, CA Sep 2021 - present

- Developed multiple stages and pipelines for antigen capture, immune profiling, and CRISPR screening products using Rust, Python, and Martian programming languages.
- Performed data analysis and provided computational biology support to the assay development team.

Data Science Intern, Dyno Therapeutics, Boston, MA Mar 2021 - Jun 2021

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

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

- Created multiple stages for the single cell immune profiling pipeline using Rust and Python programming languages.

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

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

Teaching Assistant, Sep 2014 - Jun 2018

- Held well-received discussion and lab sessions, designed and graded homework and tests, provided mentorship, and assisted course administration.

Advanced Bioinformatics Lab (UCSD), *Digital Systems* (UCSD), *Computer Structures and μ Processors Lab* (Lead Assistant, Sharif), *Principles of Electrical Engineering* (Sharif)

Volunteer Work, Iranian Student Association, UCSD, La Jolla, CA May 2016 - Apr 2018
Vice President (May 2017- Apr 2018), *Financial Director* (May 2016-May 2017)

EDUCATION

PhD, Electrical and Computer Engineering University of California San Diego
Advisor: Prof. Melissa Gymrek (Bioinformatics and Human Genetics) 2015 - 2021
GPA: 3.87 / 4.0

BSc, Electrical Engineering: Digital Systems Sharif University of Technology, Iran
GPA: 3.94 / 4.0 2011 - 2015

PUBLICATIONS

- **N. Mousavi**, R. Yanicky, S. Shleizer-Burko, M. Gymrek. “Profiling the genome-wide landscape of tandem repeat expansions”, **Nucleic Acids Research**, 47.15 (2019): e90
<https://doi.org/10.1093/nar/gkz501>
- I. Mitra, B. Huang, **N. Mousavi**, N. Ma, M. Lamkin, R. Yanicky, S. Shleizer-Burko, K. Lohmueller, M. Gymrek. “Patterns of de novo tandem repeat mutations and their role in autism”, **Nature** (2021) <https://doi.org/10.1038/s41586-020-03078-7>
- **N. Mousavi**, J. Margoliash, N. Pusarla, S. Saini, R. Yanicky, M. Gymrek. “TRTools: a toolkit for genome-wide analysis of tandem repeats”, **Bioinformatics**, btaa736 (2020)
<https://doi.org/10.1093/bioinformatics/btaa736>
- S. Saini, I. Mitra, **N. Mousavi**, S. F. Fotsing, M. Gymrek. “A reference haplotype panel for genome-wide imputation of short tandem repeats”, *Nature communications* 9.1 (2018): 4397
<https://doi.org/10.1038/s41467-018-06694-0>

Google Scholar

RESEARCH

- GangSTR: Genotyping STR Expansions**, UCSD, La Jolla, CA Jun 2017 - Present
- Created a novel software tool for genome-wide profiling and genotyping germline short tandem repeats from aligned short read sequencing data.
 - Developed maximum likelihood model based on the local realignment of paired-end reads and implemented with object oriented C++ after prototyping with Python.
 - Performed simulation and experimental validation (capillary electrophoresis).
 - Presented findings in major human genetics conferences (ASHG 2018, ISMB 2018).
 - Abstract selected for **Reviewers’ Choice award** at ASHG 2020 by scoring in the top 10% of all poster abstracts.
- TRTools: a toolkit for genome-wide tandem repeat analysis**, UCSD Jan 2020 - Aug 2020
- Created a suite of methods for handling and analysis of tandem repeat (TR) genotype datasets.
 - Contributed to a TR harmonizing module that allows TRTools to support multiple variant calling platforms.
 - Implemented the method as an open-source Python package available to the community.
- Context Engine**, University of California San Diego, La Jolla, CA May 2016 - Nov 2016
- Developed the object oriented design of a modular middleware for Internet of Things.
 - Supervised development of machine learning code and performed system integration.
 - Implemented embedded system interface with local sensors and actuators and cloud-based database.
 - Showcased the capability of system using an end-to-end application alongside poster presentation.