

Nima Mousavi

Address: 9500 Gilman Dr, Mail Code 0639, La Jolla, CA 92093
http://nmmsv.com — (858) 291-2083 — mousavi@ucsd.edu

EDUCATION

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

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

SKILLS

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

EXPERIENCE

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

- (Ongoing) Analyzing data and creating 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 steps 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 in close collaboration 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)*

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. Pulara, 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>
- **N. Mousavi**, B. Aksanli, A. Akyurek, T. Rosing. “Accuracy-Resource Tradeoff for Edge Devices in Internet of Things”, **SmartEdge17**, in conjunction with IEEE PerCom17.
<https://doi.org/10.1109/PERCOMW.2017.7917627>

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.