Nima Mousavi

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EDUCATION

PhD, Electrical and Computer Engineering   University of California San Diego

Advisor: Prof. Melissa Gymrek (Bioinformatics and Human Genetics)   2015 - 2020 (Expected)

GPA: 3.87 / 4.0

BSc, Electrical Engineering: Digital Systems   Sharif University of Technology, Iran

GPA: 3.94 / 4.0   2011 - 2015

SKILLS

- Solid research and implementation experience in inference models for variant calling using next-generation sequencing data.
- Strong background in software development and object oriented C++, C# and Python.
- Deep mathematical and probabilistic knowledge and experienced in theoretical problem analysis and statistical methods.
- Profound knowledge of algorithms and demonstrated proficiency in problem solving by deriving creative and innovative solutions.
- Experienced with Git version control and familiar with Amazon Web Services (AWS).
- Excellent teamwork and communication skills, shown as constructive cooperation with colleagues.

EXPERIENCE

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

- Implemented algorithmic improvements to increase accuracy of somatic variant caller to meet pipeline requirements.
- Utilized object oriented design and GitHub code review to facilitate test-driven C# development.
- Worked in close collaboration and presented findings to technical and marketing groups.

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 μProcessors 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)

- Collaborated with board members, university officials, and volunteers to hold events with upwards of 300 attendance from the community.

PUBLICATIONS

- **N. Mousavi**, R. Yanicki, 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
- 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

RESEARCH

GangSTR: Genotyping STR Expansions, UCSD, La Jolla, CA   Jun 2017 - Present

- Created a novel software tool for genome-wide profiling and genotyping short tandem repeats from aligned short read sequencing data.
- Developed maximum likelihood model based on 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 large human genetics conferences (ASHG 2018, ISMB 2018)