Nima Mousavi

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Summary

Motivated PhD student looking for an internship position.

EDUCATION

PhD, Electrical and Computer Engineering — University of California San Diego
Advisor: Prof. Melissa Gymrek (Bioinformatics and Population Genetics) — 2015 - 2021 (Expected)
GPA: 3.85 / 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++ 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.
- Excellent teamwork and communication skills, shown as constructive cooperation with colleagues.

EXPERIENCE

Bioinformatics Intern, illumina, San Diego, CA — Jun 2018 - Sep 2018

- Improved accuracy of somatic variant callers to meet pipeline requirements.
- Suggested and implemented design changes to address previously reported issues.

Teaching Assistant, — Sep 2014 - Mar 2017
Advanced Bioinformatics Lab — UC San Diego
Components and Design Techniques for Digital Systems — UC San Diego
Computer Structures and μProcessors Lab (Lead Assistant) — Sharif Univ. of Tech.
Principles of Electrical Engineering — Sharif Univ. of Tech.

- Clarified lecture material for students by holding well-received problem solving sessions.
- Communicated with groups and individual students and provided mentoring and advising.

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 university officials, other board members, and volunteers in holding events with upwards to 300 attendance from the community

PUBLICATIONS

- *(Preprint)* **N. Mousavi**, S. Shleizer-Burko, M. Gymrek. Profiling the genome-wide landscape of tandem repeat expansions, https://doi.org/10.1101/361162
- **N. Mousavi**, B. Aksanli, A. Akyurek, T. Rosing. Accuracy-Resource Tradeoff for Edge Devices in Internet of Things, SmartEdge17, in conjunction with IEEE PerCom17.

RESEARCH

GangSTR: Genotyping STR Expansions, UCSD, La Jolla, CA — May 2016 - Nov 2016

- 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++.
- Performed simulation and experimental validation (capillary electrophoresis). exome datasets.