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 - 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.
• Solid research and implementation experience in method development and NGS data processing using short-read genomic sequencing data and single cell transcriptomic data. Familiar with Immunology.
• 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, scipy, and seaborn.
• 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

***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 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)

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
  • **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

- I. Mitra, **N. Mousavi**, N. Ma, M. Lamkin, R. Yanicky, S. Shleizer-Burko, M. Gymrek. "The contribution of de novo tandem repeat mutations to autism spectrum disorders", bioRxiv (2020) https://doi.org/10.1101/2020.03.04.974170
- **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.