

Ramin Dehghanpoor

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EDUCATION

- **University of Massachusetts Boston** Boston, MA
Ph.D. in Computer Science (Bioinformatics, Advisor: Professor Nurit Haspel); GPA: 3.91 2022
- **University of Massachusetts Boston** Boston, MA
MSc in Computer Science; GPA: 3.91 2021
- **Amirkabir University of Technology (Tehran Polytechnic)** Tehran, Iran
B.S. in Computer Science; GPA: 3.80 2016

SKILLS

- **Programming Languages:** Python, R, Java, C++, C
- **Techniques:** Pipeline and CLI tool development, Machine learning, Neural networks, CNNs, VAEs, NGS data analysis
- **Software and libraries:** TensorFlow, Git, AWS and HPC computing environments, DolphinNext (based on NextFlow), R Shiny, Docker, VMD
- **Experience in working with:** NGS data, High dimensional biological sequences (RNA and Protein), SHAPE and DMS data, RNA secondary structure prediction tools

WORK EXPERIENCE AND PROJECTS

- **Bioinformatics Scientist at Orna** 10/2022 - present
 - Developing machine learning models to enhance circular RNA design
 - Processing, analyzing, and interpreting high dimensional NGS data
 - Using model interpretation tools to shape experimental strategies that leverage NGS- and screening-related approaches
- **Computational Science, Bioinformatics Co-Op at Moderna** 1/2022 - 7/2022
 - Comparing and benchmarking chemical probing software tools using NGS data, creating a Tyler Command Line Interface tool and a NextFlow (DolphinNext) pipeline
 - Analyzing end-seq data and predicted RNA structural elements to find RNA degradation signals
- **Graduate Research and Teaching Assistant at University of Massachusetts Boston** 9/2016 - 8/2022
 - Classifying protein families using variational autoencoder and Convolutional Neural Networks classifier
 - Characterizing Protein Conformational Space Using Robotics-Based Search and Topological Data Analysis
 - Integrating Rigidity Analysis into the Exploration of Protein Conformational Pathways Using RRT* and MC
 - Predicting the effect of single and multiple mutations on protein structural stability
 - Writing a book chapter about machine-learning based approaches in protein conformational changes on Springer Nature
 - Contributing in Proposal Development Grant "Towards Developing Deep Learning Approaches for Protein-Protein Interaction Detection"
 - Instructor of Applied Discrete Mathematics

- Instructor of Programming in C
- Research Intern at MGH Institute for Technology Assessment, Harvard Medical School 7/2020 - 2/2021
 - Identifying Online Advice-Seekers for Recovering from Opioid Use Disorder by combining text annotation, social network analysis, and statistical modeling
- Data Science and UI Designer Intern at Trace Matters Scientific 5/2019 - 9/2019
 - Creating a data acquisition system and implementing signal processing and machine learning algorithms to detect picks for a mass spectrometer
 - Designing an R shiny interactive UI with the ability to tune the parameters of the mass spectrometer hardware and see the realtime results

PEER-REVIEWED PUBLICATIONS

- **Journal Publications**

- Garcia, G.-G. P., Dehghanpoor, R., Stringfellow, E. J., Gupta, M., Rochelle, J., Mason, E., Pujol, T. A., & Jalali, M. S. (2022). **Identifying and Characterizing Medical Advice-Seekers on a Social Media Forum for Buprenorphine Use.** In International Journal of Environmental Research and Public Health (Vol. 19, Issue 10, p. 6281). MDPI AG. <https://doi.org/10.3390/ijerph19106281>
- Afrasiabi, F., Dehghanpoor, R., & Haspel, N. (2021). **Integrating Rigidity Analysis into the Exploration of Protein Conformational Pathways Using RRT* and MC.** *Molecules*, 26(8), 2329. <https://doi.org/10.3390/molecules26082329>
- Dehghanpoor, R., Ricks, E., Hursh, K., Gunderson, S., Farhoodi, R., Haspel, N., Hutchinson, B., & Jagodzinski, F. (2018). **Predicting the Effect of Single and Multiple Mutations on Protein Structural Stability.** *Molecules*, 23(2), 251. <https://doi.org/10.3390/molecules23020251>

- **Conference proceedings publications**

- Dehghanpoor, R., Afrasiabi, F., & Haspel, N. (2022). **Using Topological Data Analysis and RRT to Investigate Protein Conformational Spaces.** In EPIc Series in Computing. Proceedings of 14th International Conference on Bioinformatics and Computational Biology. EasyChair. <https://doi.org/10.29007/57fw>

- **Book chapters**

- Afrasiabi, F., Dehghanpoor, R., & Haspel, N. (2022). **Machine Learning-Based Approaches for Protein Conformational Exploration.** In Algorithms and Methods in Structural Bioinformatics (pp. 47–61). Springer International Publishing. https://doi.org/10.1007/978-3-031-05914-8_3

REVIEWER AND EDITOR

- **Reviewer**

- Bioinformatics Advances
- Computational Biology and Bioinformatics
- International Conference on Bioinformatics and Biomedicine (IEEE BIBM)
- International Conference on Biomedical and Bioinformatics Engineering (ICBBE)
- Computer Methods in Biomechanics and Biomedical Engineering

- **Editor**

- Journal of Biomedical Research & Environmental Sciences

ATTENDED CONFERENCES

- RNA Therapeutics: From Concept to Clinic Preliminary Program (RNATx), 2022
- The 14th International Conference on Bioinformatics and Computational Biology (BICOB), 2022
- The 8th and 11th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB), 2017 and 2020

CERTIFICATIONS

- Introduction to the Biology of Cancer, Johns Hopkins University (Coursera), 2022
- Moderna AI Academy: AI Awareness (Carnegie Mellon University), 2022
- Applied Data Science with Python Specialization, University of Michigan (Coursera), 2021
- Deep Learning Specialization, DeepLearning.AI (Coursera), 2021