HOSSEIN SHARIFI-NOGHABI

Machine Learning Researcher | Bioinformatics Researcher

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HIGHLIGHTS

- Expertise in developing machine learning methods for real-world challenges (five years of experience in employing machine learning in biology and medicine with two top-tier publications).
- Experienced in teamwork particularly when members have diverse backgrounds (three years of experience in collaboration with life scientists).
- Interested and passionate about learning (10 online certificates on different topics such as deep learning and reinforcement learning).
- Skilled in Python, R, Pytorch, MATLAB, Keras, Scikit-learn, and Pandas (three years of experience in deploying them for real-world problems).

EDUCATIONS

Ph.D. in Computer Science
Simon Fraser University

📅 Sep 2016 – Sep 2021 (Expected)   📍 Burnaby, Canada

- GPA: 4.08/4
- Awards: Computing Science Graduate Fellowship (four times), Travel Award (three times)
- Teaching Assistant: Introduction to computer programming I (Python)

M.Sc. in Artificial Intelligence
Ferdowsi University of Mashhad

📅 Sep 2012 – Feb 2015   📍 Mashhad, Iran

- GPA: 17.05/20

B.Eng. in Information Technology
Sadjad University of Technology

📅 Sep 2008 – July 2012   📍 Mashhad, Iran

- GPA: 17.92/20
- Honor: Ranked 1st among 67 students of Information Technology

SELECTED PUBLICATIONS

- H. Sharifi-Noghabi, H. Asghari, N. Mehrasa, M. Ester, **"Domain Generalization via Semi-supervised Meta Learning"** *arXiv 2020*.
- H. Sharifi-Noghabi, S. Peng, O. Zolotareva, C. Collins, M. Ester, **"AITL: Adversarial Inductive Transfer Learning with input and output space adaptation for pharmacogenomics"** *Bioinformatics 36 (supplement1), i380-i388 2020*.
- H. Sharifi-Noghabi, O. Zolotareva, C. Collins, M. Ester, **"MOLI: multi-omics late integration with deep neural networks for drug response prediction"** *Bioinformatics 35 (14), i501–i509 2019*.
- [1]M. Mohammadi, H. Sharifi-Noghabi, H. Rajabi Mashhadi, and G. Hodtani **"Robust and stable gene selection via Maximum-Minimum Correntropy Criterion"** *Genomics (170) 83-87 2016*.
- For the complete list please visit HERE

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[1] Joint first authorship

MACHINE LEARNING SKILLS
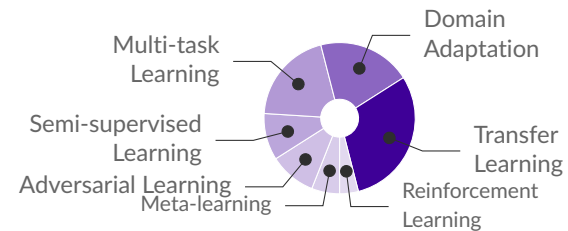
ORAL PRESENTATIONS

- H. Sharifi-Noghabi, S. Peng, O. Zolotareva, C. Collins, M. Ester, **"AITL: Adversarial Inductive Transfer Learning with input and output space adaptation for pharmacogenomics"** *ISMB 2020, Montreal, Canada*.
- H. Sharifi-Noghabi, O. Zolotareva, C. Collins, M. Ester, **"MOLI: multi-omics late integration with deep neural networks for drug response prediction"** *ISMB/ECCB 2019, Basel, Switzerland*.
- H. Sharifi-Noghabi, O. Zolotareva, C. Collins, M. Ester, **"MOLI: multi-omics late integration with deep neural networks for drug response prediction"** *The 13th Lorne D. Sullivan Lectureship & Research Day 2019, Department of Urologic Sciences, University of British Columbia, Vancouver, Canada*.
- H. Sharifi-Noghabi, Y. Liu, N. Erho, R. Shrestha, M. Alshalalfa, E. Davicioni, C. Collins, M. Ester, **"Deep Genomic Signature for early metastasis prediction in prostate cancer"** *RECOMB Computational Cancer Biology 2019 (RECOMB-CCB 2019), Washington D.C., United States* (also available on *bioRxiv*).

POSTERS

- O. Snow, H. Sharifi-Noghabi, J. Lu, O. Zolotareva, M. Lee, M. Ester , **"BDKANN - Biological Domain Knowledge-based Artificial Neural Network for drug response prediction"** *Machine learning in Computational Biology (MLCB) 2019, Vancouver, Canada*.
- H. Sharifi-Noghabi, S. Peng, O. Zolotareva, C. Collins, M. Ester, **"Deep Neural Networks for Precision Oncology: Multi-Omics Integration and Transfer Learning"** *School of Computing Science Research Day 2019, Simon Fraser University, Burnaby, Canada*.
- H. Sharifi-Noghabi, O. Zolotareva, C. Collins, M. Ester, **"MOLI: multi-omics late integration with deep neural networks for drug response prediction"** *Deep Learning Reinforcement Learning (DLRL) Summer School 2019, University of Alberta, Edmonton, Canada*.

EXPERIENCES

Research Student (co-op)

Princess Margaret Cancer Centre

📅 Jun 2020 – Dec 2020 (Expected) 📍 Toronto, Canada

- Leading a project to propose the first guideline on how to employ machine learning in pharmacogenomics. The guideline investigates generalization of machine learning methods in cross-domain drug response prediction using RNA-Seq data and provides solution to improve that.
- Implemented codes in Python and R, and utilized Pytorch and scikit-learn.
- Supervisor: Dr. Benjamin Haibe-Kains.

Research Assistant

Simon Fraser University

📅 Sep 2016 – Sep 2021 (Expected) 📍 Burnaby, Canada

- Led multiple projects on improving the accuracy of drug response prediction in patients using gene expression data. I developed 3 methods based on multi-modal representation learning, transfer learning with input and output space adaptation, and semi-supervised domain generalization. On average, these methods improved the prediction accuracy by 9% compared to state-of-the-art methods.
- Implemented codes in Python and utilized Pytorch and Keras frameworks.
- Mentored undergraduate research assistants in Database and Data Mining Laboratory.
- Collaborated with life scientists, and clinical fellows at the Vancouver Prostate Centre (VPC).
- Supervisors: Prof. Martin Ester and Prof. Colin C. Collins (VPC).

Collaboration

Vancouver Prostate Centre

📅 March 2017 – Present 📍 Vancouver, Canada

- Obtained a fundamental understanding of cancer biology.
- Obtained a fundamental understanding of prostate cancer and urologic sciences.
- Developed skills in data analysis and visualization via R.
- Collaborated closely with life scientists, clinical fellows, and bioinformaticians.
- Contributed to grant and proposal writing.
- Supervisor: Prof. Colin C. Collins

Collaboration

GenomeDx Inc.

📅 Sep 2017 – Jan 2018 📍 Vancouver, Canada

- Developed a novel method to predict metastasis (a binary outcome) in prostate cancer from early stages using gene expression data. This method was based on denoising autoencoders and transfer learning on unlabelled and labelled clinical samples and improved the prediction accuracy by 2% compared to state-of-the-art clinical studies.
- Implemented codes in Python and R, and utilized Tensorflow framework.
- Supervisor: Dr. Seagle Liu.

RESEARCH INTERESTS

- Multi-omics and multi-modal data integration.
- Pharmacogenomics, precision medicine, and drug response prediction.
- Out-of-distribution generalization.
- Developing learning systems with limited labeled data.
- Reinforcement learning and sequential decision making in biomedical domains.

AI PROJECTS

- Representation Learning: Automatic chemical design via Variation AutoEncoders (VAE) using SMILES representation.
- Feature Selection: Biomarker discovery and prediction of clinical Alzheimer's diagnosis based on plasma signaling proteins via ensemble feature selection and classification.
- Computer Vision: Applied Convolutional Neural Networks to image verification and recognition tasks and neural style transfer to generate new arts.
- Natural Language Processing: Applied LSTM and GRU models to synthesize Shakespeare's text, speech recognition, and music synthesis.
- Reinforcement Learning: Implemented Q-Learning and Expected Sarsa both with ϵ-greedy action selection on Cliff World.
- Reinforcement Learning: Implemented semi-gradient TD with a Neural Network as the function approximator for an RL agent in 500-State Random Walk Environment.

TECHNICAL SKILLS

- Programming: Python, R, and C.
- Frameworks: Scikit-learn, Pandas, Numpy, MATLAB, Pytorch, Keras, and Tensorflow.
- Other: Unix/Linux and Bash, Windows and Office packages, Slack, Photoshop, and Latex.

VOLUNTEER POSITIONS

- Program Committee member: Machine Learning in Computational Biology (MLCB 2020) conference, Vancouver, BC, Canada.
- Program Committee member: Machine Learning in Computational Biology (MLCB 2019) conference, Vancouver, BC, Canada.
- Group organizer at SFU Omics (2018-2019): SFU Omics is a student group to provide an environment for students and other academics to come together to talk about their work related to genomics, proteomics, and metabolomics via organizing monthly seminars, research days, and workshops.