

# Hossein Sharifi-Noghabi

Machine learning researcher/ Bioinformatics researcher/ Data scientist

Contact: (778) 885-4633/ Email: [hsharifi@sfu.ca](mailto:hsharifi@sfu.ca)/ Website: <https://hosseinshn.github.io/>

## Research interests

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Deep transfer learning, Unsupervised domain adaptation, few- and zero-shot adversarial learnings, interpretability of deep models, precision oncology, prostate cancer, metastasis

## Education

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### Ph.D. in Computer Science (GPA: A+)

Sep 2016-Present

Simon Fraser University, Burnaby, BC, Canada.

- ❑ Supervisors: Prof. Martin Ester and Prof. Colin Collins
- ❑ Awards: Computing Science Graduate Fellowship (\$6,500, \$7,400, and \$8,000)
- ❑ Teaching Assistant: Introduction to computer programming I (Python)

### M.Sc. in Artificial Intelligence (GPA: 17.05/20)

Sep 2012-Feb 2015

Ferdowsi University of Mashhad, Iran.

- ❑ Supervisor: Prof. H. Rajabi Mashhadi
- ❑ Honor: Admitted as exceptional talents student without entrance exam and with tuition remission

### B.E. in Information Technology (GPA: 17.92/20)

Sep 2008-July 2012

Sadjad University of Technology, Mashhad, Iran.

- ❑ Honor: Ranked 1st among 67 students of Information Technology

## Selected publications

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**H. Sharifi-Noghabi**, O. Zolotareva, C. C. Collins, M. Ester. (2019), "MOLI: Multi-Omics Late Integration with deep neural networks for drug response prediction", Accepted at ISMB/ECCB 2019 and in press at *Bioinformatics* journal. Received 1,500 USD travel award from the conference.

**H. Sharifi-Noghabi**, Y. Liu, N. Erho, R. Shrestha, M. Alshalalfa, E. Davicioni, C. Collins, M. Ester. (2018), "Deep Genomic Signature for early metastasis prediction in prostate cancer", *Recomb-CCB* 2019.

**H. Sharifi-Noghabi**, H. Rajabi Mashhadi, K. Shojaee. (2016), "A novel mutation operator based on the union of fitness and design spaces information for Differential Evolution", *Soft computing* (21) 6555-6562

M. Mohammadi, **H. Sharifi-Noghabi**, H. Rajabi Mashhadi, G. Hodtani. (2016), "Robust and stable gene selection via Maximum-Minimum Correntropy Criterion", *Genomics* (170) 83-87. (joint first authorship)

## Work experience

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### Research Assistant, Vancouver Prostate Centre (Full time)

Mar 2017-Present

- ❑ Member of Laboratory for Advanced Genome Analysis directed by Prof. C. Collins
- ❑ Obtained basic understanding of cancer biology-particularly prostate cancer
- ❑ Presented a project on metastasis prediction at 12th annual Robert Sullivan Research Day

- ❑ Participated in numerous research projects and grants as one of the bioinformaticians

**Research Assistant, Simon Fraser University (Full time)**

**Sep 2016-Present**

- ❑ Developed skills on deep unsupervised learning such as different Autoencoders, deep multi-task learning, and deep transfer learning (inductive and adversarial transfer learning)
- ❑ Developed skills on implementing in Python-particularly deep learning frameworks
- ❑ Designed and developed a novel method in Pytorch to predict drug response using multi-omics profiles. This method is an end-to-end multi-modal deep neural networks consisting of a triplet loss and a classification loss. It improved the performance (AUROC) of the state-of-the-art single- and multi-omics methods for drug response prediction.

**Research Intern, GenomeDx Inc. (Research collaboration)**

**Sep 2017-Jan 2018**

- ❑ Developed a novel method in Tensorflow to predict metastasis in prostate cancer using Autoencoders and transfer learning on unlabelled and labelled genomic data and improved the accuracy compared to the state-of-the-art studies
- ❑ Developed skills to analyze data via R such as survival analysis and data visualization
- ❑ Obtained experience to collaborate with researchers with different backgrounds
- ❑ Supervisors: Dr. Elai Davicioni, Nicholas Erho, and Dr. Yang Liu (Seagle)

**Research Assistant, Ferdowsi University of Mashhad (Full time)**

**Sep 2012- Feb 2015**

- ❑ Designed and implemented a project in Matlab on feature selection for genomic data using a novel information theoretic method based on correntropy for cancer classification

**Selected course/personal projects during Ph.D.**

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**Automatic chemical compounds design via Autoencoders using SMILES representation.**

- ❑ The goal was to generate new molecules via Variational Autoencoders. The hypothesis is that its learned representation is rich enough to sample and generate new molecules from it
- ❑ Used SMILES representations of existing chemical compounds and trained the Autoencoder on them

**Mini personal projects on Convolutional and Recurrent Neural Networks**

- ❑ Vision: Applied CNN to image verification and recognition tasks
- ❑ Vision: Used neural style transfer to generate new arts
- ❑ NLP: Applied RNN models to synthesize Shakespeare's text
- ❑ NLP: Applied RNN to speech recognition and music synthesis

**Technical skills**

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Programming languages: Python, C

Data science: Tensorflow, Pytorch, Keras, Matlab, R

Desktop and OS: Microsoft office, Latex, Photoshop, Windows, Ubuntu

**Volunteer positions**

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SFU Omics organizer—a group to provide an environment for students and other academics to come together to talk about their research related to Genomics, Proteomics, and Metabolomics. (2018-Present)