

Curriculum Vitae

PERSONAL DATA

FIRST NAME:	Iman	Last Name:	Nazari
Date of Birth:	11 August 1987	Nationality:	Iranian
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EDUCATION

2019-Now	PhD in Computational biology European School of Molecular Medicine (SEMM), Italy
2017- 2019	Master in Electronic Engineering CGPA (3.7/4.0) Faculty of Electronic and information Engineering Chonbuk National University, South Korea
2010	Bachelor in electronics Faculty of electronic Pasargad higher education institute, Iran

PROJECTS

2020-CURRENT	Role of p21 in the immune response against breast cancer Objective: <i>RNA Sequencing and analysis of WT and p21^{-/-} CD11B⁺ cells.</i> We characterized WT and p21 ^{-/-} cellular subpopulations and identify transcribed genes that distinguish different subpopulations, with particular emphasis to the antigen presentation machinery and also integrate these data with new bulk RNA sequencing data of 3 WT and 3 p21 ^{-/-} samples.
2020-CURRENT	Integrative computational analyses of single-cell/single-molecule transcriptional and mutational profiling to understand the Myelodysplastic syndrome (MDS) to secondary acute myeloid leukemia (sAML) evolution system Objective: <i>integrative analysis of mutational and transcriptional profile setting up a method to overcome the coverage bias of the high-throughput short-read single cell (SC) RNA-sequencing, combining single-cell and single-molecule sequencing (SCM-seq)</i>

Briefly, we plan to exploit a droplet-based SC RNA-sequencing platform (Chromium 10x, 3' gene expression kit v3) both to perform conventional SC gene expression analysis and to obtain full-length cDNA attached to cell barcodes and unique molecular identifiers (UMIs); this latter will be then used as an input for single-molecule long-read sequencing (Oxford Nanopore Technologies, ONT), which should provide sufficient coverage to assess the presence of mutations previously identified by bulk whole exome sequencing (WES). Shared cell barcodes provide the link between transcriptional and mutational analyses. While bulk RNA sequencing will serve as control method for both SC and long-read transcriptional analysis, we will take advantage of SCM-seq to uncover SC splicing isoforms and aberrancies, given that single-molecule sequencing is the only technology allowing the direct analysis of fully assembled transcripts.

2019

Identifying RNA N6-methyladenosine sites using deep learning

Objective: *Utilize deep learning to analyze the sequence characteristics of N6-methyladenosine sites and build their predictive models.*

We trained a convolutional neural network based on the features which extracted by word2vec model. N6-methyladenosine (m6A) is an RNA methylation modification and it is involved in various biological progresses such as translation, alternative splicing, degradation, stability, etc. We utilize an automatic feature learning approach based on the widely used natural language technique word2vec. The learnt features are extracted automatically from the human genome without any explicit definition. Then, these learnt features are fed to a simple convolution neural network model for classification.

2017- 2018

Branch Point Selection in RNA Splicing Using Deep Learning

Objective: *Developing deep learning based algorithms and tools for predicting and analyzing RNA Branchpoint sites.*

Generally, branch point site is located at 20 to 50 nucleotides upstream from 3'ss. In this study, we identify the branch point location using a computational model based on deep learning. We propose a hybrid model based on a combination of dilated convolution neural network and recurrent neural network. Integrating additional inputs to the raw RNA sequence has been studied such as conservation, binding energy, and dinucleotide. Applying the developed models in diseases study: analyze the effects of various mutations on RNA introns nucleotides near the Branch-point site and analyse the effect of them on the branchpoint.

2011- 2016

Nonlinear control of Industrial Robot Manipulator for Experimental Research and Education

Objective: *Designing robust linear and non-linear controllers to control the robot arm in matlab and their implementation on FPGA .*

We targeted developing linear and non-linear controllers to controll the robot arm with high accuracy .

WORK EXPERIENCE

2011-2016	ELECTRONIC ENGINEER, <i>South zagros Oil and Gas extraction company, Fars, Iran</i> I was assigned to Install and Maintain Communication equipment, testing and fault diagnosing in long range communication sytems and repair electronic boards in company.
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PRIZE HONNOR

2020	Achieving the certificate of participation in workshop of Neutral network in scRNS-seq by YALE university
2019	Achieving the PhD scholarship from European School of Molecular Medicine (SEMM), Milan, Italy
2017	Achieving the Master scholarship from Brain Korea (BK), Jeunjo, South Korea
2017	Achieving the certificate of award on ICIARE 2017 Japan (Innovative Application Research and Education)
2010	Holding training programs headed by scientific society of university In B.Sc. degree (Position: Instructure)
2007-2011	Registration of 10 inventions in Tehran general dept. of registration of compa-nies and industrial ownership
2007-2012	Participation in Iran open international robotic festival (For five Times)
2004	Participation in kharazmi youth festival in 2004 and achieving provincial 3rd rank and being awarded a token of appreciation from Mr.Hamidreza Azari, The director of fars province education organization.

LANGUAGES

PERSIAN:	Native
ENGLISH:	Fluent
KOREAN:	Basics

PROGRAMMING LANGUAGES

Programming:	Python, R, Deep learning programming (keras), Assembly, C, Mikrobasic, ISE(FPGA), Visual Basic
Simulation:	Matlab

DEVELOPED TOOLS

RNAbps:	Deep learning-based model for predicting RNA branchpoint sites. Fields: Computational Biology Bioinformatics Deep Learning Link: https://home.jbnu.ac.kr/NSCL/rnabps.htm
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PUBLICATIONS

Sehi Park, Abdul Wahab, **Iman Nazari**, Ji Hyoung Ryu, Kil To Chong, i6mA-DNC: Prediction of DNA N6-Methyladenosine sites in rice genome based on dinucleotide representation using deep learning, *Chemometrics and Intelligent Laboratory Systems*, <http://www.sciencedirect.com/science/article/pii/S0169743919306276> (2020)

J. Khanal, **I. Nazari**, H. Tayara and K. T. Chong, "4mCCNN: Identification of N4-Methylcytosine Sites in Prokaryotes Using Convolutional Neural Network," in *IEEE Access*, vol. 7, pp. 145455-145461, 2019, doi: 10.1109/ACCESS.2019.2943169.

Nazari, Iman, et al. "iN6-Methyl (5-step): Identifying RNA N6-methyladenosine sites using deep learning mode via Chou's 5-step rules and Chou's general PseKNC." *Chemometrics and Intelligent Laboratory Systems* (2019): 103811.

I. Nazari, H. Tayara and K. T. Chong, "Branch Point Selection in RNA Splicing Using Deep Learning," in *IEEE Access*. doi: 10.1109/ACCESS.2018.2886569 (IEEE. 2018).

I. Nazari, F Piltan, A Roshanzamir, A Jahed, S Namvarrechi, NB Sulaiman, "FPGA-Based Model-Free Nonlinear Control Approach with Application to First Order Delays System" *International Journal of u- and e- Service, Science and Technology* Vol.10, No. 1 (2017), pp.117-128 <http://dx.doi.org/10.14257/ijunesst.2017.10.1.10> (2017).

Iman Nazari, Ali Hosainpour, Farzin Piltan, Sara Emamzadeh, Mina Mirzaie, "Design Sliding Mode Controller with Parallel Fuzzy Inference System Compensator to Control of Robot Manipulator", *International Journal of Intelligent Systems and Applications*, vol.6, no.4, pp.63-75, 2014. DOI: 10.5815/ijisa.2014.04.07.

SPEECH AND POSTER PRESENTATION

Iman Nazari, Kil to Chong, "Human Splicing branchpoint prediction Based on LSTM model" *International Symposium on Information Technology Convergence (ISITC 2018)*.

Hilal Tayara, **Iman Nazari**, Kil to Chong, "Deep Learning Approaches For Prediction Of Sequence Specificities of DNA-Binding Proteins" *Innovative Application Research and Education (ICIARE2017)* japan.

BOOK

Translation, Completion and Publish of the Book of "Advanced Training Of Microcontrollers (PIC) "

SOCIAL SKILLS

Effective communication and leadership skills

Self-starter, believe in creativity

Problem solving skills

Ability to analyze and think logically

Enthusiastic team player with a drive to excel

REFERENCES

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