Personal information

- First name: Edris
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- Language: Kurdish, Persian, English
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- GitHub

Education

Degree	Field	Institution	Date	Score [1]
M.Sc.	Medical Biotechnology	Iran University of Medical Sciences	2014-2017	17.28
B.Sc.	Biology	Tabriz University	2009-2013	15.33

Research interests

- Bioinformatics
- NGS (Exome sequencing, Single-Cell RNA-Seq, RNA-Seq)
- AI (Machine learning and deep learning)
- Cancer research
- R and Python software development (Package and Web application)
- Medical genetics

Msc thesis

Edris Sharif Rahmani, **Study of genetic variations in patients with familial hemophagocytic lymphohistiocytosis by means of whole exome sequencing**. Department of Medical Biotechnology, School of Allied Medicine, Iran University of Medical Sciences. Supervised by Dr. Arashad Hosseni & Dr. Hamzeh Rahimi, 2017.

Publication

Edris Sharif Rahmani, Ankita Sunil Lawarde, Vijayachitra Modhukur. **MBMethPred: an AI-Based Framework for Classification of Childhood Medulloblastoma Subgroups based on**

[1] In Iran's education system, the maximum score is 20.

Publicly Available Methylation Data (Submitted, December 2022)

Edris Sharif Rahmani, Hasan Azarpara, Mohammad Foad Abazari, Mohammad Reza Mohajeri, Maryam Nasimi, Raziyeh Ghorbani, Arghavan Azizpour, Hamzeh Rahimi. **Novel Mutation C.7348C>T in NF1 Gene Identified by Whole-Exome Sequencing in Patient with Overlapping Clinical Symptoms of Neurofibromatosis Type 1 and Bannayan–Riley–Ruvalcaba Syndrome**. *Cytology and Genetics*. 54, pages353–362(2020).

Edris Sharif Rahmani, Majid Fathi, Mohammad Foad Abazari, Hojat Hhahraki, Vahid Ziaee, Hamzeh Rahimi, Arshad Hoseini. **Whole Exome Sequencing for Mutation Screening in Hemophagocytic Lymphohistiocytosis**. *Iran J Ped Hematol Oncol*. 2020, 10(1): 38-48.

Majid Fathi, Hojat Shahraki, **Edris Sharif Rahmani**, Hamzeh Rahimi, Pouria Omidi, Saeedeh Darvishi, Mohammad Foad Abazari, Arshad Hosseini. **Whole Exome Sequencing of an X-linked Thrombocytopenia Patient with Normal Sized Platelets**. *Avicenna J Med Biotechnol*. 2019 Jul-Sep; 11(3): 253–258.

Reyhaneh Nassiri Mansour, Fatemeh Soleimanifar, Mohamad Foad Abazari, Sepehr Torabinejad, Abdolreza Ardeshirylajimi, Pegah Ghoraeian, Seyed Ahmad Mousavi, **Edris Sharif Rahmani**, Hadi Hassannia & Seyed Ehsan Enderami. **Collagen coated electrospun polyethersulfon nanofibers improved insulin producing cells differentiation potential of human induced pluripotent stem cells**. *Artificial Cells, Nanomedicine, and Biotechnology*. 2018, 46(3): S734-S739.

E. S. Rahmani, H. Azarpara, M. Karimipoor, H. Rahimi. **Whole exome analysis of primary immunodeficiency**. *Vavilov Journal of genetics and breeding*. Vol 22, No 5 (2018).

Experiences

Teaching

- 2020- Today, Teaching R and Python for post-graduate students.
- January 8-18, 2017, "International Applied Bioinformatics Workshop" in Pasture Institute of Iran (with certificate).
- March 6, 2017, "Genetic Engineering course" in Iran University of Medical Sciences (with certificate).

English language

- IELTS overall band score 6

Molecular & cellular techniques

- Cell and Bacterial cultures
- DNA and RNA extraction and preparation
- Bioassay with Spectrophotometry
- Gel electrophoresis
- Primer design (Oligo 7, Primer 3)

- PCR and Real-time PCR

Computational skills

Statistics

- Descriptive
- Analytical (t-test, ANOVA , Chi-square, Regression)
- Meta-analysis

Programming language

Python

- Syntax
- Jupyter notebook
- Spider
- Libraries (pandas, numpy, seaborn, matplotlib, scikit-learn, keras, tensorflow, biopython, beautiful soup)

R programming language

- Syntax
- RStudio
- Packages (shiny, shinydashboard, shinyjs, shinyWidgets, shinyBS, shinyDarkmode, leaflet, tidyverse, DT, limma, reshape2, dlookr, caTools, e1071, caret, pROC, MLmetrics, class, ElemStatLearn, RColorBrewer, FNN, cluster, randomForest, factoextra, MASS, psych, Boruta, glmnet, igraph, ComplexHeatmap, car, parallel, Survival, Surat, minfi)

Shell scripting language

- Syntax
- Regular expression
- awk
- sed

High-throughput sequensing data analysis

1. Whole-exome sequensing 2. Bulk RNA-Seq 3. scRNA-Seq, 4. Methylation 5. Microarray

- Databases(NCBI, UCSC, Ensemble, HGMD, OMIM, COSMIC, PDB, KEGG, GEO, SRA, ArrayExpress, 1000Genomes, gnomAD)
- QC (Fastqc, Fastx-toolkit, Prinseq++, Trimmomatic
- Mapping(Reference indexing, Bwa, Bowtie2, Tophat2, STAR, Trinity)
- Post-alignment processing (Picard, Samtools)
- Variant discovery (GATK)
- Visualization (IGV)

- Prioritization, filtering, and annotation (KGGSeq, Ensemble Variant Effect Predictor (VEP), Shell script)
- Quantification, deferentially gene expression, and annotation (Cufflinks, eXpress, DESeq2, edgeR, limma, AnnotationDbi

Machine learning algorithms

- Regression (Simple, Multiple, Polynomial, Logistic)
- Decision Tree (Classification, Regression)
- Random Forest (Classification, Regression)
- K-Nearest Neighbors (K-NN)
- Support Vector Machine (SVM)
- Naive Bayes
- K-Means Clustering
- Hierarchical Clustering

Deep learning

- Artificial Neural Networks (ANN)
- Convolutional Neural Networks (CNN)

Documentation

- Microsoft Office
- Rmarkdown

Web development

- HTML
- CSS
- Shiny R package
- Rmarkdown

Projects

- MBMethPred
  - An R package: Utilizing a combination of machine learning models (Random Forest, Naive Bayes, K-Nearest Neighbor, Support Vector Machines, Extreme Gradient Boosting, and Linear Discriminant Analysis) and a deep Artificial Neural Network model, MBMethPred can predict medulloblastoma subgroups, including wingless (WNT), sonic hedgehog (SHH), Group 3, and Group 4 from methylation data.
- DeepBC
  - A fully automated online web application to perform the most famous data preprocessing and machine learning algorithms and microarray data analysis Tutorials.
- scRNA-SeqAnalyzer

  - A fully automated web application to analyze single-cell transcriptomic data (10X Genomics) from matrix market file to Gene ontology analysis level Tutorials.
- MethSurv (Offline)
  - A framework to analyse survival, differentially methylated probes, and deep neural network modeling of the methylation datasets.
- TCGA-Downloader (Offline)
  - For easy and graphical user interface downloading of all available TCGA datasets.
- fq2vcf
  - A fully automated shell script to analyze exome sequencing data from fastq files to fully annotated variants.
- GfantoR
  - A shell script to plot the entire output of whole-exome sequensing.
- varfilter
  - A shell script to automatic filter and annotate NGS variants from a VCF file.

Reference

- **Dr. Arashad Hosseni**
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