

Mohammadreza Sehhati



Date of birth:	9 July 1981
Place of birth:	Isfahan, Iran
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Position:	Assistant Professor at Isfahan University of Medical Sciences (Department of Bioinformatics)
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Profile

Ph.D. degree in biomedical engineering with experience in Bioinformatics, Machine Learning, Mathematical Modeling, and Programming.

Education

- **2010-2015:** Ph.D. in Biomedical Engineering, [Isfahan University of Medical Sciences](#), Isfahan, Iran.
 - *GPA* = 18.6
 - *Thesis Title:* Seeking an appropriate feature extraction method for breast cancer recurrence prediction based on microarray gene expression data
- **2003-2006:** M.Sc. in Biomedical Engineering from [University of Tehran](#), Tehran, Iran.
 - *GPA* = 16.68
 - *Thesis Title:* Design and implementation of software infrastructures for an standard hospital information system based on HL7 protocol
- **1999-2003:** B.Sc. in Biomedical Engineering from [Shahed University](#), Tehran, Iran.
 - *GPA* = 16.99
 - *Thesis Title:* Design and manufacturing of a Holter-Monitoring device prototype

Teaching Experience

- **Isfahan University of Medical Sciences (2011-now):**
 - Pattern Recognition
 - Modeling of Physiological Systems
 - Machine Learning
 - Mathematics in Medicine
 - Basics of Programming,
 - Data Structure and Algorithms,
 - Basics of Electrical and Electronic Circuits,
 - Digital Signal Processing,

Work Experience

Isfahan University of Medical Sciences

Assistant professor at Dept. of Bioinformatics, School of Advanced Technologies in Medicine, Isfahan, Iran, 2015-now.

The Green Science Institute (GSI)

Dept. of R&D, Image Processing Group, Tehran, Iran, 2005-2010.

- *Job title:* System Design, Algorithm Development, Programming.

Safe Soft Company

Dept. of Software Development, Tehran, Iran, 2008.

- *Job title:* Project Manager.

Key Skills

- **Special skills:**
 - Bioinformatics (data mining, microarray gene expression analysis, full pipeline for NGS analysis and variant calling, Network analysis),
 - Machine Learning (design and development of algorithms and software),
 - Mathematical modeling of physiological systems
 - Hospital Information System design/development/evaluation,
 - Design and manufacturing of electronic circuits for biological signal measurement.
- **Computer skills:**
 - Programming (R, C++, MatLab, VB), Web (PHP, HTML, XML), Database (MySQL), OS (Windows, Linux, Mac).
- **Languages:**
 - English (MHLE certificate), Persian (Native), Arabic (Beginner).

Selected Publications

- E Mousavi, **M Sehhati**, “A generalized multi-aspect distance metric for mixed-type data clustering”, Pattern Recognition (IF=**8.518**), 2023, 138: 109353
- Z Nouri, A Sarmadi, S Narrei, **M Sehhati**, MA Tabatabaiefar, “Whole exome sequencing identified a novel LAMA2 frameshift variant causing merosin-deficient congenital muscular dystrophy in a patient with cardiomyopathy, and autism-like behavior”, Neuromuscular Disorders (IF=**3.538**), 2022, 32(9):776-784.
- **M Sehhati**, MA Tabatabaiefar, AH Gholami, M Sattari, “Using classification and K-means methods to predict breast cancer recurrence in gene expression data”, Journal of Medical Signals & Sensors, 2022, 12(2), 122-126.
- AA Arani, **M Sehhati**, MA Tabatabaiefar, “Predicting deleterious missense genetic variants via integrative supervised nonnegative matrix tri-factorization”, Scientific Reports (IF=**4.379**), 2021, 11(1):1-13.
- N. Tavasoli, K. Rezaee, M. Momenzadeh, **M. Sehhati**, “An ensemble soft weighted gene selection-based approach and cancer classification using modified metaheuristic learning”, Journal of Computational Design and Engineering (IF=**5.860**), 2021, 8(4):1172-1189.
- A. Amousoltani Arani, **M. Sehhati**, M.A. Tabatabaiefar, “Genetic variant effect prediction by supervised nonnegative matrix tri-factorization”, Molecular Omics (IF=**3.743**), 2021, <http://dx.doi.org/10.1039/D1MO00038A>
- M. Shahhosseini, Newsha Molavi, MA. Tabatabaiefar, **M. Sehhati**, “Optimization of annotation and interpretation step of next generation sequencing data analysis for non-syndromic autosomal recessive hearing loss disease”, Journal of Health and Biomedical Informatics 2020, 7 (4), 435-444.
- M. Momenzadeh, H. Rabbani, **M. Sehhati**, “Using Hidden Markov Model to Predict Recurrence of Breast Cancer Based on Sequential Patterns in Gene Expression Profiles”, Journal of Biomedical Informatics (IF= **6.317**), 2020, 111, 103570.

- H. Mohammadi, M.A. Tabatabaiefar, **M. Sehhati**, “Selection of Optimal Bioinformatic Tools and Proper Reference for Reducing the Alignment Error in Targeted Sequencing Data”, *Journal of Medical Signals & Sensors* 2020, 11 (1), 37.
- M Momenzadeh, **M. Sehhati**, H. Rabbani, “A novel feature selection method for microarray data classification based on hidden Markov model”, *journal of biomedical informatics* (IF= **6.317**), 2019, 95, 103213
- E Saghapour, M Sehhati, “Physicochemical Position-Dependent Properties in the Protein Secondary Structures”, *Iranian Biomedical Journal* 2019, 23 (4), 253
- F. Safaei Firouzabadi, A. Vard, **M. Sehhati**, M Mohebian, “An Optimized Framework for Cancer Prediction Using Immunosignature”, *Journal of Medical Signals & Sensors* 2018, 8(3):161-170.
- E. Saghapour, S. Kermani, **M. Sehhati**, “A novel feature ranking method for prediction of cancer stages using proteomics data”, *PLoS ONE* (IF= **3.240**), 2017; 12(9): e0184203.
- E. Saghapour, **M. Sehhati**, “Prediction of metastasis in advanced colorectal carcinomas using CGH data”, *Journal of Theoretical Biology* (IF= **2.691**), 2017, 429:116-123.
- **M. Sehhati**, M. Kayed, “Evaluation of Different Classification Models to Extract Gene Signatures for Breast Cancer Recurrence Using Microarray Data”, *Journal of Isfahan Medical School* 2017; 35(419):98-103.
- A. Mehridehnavi, H. Zand, **M. Sehhati**, “Dimensionality reduction on topological features of the gene network constructed from microarray data for the prediction of breast cancer recurrence”, *Journal of Isfahan Medical School* 2016; 33(359).
- **M. Sehhati**, A. Mehridehnavi, H. Rabbani, M. Pourhossein, “Stable gene signature selection for prediction of breast cancer recurrence using joint mutual information”, *IEEE/ACM Transaction on Computational Biology and Bioinformatics* (IF= **3.710**), 2015; 12(6): 1440-1448.
- A. Mehridehnavi, **M.R. Sehhati**, H. Rabbani, “Hybrid method for prediction of metastasis in breast cancer patients using gene expression signals”, *Journal of Medical Signals and Sensors* 2013; 3(2):79-87.
- **M.R. Sehhati**, A. Mehridehnavi, H. Rabbani, S.H. Javanmard, “Using protein interaction database and support vector machine to improve gene signatures for prediction of breast cancer recurrence”, *Journal of Medical Signals and Sensors* 2013; 3(2):87-93.

References

References, letters of recommendation and other documents available upon request