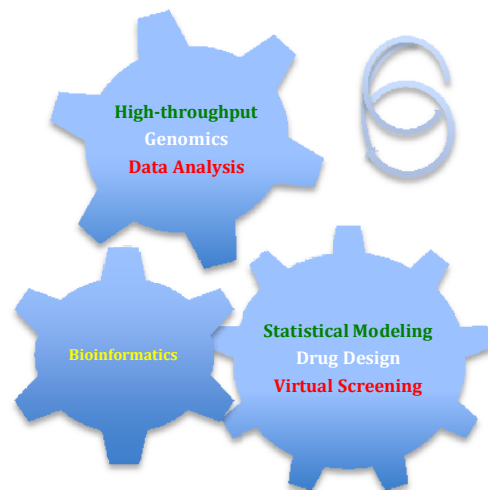


**Bioinformatics & System Biology
Research & Educational Group**
**School of Advanced Technologies in
Medicine**
Isfahan University of Medical Sciences



Introduction

In 2011 the School of Advanced Technologies in Medicine started its activities by setting up a research group in the bioinformatics field. In the weekly sessions of this research group the following goals have been followed:

- ✓ Training the members by the experts through lecture on the fundamental concepts of biology and computational algorithms
- ✓ Evaluating the progress of theses and conducting them by the experts' comments on the presentations of students

In the recent years significant number of PhD and MSc theses were supervised in this field and some are ongoing. In this regard, the computational tools required for fast processing of large data is purchased and launched. Also according to the reality that a great number of professors and experts are collaborating with our faculty in this area.

Objectives

The fast growth of biological data has produced a huge amount of information. It is obvious that without using new information technology it is not possible to manage this data. Although computer science and information science are two majors that are used in all current sciences, as knowledge related to medicine and health is now the biggest and the most challenging area of knowledge, Bioinformatics has become a unique academic field of science.

Bioinformatics is a novel field of science, which incorporates, applied mathematics, statistics, computer science, artificial intelligence, biochemistry and biology to answer the questions and aided in cellular and molecular biologic issues.

The key areas of research in bioinformatics are:

- ✓ Modeling existing structures as symbols of data and information that makes the relationship of concepts and facts more clear.
- ✓ Development and enhancement of computer aided systems to increase the

quality of patient treatment and biomedical research.

- ✓ Bioinformatics work flow management systems.
- ✓ Developing ways to assess models and systems of research in health, data mining, education and management.
- ✓ Drug lead identification and optimization, using computer, for high-throughput docking and quantitative biological activity prediction.

Selected Theses

- ✓ *PhD Thesis*: Seeking an appropriate feature extraction method for breast cancer recurrence prediction based on microarray gene expression data. Supervised by A. Mehridehnavi and Hossein Rabbani.
- ✓ *PhD Thesis*: Using a new adaptive deep learning method for drug discovery with application in investigating Parkinson disease. Supervised by A. Mehridehnavi and A. Fasihi.
- ✓ *MSc Thesis*: Classification and diagnosis of Lymphoma cancer and normal tissues based on gene expression data using artificial neural networks. Supervised by A. Mehridehnavi and M. Salehi.
- ✓ *MSc Thesis*: Implementing of pattern recognition algorithms for design of a method to find genes in prokaryotes. Supervised by A. Mehridehnavi.
- ✓ *MSc Thesis*: Extracting gene regulatory modules using biclustering on microarray

data. Supervised by A. Mehridehnavi and M. Mohammadbeigi.

- ✓ *MSc Thesis*: Dimensionality reduction on the prediction of breast cancer recurrence by using topological features of the gene network constructed from microarray data. Supervised by A. Mehridehnavi.

Selected Publications

- ✓ A Vaez, PJ van der Most, BP Prins, et al. "lodGWAS: a software package for genome-wide association analysis of biomarkers with a limit of detection", *Bioinformatics* 2016, 32 (10), 1552-1554.
- ✓ 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* 2015; 12(6): 1440-1448.
- ✓ F Ghasemi, A Mehri, J Pena-Garcia, et al. "improving activity prediction of adenosine A2B receptor antagonists by nonlinear models", *IWBBIO 2015, Part II, LNCS* 2015, 635-644.
- ✓ E Saghapour, S Kermani, M Sehhati "A novel feature ranking method for prediction of cancer stages using proteomics data", *PLoS ONE* 2017, 12(9): e0184203.
- ✓ E Saghapour, M Sehhati, "Prediction of metastasis in advanced colorectal carcinomas using CGH data", *Journal of Theoretical Biology* 2017, 429:116-123.

- ✓ A Vaez, R Jansen, BP Prins, et al. "An in silico Post-GWAS Analysis of C-Reactive Protein Loci Suggests an Important Role for Interferons", *Circulation: Cardiovascular Genetics* 2015.
- ✓ A Juluri, F Ghasemi, H Perez-Sanchez, R N Murthy, N Murthy, "IONTOPHORESIS-Captisol-Enabled (TM) Lipophilic drug complex delivered transdermally by Iontophoresis" *Journal of Drug Development and Delivery*, 2015.
- ✓ M Sehhati, A Mehri Dehnavi, H Rabbani, S Haghjoo 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.
- ✓ A Mehridehnavi, M 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): 79-86.
- ✓ A Mehridehnavi, L Ziaei, "Minimal gene selection for classification and diagnosis prediction based on gene expression profile", *Advanced Biomedical Research*, 2013; 2(2): 1-5.

People

- Prof. Dr. Alireza Mehridehnavi
- Prof. Dr. Afshin Fasihi
- Dr. Hossein Rabbani
- Dr. Ahmad Vaez

- Dr. Fahimeh Ghasemi
- Dr. Mohammadreza Sehhati
- Fatemeh Kazemi
- Mohammadali Allahyari
- Fatemeh Safayi
- Ehsan Saghapour
- Hannaneh Mohammadi

Computational Facilities

The School of Advanced Technologies in Medicine features extensive computational resources available for a wide range of applications including, data archiving, numerical analysis, signal & image processing, etc. The main resource is a parallel cluster with a server and five computing nodes including 12 AMD Opteron processors (2.2 Ghz, 16 core, 16MB L3 cache)
Total memory: 304 GB DDR3
Total processor cores: 192

