

# Hanie Samimi

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## RESEARCH INTERESTS

Bioinformatics, Computational Biology, Cancer Research, Data Mining,  
Machine Learning, Algorithm, Cell Biology, Genetics

## Work Experiences

### Doctoral Instructional Assistant

Department of Computer Science, Texas State University, Aug 2018-Present

### Graduate Instructional Assistant

Department of Computer Science, Texas State University, June 2018-Aug 2018

### Graduate Research Assistant

Department of Computer Science, Texas State University, Sept 2016-May 2018

- Under supervision of Dr. Habil Zare.

### Teaching Assistant

Department of Mathematics, Statistics and Computer Science, The University of Tehran

- Digital Design, Spring 2016
- Principles of Computer Systems, Spring 2015

### Mentoring

- Mentoring three high school students in the Summer Math Camp, Texas State University, Summer 2017.
- Computer Programming Teacher, teaching Java and C++, Tehran, Iran, 2015-2016.
- High school mathematics teacher, Tehran, Iran, 2014-2016.

## EDUCATION

**Ph.D** in Computer Science, Texas State university, USA, Fall 2018- Spring 2022 (expected)

**M.Sc.** in Computer Science, Texas State university, USA, Spring 2017-Summer 2018

*Thesis:* Identification of gene sets that predict Acute Myeloid Leukemia prognosis using integrative gene network analysis

Current techniques analyze genetic and epigenetic data separately, and then combine the results together. These approaches fail to find variations that are supported by both individual experiments. Integrating data using network analysis is a novel robust technique that can analyze these complex data. In this project, we are trying to integrate gene expression and DNA-methylation data by using network analysis. This will lead us to find bio-marker genes that enhance the prognosis of the AML disease.

*Selected Coursework:* Molecular biology and genetics, Current topics in Biochemistry and Molecular Biology, Algorithm design, Data mining, Artificial Intelligence, Database systems.

**B.Sc.** in Computer Science, University of Tehran, Iran, Fall 2011-Spring 2016.

*Final senior project:* Online signature authentication using Dynamic Time Wrapping Algorithm; In the field of biometrics, one common technique is the use of signature-based authentication of the hand-written signature. Among common techniques, the dynamic synchronization algorithm, DTW, has the highest efficiency and simplicity. During this project, I studied and evaluated DTW-based online authentication systems and implemented some parts of an authentication systems.

*Selected Coursework:* Biology (19/20), Bioinformatics (19.25/20), advanced programming (18.5/20), Foundation of programming (17.5/20), Foundation of programming languages (19.5/20), Theory of Computation (18/20), Software Engineering (18/20)

## PREVIOUS RESEARCH

*Department of Computer Science, Texas State University, January 2017-Present.*

- Molecular mechanisms of Alzheimer's disease; The deposition of tau protein aggregates in the brains of affected individuals has a critical role in Alzheimer's disease (AD). We used Drosophila as a model organism to identify the molecular mechanisms that cause Alzheimer's disease and associated tauopathies
- Designed and implemented a novel data reduction scheme to reduce size of flow cytometry data without significant loss in biological information. My approach resulted in enhancing spectral clustering technique such that it could be efficiently applied on flow cytometry data for the first time.

## PUBLICATIONS

### *Published Journal Articles*

- Sun, W., Samimi, H., Gamez, M., Zare, H., Frost, B. (2018). Pathogenic tau-induced piRNA depletion promotes neuronal death through transposable element dysregulation in neurodegenerative tauopathies. *Nature neuroscience*, 21(8), 1038. Impact factor: 18.

### *Journal Articles In Preparation*

- **Samimi** H., Docking R., Chang L., Duns G., Hudoba M., Karsan A., Zare H., iNETgrate: How to leverage epigenome data when they are missing? *PLOS Computational Biology* 2017. Impact factor: 4.9.
- Bordiya Y., Hurtado G., **Samimi** H., Zare H., Kang H., Small RNAs regulate the transcriptional dynamics of defense genes under biotic stress in Arabidopsis *Plant Cell* 2018. Impact factor: 8.5.

## Programming Skills and Bioinformatics Tools

- Expert: R, Java, C++, MySQL, PL/SQL,HTML, PHP, CSS.
- Familiar: MATLAB, Python, CUDA, OpenMp, LaTeX, UCSS Genome Browser, HOMER, etc.
- skilled in working with Linux operating system

## REFERENCES

**Dr. Habil Zare**

(my MSc supervisor)

Assistant Professor

Department of Computer Science

Texas State University

San Marcos, TX, USA.

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**Dr. Bess Frost**

Assistant Professor

Barshop Institute for Longevity and Aging  
Studies

Department of Cell Systems and Anatomy

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