

# Alireza Karbalayghareh

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CONTACT INFORMATION	Mortimer B. Zuckerman Research Center, 417 E 68th St., New York, NY 10065	<i>Phone:</i> (979) 676-9777 <i>E-mail:</i> karbalaa@mskcc.org
RESEARCH INTERESTS	Machine Learning, Computational Biology	
CURRENT POSITION	<b>Memorial Sloan Kettering Cancer Center</b> , New York, NY <b>Computational &amp; Systems Biology Program</b> Postdoctoral Research Scholar	Sept. 2019 - present
EDUCATION	<b>Texas A&amp;M University</b> , College Station, TX Ph.D. in Electrical Engineering GPA: 4.0/4.0	Sept. 2014 - Aug. 2019
	<b>Sharif University of Technology</b> , Tehran, Iran M.Sc. in Electrical Engineering GPA: 17.84/20.00	Sept. 2011 - Aug. 2014
	<b>Iran University of Science and Technology</b> , Tehran, Iran B.Sc. in Electrical Engineering GPA: 18.08/20.00 ( $3^{rd}$ rank in class)	Sept. 2007 - Aug. 2011
RESEARCH PROJECTS	<b>Learning Gene Regulation Mechanisms by Integrating 3D DNA Architectures and 1D Genomic/Epigenomics Data:</b> <ul style="list-style-type: none"><li>Developed a gene regulation model with graph attention networks which integrates the chromatin interaction data (Hi-C/HiChIP/Micro-C) data and 1D genomic/epigenomic data to predict the gene expressions.</li><li>Identified enhancers of the genes by interpreting the models using feature attribution methods.</li></ul> <b>Domain Invariant Cell Type Identification Using scRNA-seq Data:</b> <ul style="list-style-type: none"><li>Identified immune cell types from heterogeneous scRNA-seq data of different patients by correcting the batch effects using domain-invariant VAEs.</li></ul> <b>Optimal Bayesian Transfer Learning:</b> <ul style="list-style-type: none"><li>Proposed a Bayesian transfer learning framework, where the source and target domains are related through the joint prior density of the model parameters.</li><li>Derived the posteriors and posterior predictive densities in closed forms in terms of generalized hypergeometric functions of matrix argument.</li><li>Proposed the Optimal Bayesian Transfer Learning (OBTL) classifier, resulting in much better performance than the rival transfer learning and domain adaptation methods.</li><li>Proposed Optimal Bayesian Transfer Regression (OBTR) operator, transferring optimally from the source domain to regression in the target domain.</li></ul> <b>Bayesian Multi-Domain Learning:</b> <ul style="list-style-type: none"><li>Generalized Bayesian transfer learning to a multi-domain scenario with count observations using negative binomial factor analysis.</li><li>Provided a Gibbs sampling inference using state-of-the-art data augmentation techniques.</li><li>Proposed the Bayesian Multi-Domain Learning (BMDL) algorithm, outperforming the rival methods.</li></ul>	

### Trajectory/Time Series Classification Using Gene Regulatory Networks:

- Proposed the optimal classifier for the gene expression trajectories using the partial knowledge of gene regulatory networks.
- Proposed an Expectation-Maximization (EM) method to the inference of the partially observable Boolean dynamical systems.
- Proposed a Bayesian classifier for the gene expression trajectories.

### Network Inference:

- Used RNA-seq time series data and proposed an efficient algorithm for gene regulatory network inference using negative binomial model.

### PUBLICATIONS

1. **A. Karbalayghareh**, M. Sahin, and C. Leslie, “Chromatin Interaction Aware Gene Regulation Model with Graph Attention Networks,” Under Review, doi: <https://doi.org/10.1101/2021.03.31.437978>.
2. **A. Karbalayghareh**, B. Lee, and C. Leslie, “Semi-supervised Identification of Immune Cell Types in Heterogeneous Single-cell RNA-seq Datasets with Domain Invariant Variational Autoencoders,” Under Prep.
3. **A. Karbalayghareh**, X. Qian, and E. R. Dougherty, “Optimal Bayesian Transfer Learning for Count Data,” IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019.
4. E. Hajiramezani, S. Zamani, **A. Karbalayghareh**, M. Zhou, X. Qian, “Bayesian Multi-Domain Learning for Cancer Subtype Discovery,” Proceedings of the 32<sup>nd</sup> Conference on Neural Information Processing Systems (NIPS), Montreal, CA, 2018.
5. **A. Karbalayghareh**, X. Qian, and E. R. Dougherty, “Optimal Bayesian Transfer Regression,” IEEE Signal Processing Letter, 2018.
6. **A. Karbalayghareh**, X. Qian, and E. R. Dougherty, “Optimal Bayesian Transfer Learning,” IEEE Transactions on Signal Processing, 2018.
7. **A. Karbalayghareh**, X. Qian, and E. R. Dougherty, “Optimal Bayesian Transfer Learning for Classifying Multivariate Gaussian Observations,” New York Scientific Data Summit (NYSDS), 2018.
8. **A. Karbalayghareh**, U. Braga-Neto, and E. R. Dougherty, “Intrinsically Bayesian Robust Classifier for Single-Cell Gene Expression Trajectories in Gene Regulatory Networks,” BMC Systems Biology, 2018.
9. **A. Karbalayghareh**, U. Braga-Neto, E. R. Dougherty, “Classification of Single-cell Gene Expression Trajectories from Incomplete and Noisy Data,” IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017.
10. **A. Karbalayghareh**, U. Braga-Neto, and E. R. Dougherty, “Classification of Gaussian Trajectories with Missing Data in Boolean Gene Regulatory Networks,” IEEE International Conference on Acoustics, Speech, and Signal Processing (ICASSP) 2017, New Orleans, LA, Mar. 2017.
11. **A. Karbalayghareh**, U. Braga-Neto, J. Hua, and E. R. Dougherty, “Classification of State Trajectories in Gene Regulatory Networks,” IEEE/ACM Transactions on Computational Biology and Bioinformatics, Oct. 2016.
12. **A. Karbalayghareh** and T. Hu, “Inference of Sparse Gene Regulatory Network from RNA-Seq Time Series Data,” IEEE Global Conference on Signal and Information Processing (GlobalSIP) 2015, Orlando, FL, Dec. 2015.

13. **A. Karbalayghareh**, M. Nasiri-Kenari, and M. Hejazi, "Convolutional Network-Coded Cooperation in Multi-Source Networks with a Multi-Antenna Relay," IEEE Transactions on Wireless Communications, 2014.

## RESEARCH EXPERIENCE

**Leslie Lab,  
Memorial Sloan Kettering Cancer Center**

*Postdoctoral Research Scholar*

Mentor: Dr. Christina Leslie

Sept. 2019 - present

**Genomic Signal Processing (GSP) Laboratory,  
Texas A&M University**

*Research Assistant*

Advisor: Prof. Edward R. Dougherty

Sept. 2014 - Aug. 2019

## KEY GRADUATE COURSES

Probabilistic Graphical Models, Pattern Recognition, Bayesian Pattern Recognition, Stochastic Systems, Bayesian Learning, Large-Scale Biological Data Analysis, Real Analysis (Math), Statistical Bioinformatics, Optimal Signal Processing Under Uncertainty, Convex Optimization, Coding Theory, Estimation Theory, Stochastic Processes.

## TECHNICAL SKILLS

**Programming Languages:** Python, R, MATLAB.

**Deep Learning:** TensorFlow, Keras, Pytorch, Variational Autoencoders (VAE), Generative Adversarial Networks (GAN), Probabilistic Generative Models (PGM), Normalizing Flows, Graph Neural Networks (GNN), Domain Adaptation, Neural Ordinary Differential Equations (ODE), Neural Stochastic Differential Equations (SDE).

**Computational Biology:** Integrated genomic, epigenomic, transcriptomic, and 3D DNA interaction data (scRNA-seq, ATAC-seq, ChIP-seq, Hi-C, and HiChIP) by developing advance machine learning algorithms to gain insights to the underlying biology.

## JOURNAL AND CONFERENCE REVIEWER FOR

Neural Information Processing Systems (NeurIPS), International Conference on Machine Learning (ICML), International Conference on Learning Representations (ICLR), Genome Research, IEEE Transactions on Signal Processing (TSP), IEEE Signal Processing Letters (SPL), IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB), Association for the Advancement of Artificial Intelligence (AAAI), Pattern Recognition Letter (PRL), BMC Bioinformatics, IEEE Access, International Joint Conference on Artificial Intelligence (IJCAI), Journal of Applied Statistics.

## LANGUAGES

English (Fluent), Persian (Native-Bilingual), Turkish (Native-Bilingual)

## REFERENCES

Dr. Christina Leslie,  
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Computational & Systems Biology Program,  
Memorial Sloan Kettering Cancer Center,  
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Prof. Edward R. Dougherty,  
Distinguished Professor,  
Department of Electrical and Computer Engineering,  
Texas A&M University,  
Email: edward@ece.tamu.edu