

Alireza Karbalayghareh

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RESEARCH INTERESTS	Machine Learning, Computational Biology, Genomics	
CURRENT POSITION	Memorial Sloan Kettering Cancer Center , New York, NY Computational & Systems Biology Program Postdoctoral Research Scholar (PI: Dr. Christina Leslie)	Sept. 2019 - present
EDUCATION	Texas A&M University , College Station, TX Ph.D. in Electrical Engineering (PI: Dr. Edward Dougherty) GPA: 4.0/4.0	Sept. 2014 - Aug. 2019
	Sharif University of Technology , Tehran, Iran M.Sc. in Electrical Engineering GPA: 17.84/20.00	Sept. 2011 - Aug. 2014
	Iran University of Science and Technology , Tehran, Iran B.Sc. in Electrical Engineering GPA: 18.08/20.00	Sept. 2007 - Aug. 2011
RESEARCH PROJECTS	GraphReg: Learning Gene Regulation Mechanisms by Integrating 3D DNA Interaction and 1D Genomic/Epigenomics Data <ul style="list-style-type: none">• Developed GraphReg, 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.• Identified functional enhancers of the genes by interpreting the models using feature attribution methods.• Learned the effects of distal TFs on gene regulation by motif ablation and validated by CRISPRi TF knockout experiments. Epiphany: Predicting Hi-C from Epigenomic Tracks <ul style="list-style-type: none">• Used five well-known epigenomic tracks to predict Hi-C maps using CNN, Bi-LSTM, and adversarial loss functions.• Interpreted the model to discover the effects of epigenomic features, especially CTCF, on 3D chromatin conformation. scBatch: Domain Invariant Cell Type Annotation Using scRNA-seq Data: <ul style="list-style-type: none">• Annotated immune cell types from heterogeneous scRNA-seq data of different patients/cancers by correcting the batch effects using domain-invariant VAEs. Optimal Bayesian Transfer Learning: <ul style="list-style-type: none">• Proposed a Bayesian transfer learning framework, where the source and target domains are related through the joint prior density of the model parameters.• Derived the posteriors and posterior predictive densities in closed forms in terms of generalized hypergeometric functions of matrix argument.• Proposed the Optimal Bayesian Transfer Learning (OBTL) classifier, resulting in much better performance than the rival transfer learning and domain adaptation methods.• Proposed Optimal Bayesian Transfer Regression (OBTR) operator, transferring optimally from the source domain to regression in the target domain.	

Bayesian Multi-Domain Learning:

- Generalized Bayesian transfer learning to a multi-domain scenario with count observations using negative binomial factor analysis.
- Provided a Gibbs sampling inference using state-of-the-art data augmentation techniques.
- Proposed the Bayesian Multi-Domain Learning (BMDL) algorithm, outperforming the rival methods.

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.

SELECTED PUBLICATIONS

1. **A. Karbalayghareh**, M. Sahin, and C. Leslie, “Chromatin interaction aware gene regulation modeling with graph attention networks,” under review in *Genome Research*, bioRxiv doi: <https://doi.org/10.1101/2021.03.31.437978>, 2021.
2. R. Yang, A. Das, V. Gao, **A. Karbalayghareh**, W. Noble, J. Bilmes, C. Leslie. “Epiphany: predicting Hi-C contact maps from 1D epigenomic signals,” under review in *Genome Biology*, bioRxiv doi: <https://doi.org/10.1101/2021.12.02.470663>, 2021.
3. **A. Karbalayghareh**, B. Lee, V. Rapolu, and C. Leslie, “Semi-supervised annotation of immune cell types in heterogeneous single-cell RNA-seq datasets with domain invariant variational autoencoders,” to be submitted, 2022.
4. **A. Karbalayghareh**, X. Qian, and E. R. Dougherty, “Optimal Bayesian transfer learning for count data,” *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2019.
5. E. Hajiramezani, S. Zamani, **A. Karbalayghareh**, M. Zhou, X. Qian, “Bayesian multi-domain learning for cancer subtype discovery,” *Proceedings of the 32nd Conference on Neural Information Processing Systems (NeurIPS)*, Montreal, CA, 2018.
6. **A. Karbalayghareh**, X. Qian, and E. R. Dougherty, “Optimal Bayesian transfer regression,” *IEEE Signal Processing Letter*, 2018.
7. **A. Karbalayghareh**, X. Qian, and E. R. Dougherty, “Optimal Bayesian transfer learning,” *IEEE Transactions on Signal Processing*, 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)*, New Orleans, LA, 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*, 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)*, Orlando, FL, 2015.

