

Seyednami Niyakan

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EDUCATION

Texas A&M University

Aug. 2018 – Present

Direct Ph.D. in Electrical Engineering

College Station, TX

- **Coursework:** Pattern Recognition, Analysis of Algorithms, Computational Biology, Convex Optimization, Statistical Bioinformatics, Advanced Bayesian Statistics, Probabilistic Graphical Modeling, Signal Processing Under Uncertainty, Spatial Statistics
- **Research:** Bayesian Machine Learning and its application in heterogeneous and high dimensional biological data, with a focus on transcriptomics

Sharif University of Technology

2013 – 2018

B.Sc. in Electrical Engineering

Tehran, Iran

EXPERIENCE

Genomic Signal Processing Laboratory, Texas A&M University

Jun. 2019 – Present

Graduate Research Assistant

College Station, TX

- Researched on Bayesian machine learning and its application in single-cell RNA sequencing data analysis
- Implemented **SimCD**, a hierarchical Bayesian model, doing simultaneous cell clustering and gene differential expression analysis for single cell RNA-seq data with superior performance comparing to the state of the art tools.
- Designed a bioinformatic pipeline for COVID-19 severity biomarker identification in BALF cells and implemented classic machine learning classifiers to classify cells based on COVID-19 severity levels. **Paper Code**
- Implemented a comprehensive bioinformatic pipeline for genome profiling of multiple bacterial strains having quality control, alignment, quantification and downstream RNA-seq data analysis steps.

Mayo Clinic

May. 2021 – Aug. 2021

Bioinformatics Scientist Intern

Rochester, MN (Remote)

- Researched on concepts of Connectivity Map (C-map), L1000 database and learning interactions between genes, drugs and diseases.
- Implemented baseline matrix completion algorithms for gene - drug relationship discovery (link prediction), specifically in L1000 database.
- Researched on and implemented Bayesian hierarchical process models to solve gene - drug relationship prediction problem.

Institute for Research in Fundamental Sciences (IPM), School of Cognitive Sciences

May 2017 – Aug. 2017

Research Assistant Intern

Tehran, Iran

- Researched on norm optimization in 2D phase congruency method and its application in image processing specifically medical images like MRI.
- Presented and published the research results in ICEE conference. **Paper**

PUBLICATIONS

- **S Niyakan**, X Qian. COVID-Datathon: Biomarker identification for COVID-19 severity based on BALF scRNA-seq data (2021), Accepted for publication in JBHI. **Preprint**
- **S Niyakan**, E Hajiramezanali, S Boluki, SZ Dadaneh, X Qian. SimCD: Simultaneous Clustering and Differential expression for single-cell transcriptomic data (2021), Under review Bioinformatics. **Preprint**
- L Noorbala, **S Niyakan**, SMM Alavi. Development of Phase Congruency to Estimate the Direction of Maximum Information (tDMI) in Images with Straight Line Segments (2019), ICEE. **Paper**
- SMM Alavi, S Fekriasl, **SN Niyakan**, M Saif. Fault detection and isolation in batteries power electronics and chargers (2019), Journal of Energy Storage. **Paper**

SKILLS

Languages : R, C/C++, Matlab, Bash scripting, Python, HTML

Environments : Linux, MacOS, slurm, High Performance Computing (HPC)

Tools : STAR, HTSeq ,Git, Latex, Microsoft Office

Awards

Won 1st place award in IEEE COVID-19 Single-cell transcriptomics data Hackathon.	2021
Awarded Graduate Research Assistantship Grant from ECEN department of Texas A&M University.	2018
Ranked 54th among +450,000 participants in the national undergraduate university entrance exam.	2013
Recipient of the 5-year grant for undergraduate studies from National Elites Foundation of Iran.	2013 - 2018
Ranked 4th in 3rd Sharif cup open robotics competition (Firefighter & Computer Vision Robots)	2014
Ranked 6th in mathematics section of 12th Khwarizmi festival	2010

Research Projects

SimCD

- Designed a unified Bayesian hierarchical model, allowing simultaneous cell clustering and differential expression analysis for scRNA-seq data.
- Implemented an efficient Gibbs sampling based model inference process.
- Showcased the superior performance of SimCD in terms of both cell clustering and differential expression analysis comparing to other state of the art tools over extensive sets of both real and simulated scRNA-seq data with various properties.

COVID-19 severity biomarker identification based on BALF scRNA-seq data

- Implemented a bioinformatics pipeline to identify some already studied and some novel potential biomarkers for COVID-19 severity.
- Implemented various classic Machine Learning classification algorithms such as Random Forest, SVM and Linear/Quadratic/Flexible Discriminant Analysis to classify BALF cells based on COVID-19 severity
- Presented findings in **IEEE healthcare Summit** conference and won first place award in the conference data hackathon with the proposed pipeline.

lncRNA biomarker identification for diagnosis of bacterial pathogen infections

- Implemented a comprehensive bioinformatics pipeline for genome profiling of multiple bacterial strains including quality control, alignment, quantification and downstream RNA-seq data analysis steps.

Transcriptome profile analysis of melon fruit RNA-seq data during ripening

- Characterized melon fruit samples based on the fruit type or cultivar location using the RNA-seq data.
- Implemented various Ridge/Lasso regression models to learn the interactions between candidate metabolites and genes.

Gene-Drug-Disease relationship discovery

- Implemented matrix completion algorithms for link prediction in gene-drug relationship discovery task.
- Designed Bayesian negative binomial/ beta process models to predict gene-drug associations in L1000 database