

# Nargesr Rezaie

BIOINFORMATICS · DATA ANALYTICS

Irvine, CA, 92617

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## Skills

<b>Programming Languages</b>	Python (NumPy, pandas, SciPy, TensorFlow and PyTorch), R, shinyapps, Matlab, C/C++, Java SQL, HTML, CSS, Django, PHP
<b>Frameworks</b>	Git, Django, Docker, Flask
<b>Software developed by me</b>	lima, minimap2, cellbender, Samtools, RSEM PyWGCNA, Topyfic
<b>Operating Systems</b>	Mac-OS, Linux, Windows

## Research Experience

### Mortazavi Lab, University of California, Irvine

California, USA

GRADUATE STUDENT

Dec 2019 – Present

- My role is developing and applying novel bioinformatic tools and analyses to both bulk and single-cell RNA-seq datasets.
- **Model-AD:** We are part of a NIA Consortium to build better late-onset Alzheimer's Disease models in mouse. Our part includes both bioinformatics as well as single-cell transcriptomics in these new models.
- **IGVF:** We are leveraging mouse genetic diversity to study the impact of genotype on molecular function in a variety of tissues using single-cell resolution.
- **ENCODE4:** We are part of the ENCODE consortium's effort to profile full-length transcriptomes in human and mouse.
- **Gene Regulatory Networks:** We are building models of gene regulatory networks using either bulk or single-cell RNA-seq, and ATAC-seq in human, rodents, and other vertebrates in order to discover how the logic of development is encoded in the genome.

### Swarup Lab, University of California, Irvine

California, USA

LAB ROTATION

Sep 2019 – Dec 2019

- Comparing various methods of doublet detection
- Analyzing single nucleus RNA sequencing (snRNA-seq) data to detect doublet.

### Bioinformatics and Computational Biology(BCB) Lab, Sharif University of Technology

Tehran, Iran

RESEARCH ASSISTANT

May 2016 – Aug 2019

**Statistical Analysis of Clinical Data - Golestan Cohort:** Designing a statistical model to predict risk of cardiovascular disease

## Education

### University of California, Irvine

California, USA

PH.D. DIRECT IN MATHEMATICAL, COMPUTATIONAL AND SYSTEMS BIOLOGY

Sep 2019 – Present

- GPA: 3.979/4.0

### Sharif University of Technology

Tehran, Iran

BACHELOR OF SCIENCE IN INFORMATION TECHNOLOGY IN COMPUTER ENGINEERING

Sep 2014 – Jul 2018

- GPA: 17.07/20

## Publications

- KM Tran, S Kawauchi, EA Kramár, N Rezaie, HY Liang, JS Sakr, A Gomez-Arboledas, MA Arreola, Cd Cunha, J Phan, S Wang, S Collins, A Walker, K Shi, J Neumann, G Filimban, Z Shi, G Milinkeviciute, DI Javonillo, K Tran, M Gantuz, S Forner, V Swarup, AJ Tenner, FM LaFerla, MA Wood, A Mortazavi, GR MacGregor, KN Green. A Trem2R47H mouse model without cryptic splicing drives age- and disease-dependent tissue damage and synaptic loss in response to plaques. *Molecular neurodegeneration* (2023).
- N Rezaie, F Reese, A Mortazavi. PyWGCNA: A Python package for weighted gene co-expression network analysis. *Bioinformatics* (2023).
- M Bayati, N Rezaie and M Hamidi, MS Tahaei, H Rabiee. A New R Package for Categorizing Coding and Non-Coding Genes. Preprints (2023).
- F Reese, B Williams, G Balderrama-Gutierrez, D Wyman, MH Çelik, E Rebboah, N Rezaie, D Trout, M Razavi-Mohseni, Y Jiang, B Borsari, S Morabito, HY Liang, CJ McGill, S Rahmanian, J Sakr, S Jiang, W Zeng, K Carvalho, AK Weimer, LA Dionne, A McShane, K Bedi, SI Elhajjajy, S Upchurch, J Jou, I Youngworth, I Gabdank, P Sud, O Jolanki, JS Strattan, MS Kagda, MP

- Snyder, BC Hitz, JE Moore, Z Weng, D Bennett, L Reinholdt, M Ljungman, MA Beer, MB Gerstein, L Pachter, R Guigó, BJ Wold, A Mortazavi. The ENCODE4 long-read RNA-seq collection reveals distinct classes of transcript structure diversity. *bioRxiv* (2023).
- H Alinejad-Rokny, R Ghavami Modegh, HR Rabiee, E Ramezani Sarbandi, [N Rezaie](#), KT Tam, ARR Forrest. MaxHiC: A robust background correction model to identify biologically relevant chromatin interactions in Hi-C and capture Hi-C experiments. *PLOS Computational Biology* (2022).
  - [N Rezaie](#), M Bayati, M Hamidi, MS Tahaei, S Khorasani, NH Lovell, J Breen, HR Rabiee, H Alinejad-Rokny. Somatic point mutations are enriched in non-coding RNAs with possible regulatory function in breast cancer. *Communications Biology* (2022).
  - DI Javonillo, KM Tran, J Phan, E Hingco, EA Kramár, Cd Cunha, S Forner, S Kawauchi, G Milinkeviciute, A Gomez-Arboledas, J Neumann, CE Banh, M Huynh, DP Matheos, [N Rezaie](#), JA Alcantara, A Mortazavi, MA Wood, AJ Tenner, GR MacGregor, KN Green, FM LaFerla. Systematic phenotyping and characterization of the 3xTg-AD mouse model of Alzheimer's Disease. *Frontiers in neuroscience* (2022).
  - S Forner, S Kawauchi, G Balderrama-Gutierrez, EA Kramár, DP Matheos, J Phan, DI Javonillo, KM Tran, E Hingco, Cd Cunha, [N Rezaie](#), JA Alcantara, D Baglietto-Vargas, C Jansen, J Neumann, MA Wood, GR MacGregor, A Mortazavi, AJ Tenner, FM LaFerla, KN Green. Systematic phenotyping and characterization of the 5xFAD mouse model of Alzheimer's disease. *Scientific data* (2021).
  - G Balderrama-Gutierrez, H Liang, [N Rezaie](#), K Carvalho, S Forner, D Matheos, E Rebboah, KN Green, AJ Tenner, F LaFerla, A Mortazavi. Single-cell and nucleus RNA-seq in a mouse model of AD reveal activation of distinct glial subpopulations in the presence of plaques and tangles. *bioRxiv* (2021).

## Presentation

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Identifying regulatory topics in the IGVF mouse bridge samples using Topyfic <a href="#">N REZAIE</a> , E REBBOAH, D TROUT, HY LIANG, G FILIMBAN, S BOESHAGHI, D SULLIVAN, M CARILLI, P MAHDIPOOR, R WEBER, J SAKR, F REESE, B WILLIAMS, I HALLGRIMSDOTTIR, S KAWAUCHI, K GREEN, G MCGREGOR, L PACTER, BJ WOLD, A MORTAZAVI	<i>Poster</i> <i>IGVF Consortium Meeting 2023</i>
Identifying robust cellular programs using reproducible latent Dirichlet allocation (LDA) with Topyfic <a href="#">N REZAIE</a> , E REBBOAH, A MORTAZAVI	<i>Invited speaker and Poster</i> <i>IGVF Consortium Meeting 2022</i>
Topyfic identified robust cellular programs using reproducible Latent Dirichlet allocation (rLDA) <a href="#">N REZAIE</a> , E REBBOAH, A MORTAZAVI	<i>Poster</i> <i>Network Biology 2023 (CHSL)</i>
Topyfic identified robust cellular programs using reproducible Latent Dirichlet allocation (rLDA) <a href="#">N REZAIE</a> , E REBBOAH, A MORTAZAVI	<i>Poster</i> <i>Probabilistic Modeling in Genomics 2023 (CHSL)</i>
Topyfic: Reproducible latent dirichlet allocation (LDA) for single cell epigenomics data <a href="#">N REZAIE</a> , E REBBOAH, A MORTAZAVI	<i>Invited speaker</i> <i>UCI GenPALS 2023</i>
Bulk and single-cell gene expression network analysis in mouse models of AD using PyWGCNA <a href="#">N REZAIE</a> , MODEL-AD, A MORTAZAVI	<i>Poster</i> <i>Alzheimer's &amp; Dementia 2022 (AAIC)</i>
Phenotypic characterization of UCI MODEL-AD mice using RNA-seq M GANTUZ, HY LIANG, <a href="#">N REZAIE</a> , MODEL-AD, A MORTAZAVI	<i>Poster</i> <i>Alzheimer's &amp; Dementia 2022 (AAIC)</i>
Trem2 R47H NSS; 5xFAD mice display age/disease progression-dependent changes in plaques and plaque-associated microglia, and increased plasma neurofilament light chain KM TRAN, S KAWAUCHI, DI JAVONILLO, CD CUNHA, J PHAN, <a href="#">N REZAIE</a> , HY LIANG, G MILINKEVICIUTE, A GOMEZ-ARBOLEDAS, S FORNER, A MORTAZAVI, AJ TENNER, F LA FERLA, GR MACGREGOR, KN GREEN	<i>Poster</i> <i>Alzheimer's &amp; Dementia 2022 (AAIC)</i>
PyWGCNA: A Python package for weighted gene co-expression network analysis <a href="#">N REZAIE</a>	<i>Invited speaker</i> <i>UCI Systems Biology RIP talk</i>
The MODEL-AD Explorer: An open-access resource for comparing phenotypic data from mouse models of Alzheimer's disease A GREENWOOD, S GELFAND, R PANDEY, <a href="#">N REZAIE</a> , AL OBLAK, S FORNER, A UYAR, J MINCER, M FAZZA, MA PETERS, R YAXLEY, AV LINDEN, J SCHNEIDER, A MORTAZAVI, L MANGRAVITE, F LA FERLA, A TENNER, B LAMB, KN GREEN, G CARTER	<i>Poster</i> <i>Alzheimer's &amp; Dementia 2021 (AAIC)</i>
Bulk and single-nucleus analysis of the 3xTgAD cortex and hippocampus transcriptome <a href="#">N REZAIE</a> , G BALDERRAMA-GUTIERREZ, HY LIANG, S FORNER, A MORTAZAVI, MODEL AD.	<i>Poster</i> <i>Alzheimer's &amp; Dementia 2021 (AAIC)</i>

Identification and characterization of UCI MODEL-AD mouse models using single-cell and single-nucleus Split-seq.

HY LIANG, M GANTUZ, N REZAIE, G BALDERRAMA GUTIERREZ, A MORTAZAVI, MODEL AD.

*Poster*

*Neuroscience 2021 (SFN)*

MODEL-AD, Ali Mortazavi. Analyzing gene expression during neurodegeneration in a 3xTgAD mouse model at transcriptome level.

N REZAIE, G BALDERRAMA- GUTIERREZ, H LIANG, MODEL-AD, A MORTAZAVI

*Poster*

*Neuroscience 2021 (SFN)*

Bulk and single-nucleus analysis of the 3xTG cortex and hippocampus transcriptome

N REZAIE, G. BALDERRAMA-GUTIERREZ, H. LIANG, C. MCGILL, A. MORTAZAVI, MODEL-AD

*Poster*

*Neuroscience 2020 (SFN)*