

Narges Rezaie

Bioinformatics, Data Analytics, Computational Biologist

☎ (949)426-8112 nargesr@uci.edu 🏠 [Personal website](#) [in narges-rezaie](#) [nargesr](#) [Google Scholar](#)

Summary

Innovative Postdoctoral Scholar specializing in bioinformatics and computational biology with a PhD. in Mathematical, Computational, and Systems Biology from UC Irvine. Over 6 years of experience developing, optimizing, and testing existing and new analysis methods and bioinformatics pipelines to analyze biomedical data such as genomic, clinical, and sequencing(NGS). Proficient in multiple programming languages, machine learning, and statistics.

Research Experience

Postdoctoral fellow *Mortazavi Lab, University of California, Irvine* **CA, USA** March 2024 – Present

- Developing/applying/optimizing novel bioinformatic tools to analyze NGS datasets including short and long read RNA-seq at bulk, single-cell resolution, and Multiome

Graduate Researcher *Mortazavi Lab, University of California, Irvine* **CA, USA** Sept 2019 – March 2024

- **Model-AD:** Analyse various Genomics data (bulk, single-cell, single-nucleus) to characterize the next generation of animal models for Alzheimer's disease and provide predictive models for the development of therapeutics. Identify gene and transcript expression changes that are found in the model-AD mice as compared to wild-type mice as well as human Alzheimer's disease patients. Implement standardized data acquisition to Synapse.
- **IGVF:** Understanding how genomic variation affects genome function and phenotype in various tissues using single-cell resolution.
- **ENCODE4:** Integrate, and interpret Single-cell omics data to profile full-length transcriptomes in humans and mice.
- **Gene Regulatory Networks:** Building models of gene regulatory networks using either bulk or single-cell RNA-seq, and ATAC-seq in humans, rodents, and other vertebrates to discover how the logic of development is encoded in the genome.
- Working with experimental scientists to understand and support their research goals.
- Educated undergraduate students on programming languages and bioinformatics pipeline.

Lab Rotation *Swarup Lab, University of California, Irvine* **CA, USA** Sep 2019 – Dec 2019

- Benchmarking doublet detection methods on single-nucleus RNA sequencing (snRNA-seq).

Research Assistant *Sharif University of Technology* **Tehran, Iran** May 2016 – Aug 2019

- **Statistical Analysis of Clinical Data - Golestan Cohort:** Designing a statistical model to predict the risk of cardiovascular disease using the Golestan Cohort Study, which evaluates the environmental and genetic risk factors for esophageal squamous cell carcinoma (ESCC) in Golestan Province, Iran, and includes approximately 50,000 adults aged 40-75 years.

Education

PhD in Mathematical, Computational, and Systems Biology *University of California, Irvine* **USA** 2019–2024

- **Thesis:** Computational approach to characterize gene dynamics using bulk and single-nucleus RNA sequencing to study Alzheimer's disease. **Supervisor:** Dr. Ali Mortazavi. **GPA:** 3.98/4.0

B.S. in Information Technology in Computer Engineering *Sharif University of Technology* **Iran** 2014–2018

Skills

- **Developed by me:** PyWGCNA and Topyfic
- **Programming Languages:** Python (Matplotlib, seaborn, NumPy, pandas, SciPy, Anndata, scikit-learn, TensorFlow, and PyTorch), R, shinyapps, Bash, Matlab, C/C++, Java, SQL, HTML, CSS, and PHP
- **Softwares:** BLAST, Lima, Minimap2, Cellbender, Samtools, bedtools, Picard, RSEM, Seurat, Scanpy, and Kallisto
- **Pipeline management:** NextFlow and Snakemake
- **Assays:** Single-cell/nucleus RNA-seq, Multi-omics, Pertub-seq, Bulk long-read RNA-seq, Bulk short-read RNA-seq, and Hi-C
- **Frameworks:** AWS, SLURM, Git, Django, Docker, and Flask

Publications

- **N Rezaie**, ..., B Wold, A Mortazavi. Identification of robust cellular programs using reproducible LDA that impact sex-specific disease progression in different genotypes of a mouse model of AD. *bioRxiv* (2024)
- **N Rezaie**, F Reese, A Mortazavi. PyWGCNA: A Python package for weighted gene co-expression network analysis. *Bioinformatics* (2023)
- **N Rezaie**, ..., H Alinejad-Rokny. Somatic point mutations are enriched in non-coding RNAs with possible regulatory function in breast cancer. *Communications Biology* (2022)
- M Bayati*, **N Rezaie*** and M Hamidi, MS Tahaei, H Rabiee. A New R Package for Categorizing Coding and Non-Coding Genes. *Preprints* (2023)
- E Rebboah, **N Rezaie**, ..., B Wold, A Mortazavi. The ENCODE mouse postnatal developmental time course identifies regulatory programs of cell types and cell states. *bioRxiv* (2024)
- LF Garcia-Agudo, ..., **N Rezaie**, ..., GR MacGregor, KN Green. BIN1^{K358R} suppresses glial response to plaques in mouse model of Alzheimer's disease. *Alzheimer's & Dementia* (2024)
- CA Butler, ..., **N Rezaie**, ..., GR MacGregor, KN Green. The Abca7^{V1613M} variant reduces A β generation, plaque load, and neuronal damage Alzheimer's & Dementia (2024)
- F Reese, ..., **N Rezaie**, ..., BJ Wold, A Mortazavi. The ENCODE4 long-read RNA-seq collection reveals distinct classes of transcript structure diversity. *bioRxiv* (2023)
- KM Tran, ..., **N Rezaie**, ..., GR MacGregor, KN Green. A Trem2^{R47H} mouse model without cryptic splicing drives age-and disease-dependent tissue damage and synaptic loss in response to plaques. *Molecular neurodegeneration* (2023)
- H Alinejad-Rokny, ..., **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**, ..., H Alinejad-Rokny. Somatic point mutations are enriched in non-coding RNAs with possible regulatory function in breast cancer. *Communications Biology* (2022)
- DI Javonillo, ..., **N Rezaie**, ..., KN Green, FM LaFerla. Systematic phenotyping and characterization of the 3xTg-AD mouse model of Alzheimer's Disease. *Frontiers in neuroscience* (2022)
- S Forner, ..., **N Rezaie**, ..., 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**, ..., 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)

Selected Talks and Posters

- 2023 Alzheimer's and Brain Awareness Month, PARSE biosciences. *Invite speaker*
Identifying Distinct Cellular Programs from Single Cell Datasets Using Topyfic.
- *Topyfic identified robust cellular programs using reproducible Latent Dirichlet allocation (rLDA)*. Poster (Network Biology 2023 (CHSL)) and (Probabilistic Modeling in Genomics 2023 (CHSL))
- *Bulk and single-cell gene expression network analysis in mouse models of AD using PyWGCNA*. Poster (Alzheimer's & Dementia 2022 (AAIC))
- The MODEL-AD Explorer: An open-access resource for comparing phenotypic data from mouse models of Alzheimer's disease. *Poster* (Alzheimer's & Dementia 2021 (AAIC))
- Analyzing gene expression during neurodegeneration in a 3xTgAD mouse model at transcriptome level. *Poster* (Neuroscience 2021 (SFN))

References

Available upon request.