Narges Rezaie

Bioinformatics, Data Analytics, Computational Biologist

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Summary

Innovative Postdoctoral Scholar specializing in bioinformatics and computational biology with a Ph.D. in Mathematical, Computational, and Systems Biology from UC Irvine. Over 6 years of experience developing bioinformatics tools and automated pipelines for biomedical data analysis. Proficient in multiple programming languages and machine learning.

Research Experience

Postdoctoral fellow *Mortazavi Lab, University of California, Irvine* **CA, USA** *March 2024 – Present*
- Developing/applying novel bioinformatic tools to analyze short and long read RNA-seq at bulk and single-cell resolution

Graduate student *Mortazavi Lab, University of California, Irvine* **CA, USA** *Dec 2019 – March 2024*
- Developing and applying novel bioinformatic tools to analyse bulk and single-cell RNA-seq datasets.

- **Model-AD**: We are part of an NIA Consortium to build better late-onset Alzheimer's Disease models in mice. I am mainly involved in analyzing/validating these new models as well as implementing standardized data acquisition and data analysis protocols for these mouse models of Alzheimer's disease

- **IGVF**: We are leveraging mouse genetic diversity to study the impact of genotype on molecular function in various tissues using single-cell resolution.

- **ENCODE4**: We are part of the ENCODE consortium's effort to profile full-length transcriptomes in humans and mice.

- **Gene Regulatory Networks**: We are 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.

Lab Rotation *Swarup Lab, University of California, Irvine* **CA, USA** *Sep 2019 – Dec 2019*
- Comparing various methods of doublet detection

- Analyzing single nucleus RNA sequencing (snRNA-seq) data to detect doublet.

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 risk of cardiovascular disease

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

- **Programming Languages:** Python (Matplotlib, seaborn, NumPy, pandas, SciPy, Anndata, scikit-learn, TensorFlow, and PyTorch), R, shinyapps, jupyter notebook, Bash, Matlab, C/C++, Java, SQL, HTML, CSS, Django, and PHP

- **Softwares:** Blast, Lima, Minimap2, Cellbender, Samtools, bedtools, Picard, RSEM, Seurat, Scanpy, and Kallisto

- **Developed by me:** PyWGCNA and Topyfic

- **Pipeline managements:** 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:** Git, Django, Docker, and Flask

Publications

- 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)

- **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)

- 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 $A\beta$ 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)

- **N Rezaie**, F Reese, A Mortazavi. PyWGCNA: A Python package for weighted gene co-expression network analysis. Bioinformatics (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)

- M Bayati, **N Rezaie** and M Hamidi, MS Tahaei, H Rabiee. A New R Package for Categorizing Coding and Non-Coding Genes. Preprints (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

- *Identifying Distinct Cellular Programs from Single Cell Datasets Using Topyfic*
  N Rezaie (2023 Alzheimer's and Brain Awareness Month, PARSE biosciences)

- *Topyfic identified robust cellular programs using reproducible Latent Dirichlet allocation (rLDA).*
  N Rezaie, E Rebboah, A Mortazavi (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.*
  N Rezaie, MODEL-AD, A Mortazavi (Alzheimer's & Dementia 2022 (AAIC))

- The MODEL-AD Explorer: An open-access resource for comparing phenotypic data from mouse models of Alzheimer's disease.
  A Greenwood, ..., **N Rezaie**, ..., G Carter. (Alzheimer's & Dementia 2021 (AAIC))

- Analyzing gene expression during neurodegeneration in a 3xTgAD mouse model at transcriptome level.
  N Rezaie, ..., A Mortazavi. (Neuroscience 2021 (SFN))

References

Available upon request.