

# Narges Rezaie

BIOINFORMATICS

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## Education

### University of California, Irvine

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

• GPA: 3.968/4.0

California, USA

Sep 2019 – Present

### Sharif University of Technology

BACHELOR OF SCIENCE IN INFORMATION TECHNOLOGY IN COMPUTER ENGINEERING

• GPA: 17.07/20

Tehran, Iran

Sep 2014 – Jul 2018

## Skills

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

## Publications

1. Alinejad-Rokny, H., Modegh, R. G., Rabiee, H. R., Sarbandi, E. R., Rezaie, N., Tam, K. T., & Forrest, A. R. (2022). Maxhic: A robust background correction model to identify biologically relevant chromatin interactions in hi-c and capture hi-c experiments. *PLOS Computational Biology*, 18(6), e1010241.
2. Rezaie, N., Bayati, M., Hamidi, M., Tahaei, M. S., Khorasani, S., Lovell, N. H., ... Alinejad-Rokny, H. (2022). Somatic point mutations are enriched in non-coding rnas with possible regulatory function in breast cancer. *Communications Biology*, 5(1), 1–13.
3. Rezaie, N., Reese, F., & Mortazavi, A. (2022). Pywgcna: A python package for weighted gene co-expression network analysis. *bioRxiv*.
4. Tran, K. M., Kawauchi, S., Kramár, E. A., Rezaie, N., Liang, H. Y., Arreola, M., ... others (2022). A trem2\* r47h mouse model without cryptic splicing drives age-and disease-dependent tissue damage and synaptic loss in response to plaques. *bioRxiv*.
5. Javonillo, D. I., Tran, K. M., Phan, J., Hingco, E., Kramár, E. A., Da Cunha, C., ... others (2022). Systematic phenotyping and characterization of the 3xtg-ad mouse model of alzheimer's disease. *Frontiers in neuroscience*, 1829.

6. Rezaie, N., Gutierrez, G. B., Liang, H. Y., Forner, S., Mortazavi, A., & AD, M. (2021). Bulk and single-nucleus analysis of the 3xtgad cortex and hippocampus transcriptome. *Alzheimer's & Dementia*, 17, e056475.
7. Forner, S., Kawauchi, S., Balderrama-Gutierrez, G., Kramár, E. A., Matheos, D. P., Phan, J., ... others (2021). Systematic phenotyping and characterization of the 5xfad mouse model of alzheimer's disease. *Scientific data*, 8(1), 1–16.
8. Balderrama-Gutierrez, G., Liang, H., Rezaie, N., Carvalho, K., Forner, S., Matheos, D., ... others (2021). 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*.
9. Alinejad-Rokny, H., Ghavami, R., Rabiee, H. R., Rezaei, N., Tam, K. T., & Forrest, A. R. (2020). Maxhic: robust estimation of chromatin interaction frequency in hi-c and capture hi-c experiments. *bioRxiv*.

## Posters

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**Narges Rezaie**, Ali Mortazavi. Bulk and single-cell gene expression network analysis in mouse models of AD using PyWGCNA. Poster presented at: Alzheimer's & Dementia 2022 (AAIC).

**Heidi Y. Liang**, Magdalena Gantuz, Narges Rezaie, MODEL-AD Consortium, Ali Mortazavi. Phenotypic characterization of UCI MODEL-AD mice using RNA-seq. Poster presented at: Alzheimer's & Dementia 2022 (AAIC).

**Narges Rezaie**, Gabriela Balderrama- Gutierrez, Heidi Liang, MODEL-AD, Ali Mortazavi. Analyzing gene expression during neurodegeneration in a 3xTgAD mouse model at transcriptome level. Poster presented at: Neuroscience 2021 (SFN).

**Narges Rezaie**, Gabriela Balderrama Gutierrez, Heidi Yahan Liang, Stefania Forner, Ali Mortazavi, MODEL AD. Bulk and single-nucleus analysis of the 3xTgAD cortex and hippocampus transcriptome. Poster presented at: Neuroscience 2021 (SFN).

**Heidi Yahan Liang**, Magdalena Gantuz, Narges Rezaie, Gabriela Balderrama Gutierrez, Ali Mortazavi, MODEL AD. Identification and characterization of UCI MODEL-AD mouse models using single-cell and single-nucleus Split-seq. Poster presented at: Neuroscience 2021 (SFN).

**Magdalena Gantuz**, Heidi Yahan Liang, Narges Rezaie, Gabriela Balderrama Gutierrez, Ali Mortazavi, MODEL AD. Phenotypic characterization of UCI MODEL-AD mice using RNA-seq. Poster presented at: Neuroscience 2021 (SFN).

**K. M. TRAN**, S. KAWAUCHI, S. FORNER<sup>1</sup>, D. JAVONILLO<sup>1</sup>, C. DA CUNDA<sup>1</sup>, J. PHAN<sup>1</sup>, K. TRAN<sup>1</sup>, N. REZAIIE, H. LIANG<sup>1</sup>, A. MORTAZAVI, A. TENNER<sup>1</sup>, F. LA FERLA, G. MACGREGOR, K. GREEN. TREM2R47Hem1Aduci; 5xFAD mice display sex-specific differences in plaques and plaque-associated microglia. Poster presented at: Alzheimer's & Dementia 2021 (AAIC).

**A. GREENWOOD**, S. GELFAND, R. PANDEY, N. REZAIIE, A. L. OBLAK, S. FORNER, A. UYAR, J. MINCER<sup>5</sup>, M. FAZZA, M. A. PETERS, R. YAXLEY, A. VANDER LINDEN, J. SCHNEIDER, A. MORTAZAVI, L. MANGRAVITE, F. LA FERLA, A. TENNER, B. LAMB, K. N. GREEN, G. CARTER. The MODEL-AD Explorer: An open access resource for comparing phenotypic data from mouse models of Alzheimer's disease. Poster presented at: Alzheimer's & Dementia 2021 (AAIC).

**N. Rezaie**, G. Balderrama-gutierrez, H. Liang, C. McGill, A. Mortazavi, MODEL-AD. Bulk and single-nucleus analysis of the 3xTG cortex and hippocampus transcriptome. Poster presented at: Neuroscience 2020 (SFN); August 2020.

## Experience

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### Mortazavi Lab, University of California, Irvine

California, USA

RESEARCH ASSISTANT

Dec 2019 – Present

- **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.
- **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