Ehsan Ramezani Sarbandi

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Research Objective

Biological systems represent the most information-dense architectures known: a single human cell's genome encodes over three billion base pairs—vastly surpassing the storage capacity of any conventional data medium. Understanding these highly nonlinear, high-dimensional systems in disease contexts is essential for improving health span and quality of life, yet traditional statistical methods often fall short of capturing their full complexity. Recent advances in artificial intelligence and machine learning offer unprecedented power to model these data, but meaningful progress demands the rare fusion of computational rigour with biological insight. As a computer scientist with industry-honed expertise and a fascination with living systems, I adopt an "AI-first" mindset to design end-to-end pipelines that are both computationally robust and biologically validated. Leveraging proficiency in multiple programming languages, reproducible workflows, and systems-level thinking, my goal is to translate complex omics and spatial datasets into actionable biomarkers and therapeutic strategies.

Core AI & Methodological Skills

- Deep Learning & AI: scVI, scANVI, TensorFlow, PyTorch, CNN architectures
- Spatial Transcriptomics: Scanpy, Squidpy, 10× Visium data analysis
- Statistical & Computational: Limma, EdgeR, Bayesian modelling, graph neural networks
- Programming & Data: Python (pandas, NumPy, scikit-learn), R (Bioconductor), SQL
- Visualization: Matplotlib, Seaborn, Plotly, ggplot2
- Reproducible Workflows: Git, Docker, Nextflow, Snakemake

Professional Experience

- **Data Scientist** | *Idekavan Group, Tehran, Iran | Mar 2023 – Feb 2024*

    - Engineered ML pipelines for fraud detection on billions of records
    - Built automated NSFW classification using CNNs

- **Hardware Product Owner** | *FANAM Co, Tehran, Iran | Jan 2019 – Mar 2023*

    - Led IoT attendance system deployment integrating hardware and analytics
    - Managed cross-functional team of 5 to deliver scalable educational solutions

Research Experience

- **PhD Candidate, Bioinformatics and Computational Biology Division, WEHI** | *Walter and Eliza Hall Institute of Medical Research | Mar 2024 – Present*

    - Conducting AI-driven bioinformatics research in spatial and multimodal transcriptomics
    - Developing novel machine learning pipelines for rare cell type identification and batch correction
    - Collaborating with clinical and laboratory teams to translate computational insights into biological hypotheses

- **Biomedical Data Science Researcher** | *UNSW Biomedical ML Lab, Sydney, Australia | Jul 2020 – Dec 2023*

  - Developed AI-based integration methods for single-cell and spatial transcriptomics
  - Co-authored PLOS Comput. Biol. publication on MaxHiC

- **Visiting Fellow, AI-Enabled Processes Centre** | *Macquarie University | Mar 2021 – Mar 2022*

  - Researched AI-enabled biomedical workflows and presented interdisciplinary findings

Key AI Projects

- MaxHiC: Deep learning model for chromatin interaction signal correction, improving SNR by 40%
- Cortical Layer Annotation: CNN-based pipeline on 10× Visium achieving >95% accuracy and F1-score >72%
- Automated Dyslamination Mapping: A first-of-its-kind transfer-learning pipeline mapping FCD dyslamination regions in human and mouse tissues
- Leveraging state-of-the-art AI to integrate 30 single-cell datasets, remove batch effects, and characterise disease contexts at atlas scale

Select Publications

1. DECODCNV: A Deep Convolutional Autoencoder implicating the immune system in neurodevelopmental disorders · Manuscript in preparation (2025)
2. Peeling Back the Layers: Automating Brain Layering Annotation in Spatial Transcriptomics Using AI · Poster, Oz Single Cell 2025 (Sydney, NSW) · May 21, 2025
3. AI-Driven Spatial Transcriptomics Characterises Dyslamination in Focal Cortical Dysplasia · Oral Presentation, Translational Neurogenetics Mini-Retreat · Feb 12, 2025
4. Deep Convolutional Network for Cortical Layer Prediction from 10× Visium Spatial Transcriptomics · Poster, AMSI BioInfoSummer 2024 (University of Melbourne) · Dec 3, 2024
5. MaxHiC: A robust background correction model to identify biologically relevant chromatin interactions in Hi-C and capture Hi-C · PLOS Computational Biology · Jun 24, 2022
6. Neural Spike Compression Based on Random Sampling and IMATI Techniques · IEEE ICEE 2018 (Oral) · May 2018
7. Neural Spike Sorting with Neural Networks Without Feature Extraction · 2nd National Conference on Electrical & Computer Engineering · 2018

Honors & Awards

- People's Choice Winner, WEHI 3MT Competition · Jun 2025
- Runner-Up, WEHI 3MT Competition · Jun 2025
- WEHI prestigious International PhD Scholar Initiative (IPSI) Scholarship · Jan 2023

Education

Degree	Institution	Period	GPA & Honours
PhD Candidate	WEHI & University of Melbourne	Mar 2024 – Present	WEHI prestigious International PhD Scholar Initiative (IPSI) Scholarship
MSc Computer Hardware Engineering	K.N. Toosi University of Technology	2014 – 2016	18.25/20, Ranked 1st; Bypassed entrance exam
BSc Computer Engineering	Shahid Bahonar University	2010 – 2013	17.26/20, Ranked 1st