Maral Maghsoudi (Zeynab)

PhD Candidate in CS | Reno, Nevada (Open to Relocation or Remote, Open to Internship)
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PROFILE SUMMARY

Computational biologist and data science researcher with extensive experience in machine learning, statistical modeling, and high-dimensional data analysis, specializing in multi-omics integration and NGS data. Proficient in R, with a strong foundation in data-driven research and biological signal extraction. Skilled in building scalable pipelines for data preprocessing, predictive modeling, and pathway analysis across diverse omics layers. Co-author of peer-reviewed publications on computational methods in biomedical research, with demonstrated expertise in translating complex biological data into actionable insights.

EDUCATION

PhD in Computer Science, University of Nevada, Reno, GPA: 3.8/4.0 — Feb 2021 – Current
– Exploration of Single/Multi-Omics Data Integration for Systems-Level Understanding.

MSc in Software Engineering, Iran University of Science and Technology, Iran, GPA: 4.0/4.0 — Sep 2014 – Apr 2017
– A New Approach to Malware Detection and Classification based on the Combination of Static Structure and Dynamic Behavior.

BSc in Software Engineering, University of Arak, Iran, GPA: 3.4/4.0 — Jan 2009 – Feb 2013
– Investigating of Attacks in Computer Networks.

SELECTED COMPUTER SKILLS

Languages:	R, Python, C++, C#, JavaScript
Bioinformatics / Statistical Analysis:	Bioconductor, DESeq2, edgeR, limma, ggplot2, WA, GATK, Samtools, Picard
Data Manipulation:	dplyr, tidyr, data.table, Numpy, Pandas, Matplotlib, Seaborn
Machine Learning:	TensorFlow, PyTorch, scikit-learn, *(Academic Experience)* Weka, Rapid Miner
Databases:	SQL Server, MySQL
Mobile Programming:	Android SDK, XML, Gradle, JSON
Software:	RStudio, Microsoft Visual Studio, VMWare, Android Studio, PyCharm, Jupyter Notebook
Version Control / Collaboration:	Git, GitHub, GitLab, Overleaf
HPC / Cloud:	AWS (S3, EC2)
Soft Skills:	Analytical Thinking, Problem Solving, Teamwork, Communication, Time Management

WORK EXPERIENCE

Data Scientist & Bioinformatics Research Assistant | University of Nevada, Reno – Nevada, Reno — Feb 2021 – Current

- Co-led development of the R package **RCPA**, enabling reproducible and scalable consensus pathway analysis workflows.
- Automated differential expression analysis for microarray/RNA-Seq with GEO support for 1,000+ species.
- Led pathway meta-analysis with **NASA GeneLab**, revealing mitochondrial dysfunction signatures across spaceflight datasets.
- Developed a personalized multi-omics pathway method using sequential NMF, improving tumor detection in TCGA breast cancer data up to 5%.
- Built an **NGS variant calling** pipeline for SARS-CoV-2 at **Renown Hospital**, ensuring accurate, reproducible mutation detection.
- Applied ResNet50/VGG-16 with BEMD for MRI-based breast mass classification, enhancing diagnostic model performance.

Teaching Assistant | University of Nevada, Reno – Nevada, Reno — Feb 2021 – Current

- Mentored students in mitochondria-centered pathway analysis in collaboration with **Purdue University Biomedical Engineering Department**.
- Teaching assistant for *Embedded System Design Lab* for 3 years, managing and mentoring around 60 students each semester, designing lab assignments, and assisting in project-based learning.

C++ Developer | R&D Team Member | AmnPardaz – Tehran, Iran — Jan 2019 – Mar 2019

- Researched and evaluated security solutions for antivirus tools.
- Designed, built, and maintained reliable and efficient C++ code.
- Collaborated with the software development team and provided technical feedback.

C# Developer | GoldIran (Representative of LG Products in Iran) – Tehran, Iran — Jan 2018 - Dec 2018

- Collaborated on programming the PDA to determine warehouse keeper's tasks.
- Implemented the Warehouse Handling project to automate inventory checks.
- Collaborated on the Sales project to automate the process of taking customer purchase orders and handling further steps.
- Implemented the Soroush project to link all subsystems automatically through an automated workflow.

Malware Analysis Researcher | Iran University of Science and Technology – Tehran, Iran — Sep 2014 - Apr 2017

- Developed a hybrid malware detection pipeline using C# programming for static/dynamic analysis and machine learning.
- Built static analysis module to extract control flow features from system calls.

- Applied dynamic analysis using `Pin` and `Cuckoo Sandbox` for behavioral profiling.
- Enhanced malware detection performance by 7% via anti-analysis detection techniques.

SELECTED PROJECTS

University of Nevada, Reno, Research Assistant in Computer Science Feb 2021 – Current

Imputation for Single-Cell RNA-seq Data – *Ongoing*

- Designing a novel imputation framework tailored to the sparsity and noise in scRNA-seq data.
- Leveraging cell similarity networks and gene co-expression patterns to enhance recovery of dropout values.
- Evaluating the method across multiple publicly available scRNA-seq datasets to assess accuracy, biological relevance, and scalability.

RCPA R Package Development

- Implemented functions for downloading and processing data from `NCBI GEO`, supporting over 1000 species.
- Developed differential analysis modules for both microarray (Affymetrix, Agilent) and RNA-Seq data.
- Integrated multiple pathway analysis techniques, including gene set enrichment and topology-based pathway analysis, supporting diverse research hypotheses.
- Implemented data integration and visualization features, enabling users to combine and compare results from different methods and datasets.

Space Mitochondria Analysis – *In Collaboration with NASA GeneLab Group*

- Prepared scripts to access RNA-seq data for mouse, worm, fly, and plant species from the GeneLab API.
- Applied gene set analysis using the `fgsea` package to identify enriched pathways across multiple species and tissue types.
- Conducted meta-analysis based on strain and tissue-specific data, integrating results to identify consistent pathways across biological conditions.
- Identified tissue-specific mitochondrial gene expression changes under different spaceflight conditions through gene- and pathway-level analysis.

Personalized Multi-Omics Pathway Analysis

- Developed a novel gene weight computation strategy using sequential `Non-Negative Matrix Factorization (NMF)`.
- Integrated mRNA, methylation, and CNV data to reveal personalized molecular signatures and pathway activity profiles.
- Conducted validation studies using both simulation tests and the real-world `TCGA breast cancer` dataset.
- Achieved performance improvements ranging from 2.43% to 5.51%.

SARS-CoV-2 Variant Calling Pipeline – *Renown Hospital, Reno*

- Developed a pipeline for SARS-CoV-2 variant detection using high-throughput sequencing data.
- Implemented sequence alignment with `BWA` and pre-processing steps including sorting, deduplication, and base quality recalibration using `Samtools`, `Picard`, and `GATK`.
- Performed variant calling with `GATK HaplotypeCaller` and applied quality filtering to obtain high-confidence SNP and Indel variants.
- Optimized pipeline efficiency for large-scale sequencing data processing, ensuring reproducibility and accuracy in variant identification.

Malignant Mass Classification in Breast MRI Images

- Applied image pre-processing techniques, including `CLAHE` enhancement, aspect ratio consideration, and resizing for mammogram ROI images from the `CBIS-DDSM` dataset, sourced from the `Cancer Imaging Archive (TCIA)`.
- Employed `BEMD` algorithm to extract `BIMFs` from mammogram ROI images, enhancing the detection of subtle patterns in mass images.
- Implemented deep learning models, including `ResNet50` and `VGG-16` architectures, to assess the effectiveness of BIMF-generated features in mass detection, utilizing advanced data augmentation techniques to enhance model performance.

PUBLICATIONS

- **1st Author, Oct 2022**. *A comprehensive survey of the approaches for pathway analysis using multi-omics data integration*. https://doi.org/10.1093/bib/bbac435

- **2nd Author, May 2024**. *RCPA: An Open-Source R Package for Data Processing, Differential Analysis, Consensus Pathway Analysis, and Visualization*. https://doi.org/10.1002/cpz1.1036

- **1st Author, Aug 2024**. *Text Mining Landscape in Bioinformatics: An In-Depth Analysis of Tasks and Techniques* — Under Review

- **1st Author, Nov 2024**. *A Patient-Specific Multi-Omics Pathway Analysis Method Using Hierarchical NNMF for Improved Gene Weighting* — Under Review

- **1st Author, Jan 2025**. *Guardians of the Mitochondria: Space Mitochondria 2.0 Systemic Analysis Reveals Bioenergetic Dysregulation Across Species*. http://dx.doi.org/10.2139/ssrn.5087025