

Maral (Zeynab) Maghsoudi

Computational Scientist | Machine Learning for Drug Discovery, Biomarkers & Multi-Omics

PhD in Computer Science (2026) | Authorized to Work in the U.S. Without Sponsorship | Open to Relocation or Remote | (775) 378-6977 | [linkedin.com/in/maral-maghsoudi/](https://www.linkedin.com/in/maral-maghsoudi/) | zmaghsoudi.unr@gmail.com | <https://maralmaghsoudi.com>

PROFILE SUMMARY

Computational scientist and PhD candidate applying machine learning and statistical modeling to large-scale proteomics and multi-omics data, with direct pharma industry experience (Johnson & Johnson Innovative Medicine) building predictive models for biomarker discovery, patient stratification, and therapeutic target prioritization. Combines strong software engineering fundamentals with deep expertise in high-dimensional biomedical data, interpretable ML, and reproducible pipeline design, with peer-reviewed publications in computational biology and multi-omics.

CORE SKILLS

Programming & Frameworks: R, Python, TensorFlow, PyTorch, Keras, scikit-learn, NumPy, Pandas, Matplotlib, Seaborn, Bioconductor

Machine Learning & Modeling: XGBoost, LightGBM, CNNs (ResNet, VGG), Autoencoders, Unsupervised Learning (PCA, NMF, Clustering), Transformers (BERT/HuggingFace), Ensemble Methods, Hyperparameter Tuning, SHAP Interpretability

Computational Biology & Bioinformatics: Proteomics, Multi-Omics Integration, scRNA-seq, NGS, Differential Expression Analysis, Pathway Analysis, Gene Set Enrichment, Biomarker Discovery, Patient Stratification

Bioinformatics Tools: DESeq2, edgeR, limma, fgsea, GATK, BWA, Samtools, Picard

Data Engineering / Databases: SQL Server, MySQL, Reproducible Pipelines, Large-scale Data Preprocessing

HPC / Cloud & Engineering: AWS (S3, EC2), GPU Acceleration (CUDA, Colab Pro), Git/GitHub/GitLab

AI Agents / Agentic Systems: Agentic architectures, MCP tool integration, context & memory engineering (short-term/long-term), agent evaluation (logging, tracing, metrics), multi-agent deployment using A2A

WORK EXPERIENCE

Data Science Intern – Population Analytics & Insights (DDSAI), Johnson & Johnson Innovative Medicine (J&J). (May 2026 – Aug 2026)

- **Developed an interpretable multi-task machine learning framework** integrating plasma proteomics and clinical phenotypes from ~18,000 UK Biobank participants and ~3,000 proteins to characterize shared and disease-specific signatures across multiple neuropsychiatric disorders.
- **Designed a PLS-enhanced classifier-chain XGBoost model** with masked multi-label learning, achieving test AUCs up to 0.85 across schizophrenia, bipolar disorder, major depressive disorder, suicide, and insomnia-related phenotypes.
- **Benchmarked modeling and feature engineering strategies**, including neural networks, XGBoost, Random Forest, PCA, PLS, protein correlation features, pathway features, protein modules, and latent representations to identify the optimal predictive architecture.
- **Applied SHAP-based interpretation and recursive feature reduction** to identify disease-specific and shared protein drivers and derive compact 5-protein signatures per disease while retaining >90% of predictive performance.
- **Discovered proteomically distinct insomnia subtypes** through unsupervised learning and differential protein analysis, identifying an immune/inflammatory subtype with improved predictive discrimination (AUC ~0.84).
- **Integrated predictive modeling with pathway enrichment, GWAS evidence, and target tractability/clinical-precedence analyses** to prioritize biologically and therapeutically relevant protein targets; selected as a featured intern presenter at the J&J Intern Symposium.

Data Scientist & Bioinformatics Research Assistant, University of Nevada, Reno. (Feb 2021 – Current)

- **Developed PathLit-Agent, an LLM-driven biomedical research assistant** that autonomously plans literature searches, retrieves and iteratively synthesizes scientific evidence, and generates structured biological insights using a deterministic, phase-based workflow with automated evaluation for multi-turn reliability.
- **Developed deep learning models** (ResNet50, VGG-16) with advanced feature engineering (BEMD) for MRI-based breast mass classification, boosting diagnostic accuracy.
- **Designed a personalized pathway analysis framework** using sequential NMF for gene weighting for three omics (mRNA, methylation, CNV), improving tumor detection in TCGA data by up to 5%.

- **Developed an autoencoder-based framework** for individual-level pathway analysis in multi-omics data, improving aberrant sample detection accuracy in TCGA datasets.
- **Co-led development of the RCPA R package**, enabling reproducible large-scale pathway analysis workflows (1,000+ species) with integrated statistical methods.
- **Led pathway meta-analysis with NASA GeneLab**, revealing mitochondrial dysfunction signatures across spaceflight datasets.
- Built an NGS variant calling pipeline for SARS-CoV-2 at Renown Hospital, ensuring accurate genomic mutation detection.

C++ Developer | R&D Team Member, AmnPardaz. (Jan 2019 – Mar 2019)

- Researched/evaluated antivirus solutions and developed reliable C++ modules for security tools.

C# Developer, Representative of LG Company. (Jan 2018 – Jan 2019)

- Designed and deployed automated inventory and sales systems for workflow optimization.

Malware Analysis Researcher, IUST. (Sep 2015 – Apr 2017)

- Built a machine learning–based malware detection pipeline integrating static code analysis (control-flow features) and dynamic behavioral profiling (system calls).
- Applied supervised ML models to extracted features, improving malware detection accuracy by 7% with anti-analysis–aware techniques.

EDUCATION

PhD in Computer Science, University of Nevada, Reno, GPA: 3.8/4.0. (Feb 2021– Expected Dec 2026)

- Development of Computational Methods for Analyzing Single/Multi-Omics Data for Systems-Level Understanding.

MSc in Software Engineering, IUST, GPA: 4.0/4.0. (Sep 2014 – Apr 2017)

- A New Hybrid Approach to Malware Detection and Classification Using Machine Learning and Behavioral Analysis.

BSc in Software Engineering, University of Arak, GPA: 3.4/4.0. (Jan 2009 – Feb 2013)

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.* https://doi.org/10.1007/978-3-031-89063-5_63
- **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>
- **1st Author, Sep 2025.** *Autoencoder-Derived Pathway Deviation Scores Reveal Individual-Level Molecular Aberrations* — Under Review
- **1st Author, Nov 2025.** *PathLit-Agent: A Multi-Stage AI Literature Mining System for Pathway-Focused Biomedical Insight* — In Press

AWARDS & HONORS

- **Featured Intern Presenter,** Johnson & Johnson Intern Symposium, 2026.
- **Best Graduate Student Researcher,** University of Nevada, Reno, 2025.
- **Outstanding Graduate Student Researcher Scholarship,** University of Nevada, Reno, 2025.
- **Fully Funded Ph.D. Fellowship,** University of Nevada, Reno.