Omid Mohajeri

▪ Portfolio of Bioinformatics Work
▪ My Advanced Shiny Application
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Bioinformatics Profile

Bioinformatician with **two MSc degrees**, with the second in Bioinformatics (both with **distinction**), **over four years of experience in R** and proficiency in **Python**. Known for developing innovative bioinformatics pipelines and **interactive tools** (e.g., Shiny apps) by combining **strong programming skills** with **creativity** and **problem-solving**. While my expertise to date has mainly focused on **transcriptomics** (**bulk** and **single-cell RNA-Seq**), I am confident in applying these techniques to other omics data types. Experienced in extracting **meaningful biological insights** from complex datasets, including **pathway interpretation**, functional annotation, and **molecular profiling**. I also have evolving experience with **AI/ML/DL**, including neural networks, and am keen to expand my programming and analytical expertise to develop innovative AI-driven solutions. Committed to translational research in **cancer** and other **disease** areas, and able to **adapt quickly**, **communicate clearly**, meeting **deadlines**, and balancing **multiple projects** while acting as a **reliable point of contact** for resolving **technical challenges** and **work effectively under pressure** in **multidisciplinary teams**. Created and maintain a personal portfolio website showcasing my tools, code, and research outputs.

Areas of Expertise

- **Programming (R / Python)**
- **Biological data interpretation**
- **Functional enrichment & pathway**
- **ML & AI (evolving expertise)**
- **Transcriptomics (bulk/ single cell)**
- **Bioinformatics pipeline development**
- **Shiny Web applications**
- **Web design with HTML/CSS**
- **Cancer and disease research**
- **Data Analysis & Visualisation**
- **Data Integration**
- **Linux & GitHub**

Career Experience

Shiny Web Application | ***Independent Bioinformatics Project*** **01/2025 – Present**

- Designed & developed a Shiny app (~2,000 lines R) to support biomarker discovery from single-cell RNA-seq data.
- Enables cell-type-specific exploration by integrating metadata, streamlining hypothesis generation for drug discovery.
- Supports 10X input, metadata, EDA, QC, normalization; identifies HVGs; performs GSEA/ORA for GO terms and KEGG.
- Tested on kidney cancer data (ICB-treated); designed for users without programming or bioinformatics expertise.
- Presented at Norwich Single-Cell & Spatial Symposium 2025 (abstract published).

Biologically Informed HVG Selection Pipeline | ***Independent Bioinformatics Project*** **06/2024 – 12/2024**

Developed an end-to-end R-based bioinformatics pipeline to generate a biologically refined HVG list from scRNA-seq data for training deep learning models. Identifies an optimal HVG threshold and intersects it with GO/pathway-informed gene sets to produce interpretable, context-relevant features.

- **Step 1**: Filtering input 10X-format scRNA-seq data by cell type to generate multiple HVG sets of varying sizes.
- **Step 2**: Evaluating biological relevance of each HVG set by calculating overlap with immune-related gene sets derived from GO terms and pathways (via biomaRt and msigdbr), identifying the point at which biological signal plateaus.
  Step 3: Producing a final, biologically curated HVG list by intersecting the selected HVG set with reference genes. This project was motivated by the need to select biologically meaningful genes for model training and outcome prediction.

Collaborative Research Project (R-based) | Teesside University **10/2023 – 06/2024**

Kidney Cancer scRNA-seq Analysis with Prof. Claudio Angione's AI Research Group

- Collaborated with AI researchers to extract biological meaning from scRNA-seq data & support model development.
- Developed a full Seurat pipeline: cell filtering, HVG selection, clustering, annotation, DEA, and functional analysis
- Conducted end-to-end scRNA-seq analysis to extract complex biological insights from ICB-treated kidney cancer data
- Interpreted AI model outputs for biological relevance and alignment with known pathways and immune mechanisms
- Supported a multidisciplinary team with clear analyses and visualizations to communicate complex biological insights
- Engaged in weekly team meetings, providing analysis updates and contributing to interdisciplinary discussions

RNA-Seq Analysis of AD: DESeq2 Differential Gene Expression | ***Independent Bioinformatics Project*** **02/2023 – 09/2023**

- Analysed GSE157194 (166 Atopic Dermatitis samples) using R (DESeq2): lesional vs. non-lesional skin.
- Conducted exploratory data analysis including PCA, boxplots, histograms, heatmaps, and other visualizations.
- Performed differential expression & functional enrichment analysis (PPI, ORA & GSEA for GO terms and KEGG pathways).
- Published visuals and methods on my personal website (full project update in progress).

Website Design & Development (My Personal Portfolio Website) | ***Self-Directed Project*** **07/2022 – 01/2023**

- Independently designed and developed a personal portfolio website from scratch using HTML and CSS coding.
- Created a multi-page, interactive platform to showcase my bioinformatics projects and communicate complex results.
- Demonstrated visual & written communication skills through well-structured documentation & intuitive structure.

- Applied creativity and problem-solving to design custom layouts and engaging interactive components.

Multi-Phase Transcriptomic Analysis of Breast Cancer | *Dissertation Research Project* | Teesside University 01/2022 – 06/2022

- Developed a 3-step pipeline using custom R functions with GEOquery, limma, GeneMeta, fgsea/msigdbr, ggplot2/plotly.
- Implemented grade-based comparisons using limma and meta-analysis to identify aggressiveness-related DEGs.
- **Phase 1:** DEG analysis on one dataset comparing tumor aggressiveness via grade vs. subtype; grade prioritized.
- **Phase 2:** Integrated 4 datasets using grade-based DEG analysis via limma package and custom R functions.
- **Phase 3:** Conducted meta-analysis with REM model to integrate DEGs, followed by pathway and functional enrichment.

Meta-Analysis Study Selection & Classification | *Internship Project* | Teesside University 09/2021 – 12/2021

- Queried PubMed with defined keywords; screened & shortlisted breast cancer transcriptomic studies for meta-analysis. Selected 4 eligible pre-treatment datasets & based on literature, identified grade & subtype as aggressiveness indicators.
- Defined classification groups (e.g. Grade 1 vs. 3, Lum A/Normal-like vs. Basal-like/Lum B/HER2) for downstream analysis.
- Performed initial DEG and functional analyses using GO2R and NetworkAnalyst platforms to assess group-level differences.
- Established classification approach and prepared datasets for integration & DEG analysis in dissertation research project.

Research Assistant, Pasteur Institute of Iran, Tehran, Iran 2018–2020

- Supported whole exome sequencing (WES) and disease projects with literature reviews and weekly research updates.
- Assisted in preparing reports, posters, presentations, manuscript drafts for the team, and delivering workshops.
- Co-authored a publication on NF1-related mutation analysis and contributed to VSD and cancer reviews.

National Institute of Genetic Engineering and Biotechnology (NIGEB), Iran (Training & Transition) 2016–2018

- Completed multiple workshops in NGS, multi-omics including transcriptomics, genomics, and epigenomics, etc.
- Built core skills through self-study and literature review during transition to human genomics.

Education

MSc Bioinformatics (with advanced practice) (Distinction 73/100) — Teesside University, Middlesbrough, UK
MSc Agricultural engineering (GPA: 89.15/100) — SRB University, Tehran, Iran
BSc Plant Products Engineering (GPA: 76.35/100) — Karaj University, Karaj, Iran

Bioinformatics Training

Intensive Course in Drug Discovery, Bioprocessing & Immunological Techniques (11 days) | Real-time PCR (16 hours) | Bioinformatics & NGS Methodologies, Bio-Linux, SNP Discovery & Analysis, RNA-Seq Data Analysis, Predict New Transcript/Isoforms, Clinical Applications & Diagnostics (24 hours) | Gene Cloning (RNA Extraction, cDNA Synthesis, Primer Designing, PCR, DNA Extraction, Cloning, Gene Transformation, Electrophoresis, Protein Expression & Purification, SDS-PAGE, Western blot) (32 hours) | Next-generation Sequencing Data Analysis: RNA Seq and Small RNA Seq (2 days) | Meta-analysis of High-throughput Sequencing data (2 days) | Computational Systems Biology: Network Analysis, Gene Ontology and Promoter analysis (2days) | Next-generation Sequencing Data Analysis: Metagenomics (2 days) | Epigenomic Data Analysis (ChIP-seq & Genome-wide Methylation) (2 days) | Data Mining and Machine Learning in Bioinformatics (2 days) | NGS Analysis and Clinical Report Writing (1 day) | Introduction to Genomic Technologies (Johns Hopkins University; Coursera)

Programming & Analytical Tools

- **R:** dplyr, ggplot2, Seurat, clusterProfiler, limma, tidyr, readr, GEOquery, plotly, data.table, ComplexHeatmap, sva, shiny, Matrix, msigdbr, org.Hs.eg.db, biomaRt, fgsea, caret, tidyverse, enrichplot, RColorBrewer, ggpubr, shinyjs, circlize, ggvenn, wordcloud, reshape2, vsn, GeneMeta, rgl
- **Python:** tensorflow, scikit-learn, shap, pandas, numpy, matplotlib, seaborn

Publications

1. **Mohajeri**, O. (**M.R.**) (2025). **An Interactive Shiny App for Biomarker Identification: Cell-Type-Specific HVGs & Functional Analysis in Single-cell RNA-Sequencing**. Norwich Single-Cell & Spatial Symposium Abstracts, p. 28. Earlham Institute.
2. E.S. Rahmani, H. Azarpara, M. F. Abazari, **M.R. Mohajeri**, M. Nasimi, R. Ghorbani, A. Azizpour & H. Rahimi. 2020. **Novel Mutation C.7348C>T in NF1 Gene Identified by Whole-Exome Sequencing in Patient with Overlapping Clinical Symptoms of Neurofibromatosis Type 1 and Bannayan–Riley–Ruvalcaba Syndrome**, Cytol Genet. vol. 54, no. 4, pp. 353–362.
3. **Mohajeri, M.R.**, Ghamari Zare, A., Naderi Shahab M. A., Kalateh Jari S., 2014. Seed Germination of Lilium Iedebourii (Baker) Boiss after Cryopreservation. Journal of Rangeland Science, 4 (4): 279- 286.