Mohammad Reza Mohajeri
Curriculum Vitae

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Detail-oriented bioinformatician with an analytical and strategic mind and proven success designing, optimising, and troubleshooting bioinformatic analyses and project pipelines. Collaborative and engaging communicator, equally adept at presenting at workshops and writing scientific reports and articles. Experienced in working independently and alongside senior team members as well as guiding assistants and students. Passionate about applying bioinformatics tools, programming, and machine learning to achieve project goals.

Areas of Expertise

- Scientific Writing & Presentation
- Data Integration & Meta-Analysis
- Biological Systems
- Programming & Analysis

- Medical & Academic Research
- Team Leadership
- Training & Mentorship
- Machine Learning (Weka)

Education and Credentials

Master of Science in Bioinformatics (with Advanced Practice) with Distinction
University of Teesside, UK

Master of Science in Agricultural Engineering
SRB University, Iran

Bachelor of Science in Plant Products Engineering
Karaj University, Iran

Research Experience

University of Teesside, UK   **2020 – 2022**
  Dissertation, Gene Expression Profiling for Aggressive Breast Cancer: A Microarray Meta-Analysis Approach in R (Jan 2022 – Jun 2022)

Executed pipeline in R to combine multiple microarray datasets consisting of more than 450 tissue samples, through comprehensive literature review and data pre-analysis in NetworkAnalyst. Recognised and implemented REM as most effective meta-analysis method using GeneMeta package in R.

- Interpreted and identified potential biomarkers for diagnostic and screening purposes based on most differentially expressed genes.
- Wrote and edited manuscript for submission to Breast Cancer Research and Treatment Journal.

Internship Project (Sept 2021 – Dec 2021)

Generated initial stages of dissertation project, including large-scale data collection and extraction.

- Differentiated between early stage (Grade I) and advanced stage (Grade III) of breast cancer through identification of DEGs as biomarkers.
- Developed in-depth understanding of GEO databases and PubMed for data analysis purposes.

Pasteur Institute of Iran   **2016 – 2020**
  Research Assistant (Oct 2017 – Jan 2020)

Interpreted research results, prepared internal project discussions, wrote reports, and organised presentations based on research results. Directed master students and junior researchers to complete project-related tasks.

- Led technical support and presented student workshops for project: Identification of Mutation in NF1 Gene, Responsible for Overlapping Clinical Symptoms of Neurofibromatosis Type 1 and Bannayan-Riley-Ruvalcaba Syndrome using Whole-Exome Sequencing.
- Independently established baselines and bioinformatic workflow of project: Meta-Analysis of the Effects of Palifermin and other Interventions on the Oral Mucositis Caused by Chemotherapy and Radiotherapy in Cancer Patients Receiving Stem Cell Transplantation.

Volunteer Research Assistant (Jan 2016 – Sept 2017)

Conducted comprehensive literature reviews, evaluated NGS techniques and meta-analysis techniques.

- Wrote reports and prepared presentations for project: Evaluation of Genetic Variations Among Patients Suffering from Ventricular Septal Defect Utilizing Whole Exome Sequencing Technique.
- Researched Epigenetics and assisted in presentations for project: Drug Resistant Prostate Cancer and Epigenetics Data.
- Translated book "RNA-seq Data Analysis – A Practical Approach" in English to Persian.

Laboratory Experience

Forests and Rangelands Institute, Iran   **2009 – 2011**
  Researcher

Conducted plant-tissue-culture research.

Technical Proficiencies

Software
  Python & R, GitHub, Microsoft Office

Online Bioinformatics Tools
  NetworkAnalyst, Galaxy, NCBI, UCSC, Ensembl, Blast, GEO, GEO2R, DAVID

Professional Development

Bioinformatics Training
  Real-time PCR (16 hours), Meta-Analysis Methods (REM, Fisher's, Stouffer's Methods, FEM), NGS Methodologies, Bio-Linux, Gene Expression Profiling, Gene Cloning (RNA & DNA Extraction, cDNA Synthesis, Electrophoresis, Protein Expression & Purification, SDS-PAGE, Western Blot), Computational Systems Biology, Genomic Technologies, Epigenetics, Cancer Etiologies and Treatments

Analysis Techniques
  Transcriptomic Data Integration, Data Processing, Visualization (Box, Density, PCA, MDS Plots, Heatmaps), RNA-Seq Data Analysis, DE Analysis (Fold Change/FDR & Z-score/FDR), Biomarker Identification & Pathway Analysis, Next-generation Sequencing Data Analysis, Epigenomic Data Analysis (ChIP-seq & Genome-wide Methylation), Data Mining, Network Analysis, Gene Ontology & Promoter Analysis

Publications

1. Rahmani E. S., Azarpara H., Abazari M. F., **Mohajeri M. R.**, Nasimi M., Ghorbani R., Azizpour A., & Rahimi H., 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; DOI: 10.3103/S0095452720040106, 2020.
2. **Mohajeri, M. R.**, Ghamari Zare, A., Naderi Shahab M. A., Kalateh Jari S., Seed Germination of *Lilium ledebourii (Baker) Boiss* after Cryopreservation, *Journal of Rangeland Science*, 4 (4): 279- 28, 2014.