

Bioinformatics Profile

Expert bioinformatics professional with advanced AI and scripting skills for sophisticated data analysis.

Possessing two MSc degrees with distinction, my expertise extends to in-depth technical proficiency in areas such as multi-omics and transcriptomics, along with talents in designing, optimizing, and troubleshooting bioinformatic analyses and project pipelines, and developing innovative computational tools. Thorough and accurate communicator, exercising clarity and conciseness in authoring scientific reports and presenting complex scientific concepts to non-scientific audiences. Proven expertise in bioinformatics tools for molecular biomarkers (diagnostics, treatments, and drug discovery), specializing in cancer research and personalized medicine. Talent for operating independently and in partnership with senior team members. Equipped to adapt rapidly to new environments, I apply my academic research background to innovate in pharmaceutical and biotech projects and contribute to academic pursuits.

Areas of Expertise

- Data Integration/ Meta-analysis
- Bulk, scRNA-seq & Microarray
- AI (DL/ML)
- Programming (R / Python)
- Familiarity with Linux & Windows
- Biological Data Statistical Analysis
- NGS
- Biomarker & Pathway Discovery
- GitHub Code Management
- Web Applications (Shiny)
- Data Visualisation / Accessibility
- Data Analysis Workflow Development
- Biological Data Report Generation
- Basic Familiarity with Nextflow

Career Experience

Voluntary Collaboration with Prof. Claudio Angione (Teesside University, UK)

10/2023 – Present

- Developed an R-based bioinformatics pipeline for scRNA-seq, enhancing AI model accuracy.
- Created a Shiny app and computational methods for key gene feature identification.
- Provided insights on immune responses and ICB therapy responsiveness.
- Engaging with cutting-edge computational tools in Systems Biology and Machine Learning.

Professional & Skill Advancement

7/2022 – 10/2023

RNA-Seq Analytics & Integration:

- Drove end-to-end RNA-sequencing analysis workflows using R, specializing in data integration and visualization.
- Applied rigorous statistical methods ensuring data integrity in biomarker and pathway discovery.
- Strengthened proficiency in Linux, elevating data processing, manipulation, visualization, and integration abilities.

Breast Cancer Project Showcase Website:

- Developed a well-developed website using HTML and CSS to showcase my breast cancer research project on GitHub.
- Created an organized interface to showcase the R code used in three phases of the breast cancer research project.

GitHub Experience:

- Managed GitHub with local Linux commands for effective code management in repositories, and consistent code updates.

Teesside University, Middlesbrough, UK

1/2022 – 6/2022

Dissertation Project

Planned and coordinated all facets of “Gene Expression Profiling for Aggressive Breast Cancer: A microarray meta-analysis approach in R” project. Conducted normalization and visualization processes. Facilitated batch effect correction. Performed in-depth analysis of various meta-analysis techniques, including REM meta-analysis method. Coordinated functional and pathway analyses.

- Devised R-based pipeline derived from comprehensive literature review and in-depth pre-analysis of data in NetworkAnalyst, determining optimal methodology for combining microarray datasets (4 datasets and 468 breast cancer tissue samples).
- Spearheaded in-depth literature review to gain insight for biological interpretation and identify potential biomarkers for diagnostic and screening purposes selected from the most differentially expressed genes.

Teesside University, Middlesbrough, UK

9/2021 – 12/2021

Internship Project

Completed project entailing data collection, extraction and pre-analysis utilising GO2R and NetworkAnalyst to identify DEGs as biomarkers for differentiating between early stage (Grade I) and advanced stage (Grade III) of breast cancer. Conducted primary analysis to identify DEGs through GO2R and NetworkAnalyst platforms. Performed extensive literature review through GEO and PubMed databases. Screened all studies based on defined criteria. Coordinated data extraction and classified studies based on grades and subtypes.

- Selected four datasets containing Grade classification to conduct thorough meta-analysis for identifying DEGs; proceeded with meta-analysis for dissertation project.

- Successfully compiled and analysed data that was integral in ascertaining effectiveness of applying molecular subtypes and grading systems for differentiating between non-aggressive and aggressive breast cancer samples in microarray gene expression profiling.

Pasteur Institute of Iran, Tehran, Iran
Research Assistant

1/2016 – 1/2020

Project1: Contributed to whole-exome Seq to identify NF1 gene mutation linked to overlapping symptoms of NF1 and Bannayan–Riley–Ruvalcaba syndrome.

- Contributed to the write-up of reports and scholarly publications for the research project (Co-authored; See Publication).
- Gained subject knowledge in whole-exome sequencing through hands-on research experience.

Project 2: Supported meta-analysis research on interventions for chemotherapy-induced oral mucositis in cancer patients treated by chemotherapy, and radiotherapy.

- Contributed to the research program under the mentorship of Dr. Hamzeh Rahimi.
- Reviewed literature, provided technical support, interpreted results, and produced reports and presentations.
- Volunteered to lead workshops for MSc students on meta-analysis
- Gained knowledge in meta-analysis, etiology of cancers and treatments.

Project 3: Aided in researching genetic variations in Ventricular Septal Defect (VSD) patients using Whole Exome Sequencing.

- Reviewed literature, drafted reports, and prepared posters and presentations

Project 4: Investigated drug resistance in prostate cancer and the impact of epigenetics on treatment outcomes.

- Gained subject knowledge in epigenetics and its role in prostate cancer drug resistance.
- Contributed to the write-up of reports.

Project 5: Assisted in translation of “RNA-seq Data Analysis-a practical Approach” book from English to Persian.

Additional Experience

Plant Propagation & Growth Project Assistant, Research Institute of Forests and Rangelands (RIFR), Tehran, Iran
Assistant Manager & Supervisor, Startup Landscape Business, Tehran, Iran
Founder / Operations Manager, Various Startup Businesses, Tehran, Iran

Education

MSc Bioinformatics (with advanced practice) (Distinction 75/100)

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

Associate Degree, Plant Products Technology (76.9/100)

Varamin University, Varamin, 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)

Technical Proficiencies

R, Python, Linux command-line, Deep learning, Data Integration, NetworkAnalyst, GitHub, Galaxy, NCBI, UCSC, Ensembl, Blast, GEO, GEO2R, DAVID, Weka, SPSS

Publications

1. 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.
2. Mohajeri, M. R., Ghamari Zare, A., Naderi Shahab M. A., Kalateh Jari S., 2014. Seed Germination of Liliun ledebourii (Baker) Boiss after Cryopreservation. Journal of Rangeland Science, 4 (4): 279- 286.