



Bioinformatics Profile

Technically savvy bioinformatics professional with advanced education and technical expertise in scripting, data integration and pathway / functional analysis to support complex bioinformatic analysis efforts.

In-depth technical savvy in areas such as high-throughput genomics and transcriptomics along with talents in designing, optimising and troubleshooting bioinformatic analyses and project pipelines. Strong theoretical understanding of epigenomics. Thorough and accurate communicator, exercising clarity and conciseness in authoring scientific reports and presenting complex scientific concepts to non-scientific audiences. Proven skills and knowledge in use of bioinformatics tools and biological systems for molecular biomarkers / diagnostics, treatments and drug discovery. Talent for operating independently and in partnership with senior team members. Able to adapt rapidly to new environments and employ academic research background to contribute to challenging pharmaceutical and biotechnology projects.

Areas of Expertise

- Data Integration & Meta-analysis
- Bulk & scRNA-seq Analysis in R (DESeq2 & Seurat)
- Machine Learning / AI (Deep Learning)
- Scripting & Programming
- GitHub Code Management
- Biological Data Statistical Analysis
- NGS
- Biomarker & Pathway Discovery
- Familiarity with Linux & Windows
- 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

- Collaborating on scRNA-seq combined with deep learning.
- Guiding biological interpretation of results.
- Offering insights on 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.
- Successfully prepared and presented manuscript for publication in Breast Cancer Research and Treatment journal.

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 sequencing to identify mutation in NF1 gene responsible for overlapping clinical symptoms of Neurofibromatosis Type 1 and Bannayan–Riley–Ruvalcaba syndrome. Delivered key support in drafting project plan. Maintained and troubleshooted computer / laboratory equipment utilised for research project. Delivered key input in informational meetings and interim progress reports. Leveraged research results to compose reports and papers.

- Integral contributor to workshops for MSc students in discussing project scope.

Project 2: Aided in research for project titled “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.” Reviewed literature on technical and medical facets of project to establish baselines and monitor project progression. Delivered technical support during meta-analysis. Contributed to results interpretation and produced reports and posters for internal presentations.

- Instrumental in compiling data that gauged efficacy of palifermin for use in pharmaceuticals.
- Successfully prepared and delivered workshops on meta-analysis for master’s students and scheduled meetings for master’s students and junior researchers to meet and discuss project tasks.
- Gained knowledge in meta-analysis, etiology of cancers and treatments.

Project 3: Supported research project focused on identification of mutations titled “Evaluation of genetic variations among patients suffering from Ventricular Septal Defect utilizing Whole Exome Sequencing technique.” Contributed to literature review on VSD and WES techniques, and on genetic causes of the disease. Drafted project reports and prepared posters and progressive presentations.

Project 4: Performed literature review on prostate cancer, drug resistant, and role of epigenetics. Attended and presented at institutional seminars on epigenetics. Generated posters and presentations.

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

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 Lilium ledebourii (Baker) Boiss after Cryopreservation. Journal of Rangeland Science, 4 (4): 279- 286.