Vahid Shariati

National Institute of Genetic Engineering and Biotechnology (NIGEB), Tehran, Iran
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Languages: English (Fluent), Italian (Good), French (Basic), Persian (Native)

Education

PhD in Genomics
Ph.D., Sant' Anna University of Advanced Studies, Pisa, Italy, 2007 – 2010. *Top student*

Professional Experience:

Senior Bioinformatician, Genome Center, National Institute of Genetic Engineering and Biotechnology, 2018-Present
- Conducted population genome diversity, pan and core genome analysis in human and other species
- Developed and implemented novel algorithms for the identification and annotation of genetic variants
- Collaborated with biologists and clinicians to provide bioinformatics support for research projects
- Conducted data mining, meta-analysis, and omics integration to identify potential biomarkers in cancer
- Presented research findings at national and international conferences

Bioinformatics Research Scientist, Genome Center, National Institute of Genetic Engineering and Biotechnology, 2011-2017
- Conducted bioinformatics analyses on large-scale genomics and transcriptomics datasets
- Designed and developed computational pipelines for data processing, quality control, and analysis
- Collaborated with cross-functional teams to identify actionable insights from genomic data
- Contributed to the development of bioinformatics tools and pipelines for data analysis
- Presented research findings to internal teams and external stakeholders

Research Assistant, University of Milan, Italy, 2010-2011
- Assisted in the analysis of genomic data and chromosome assembly for research project
- Conducted statistical analysis and data collection and visualization to interpret research results
- Assisted in the preparation of publications and research reports

Skills

- Strong programming skills in Python, Bash, R, and JavaScript
- Proficient in analyzing and interpreting high-throughput biological data, including genomics, transcriptomics, and metagenomics
- Proficiency in next-generation sequencing (NGS) data analysis (WGS, WES, RNA-seq, miRNA-seq, lncRNA-seq, ATAC-seq)
- Proficiency in single-cell RNA sequencing (scRNA-seq) data analysis
- Proficiency in PPI, co-expression, differential co-expression, and meta co-expression network analysis
- Proficiency in meta analysis and statistical analysis
- Proficiency in data analysis pipelines development
- Proficiency in GWAS & post-GWAS analysis
- Proficiency in functional genomics, comparative genomics, and conservation analysis
- Proficiency in database development
- Proficiency in structural analysis and molecular docking
- Proficiency in data visualization
- Knowledge of Machine Learning, Deep Learning algorithms and frameworks (e.g., TensorFlow, scikit-learn)
- Excellent problem-solving and critical thinking abilities
- Strong communication and presentation skills (written and verbal)
- Ability to work independently as well as collaboratively in interdisciplinary and international research teams

Project Experiences

- **Whole Genome Sequencing**: Several genome sequencing and population diversity projects in human, plants, and bacteria
- **Transcriptome Meta-analysis**: Discovered metagenes and their correlation to SVs and methylation in Breast, Gastric, Lung, and Colorectal Cancers
- **Pan-cancer analysis**: Cancer-specific UPR regulation and differential co-expression networks identified through Meta and ML analysis
- **Predictive AI Model**: Detected key histones responsible for the nucleosome structure using AI models in breast cancer
- **Pipelines and Database Development**: Developed highly efficient NGS analysis tools and databases for RNA-seq and WES

Selected Recent Publications

1. **Intratumoral IL-12 Immunotherapy Suppresses Tumor Growth and Metastasis Promoted by Tumor-Associated Mesenchymal Stem Cells in Triple-Negative Breast Cancer,** B Jahangiri, ZS Soheili, M Shamsara, V Shariati, A Zomorodipour, Cell Journal (Yakhteh), 2025
2. **Interaction between high-intensity interval training and high-protein diet on gut microbiota composition and body weight in obese male rats,** M Aliabadi, M Saghebjoo, B Yakhchali, V Shariati, Applied Physiology, Nutrition, and Metabolism, 2023
3. **Genomic palaeoparasitology traced the occurrence of *Taenia asiatica* in ancient Iran (Sassanid Empire, 2th cent. CE–6th cent. CE),** Z Askari, F Ruehli, A Bouwman, V Shariati, *et al.*, Scientific reports, 2022
4. **Transcriptional profile of ovine oocytes matured under lipopolysaccharide treatment in vitro,** M Rasekhi, A M-Sangcheshmeh, M Daliri, M Bakhtiarzadeh, V Shariati, *et al.*, Theriogenology, 2020
5. **PrESOgenesis: A two-layer multi-label predictor for identifying fertility-related proteins using support vector machine and pseudo amino acid composition approach,** MR Bakhtiarizadeh, M Rahimi, V Shariati, Scientific reports, 2018
6. **Comprehensive genomic analysis *Pantoea agglomerans* strain P5,** V Shariati, MA Malboobi, Z Tabrizi, E Tavakol, Scientific reports, 2018

References:

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