Vahid Shariati (🆔 0000-0003-3745-4949)

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Languages: English (Fluent), Italian (Good), French (Basic), Persian (Native)

Professional Summary

Accomplished staff bioinformatician with over 10 years of experience in computational genomics and multi-omics data integration. Proven expertise in developing advanced custom analysis pipelines, applying artificial intelligence and machine learning for OMICS data analysis. Skilled in managing large-scale projects and translating complex genomic data into actionable biological insights for cancer, microbiology, and agricultural genomics.

Education

PhD in Genomics, Sant' Anna University of Advanced Studies, Pisa, Italy, 2007 – 2011. *Top student*

Professional Experience:

Staff Bioinformatics Scientist, NIGEB, 2020–Present
- Lead bioinformatics research in population genome diversity, pan- and core-genome analysis in human and other species
- Oversee project development, collaborations with clinicians and biologists
- Conduct multi-omics integration, data mining, and biomarker discovery in cancer
- Supervise, mentor, and coordinate PhD and Master's students and junior researchers

Senior Bioinformatician, NIGEB, 2016–2020
- Designed and implemented new algorithms for genetic variant identification and annotation
- Coordinated collaborative bioinformatics projects with multidisciplinary teams
- Provided advanced data analysis, meta-analysis, and omics integration
- Delivered invited presentations and contributed to building international collaborations
- Initiated mentorship and supervision of graduate students in bioinformatics projects

Bioinformatics Research Scientist, NIGEB, 2012–2016
- Performed large-scale bioinformatics analyses on genomics and transcriptomics datasets
- Built computational pipelines for reproducible processing and analysis
- Contributed to developing new bioinformatics service platforms at the center
- Supported cross-functional projects translating genomic results into actionable insights

Skills

- **Programming & Bioinformatics:** Expert in Python, R, and Bash for developing custom data analysis pipelines. Experienced with TensorFlow and scikit-learn for machine learning applications.
- **Genomic Data Analysis:** Skilled in analyzing diverse high-throughput biological data, including genomics, transcriptomics, and metagenomics. Extensive experience with Next-Generation Sequencing (NGS) data at bulk and single-cell sequencing levels.
- **Image Processing & Artificial Intelligence:** Proficient in biomedical image processing and analysis using deep learning methods for feature extraction, integration of omics and imaging data, tissue annotation, and cell type decomposition of spatial transcriptomics (ST) or H&E images; familiar with approaches relevant to high-content imaging.
- **Advanced Analysis:** Expertise in GWAS & post-GWAS analysis, functional and comparative genomics, conservation analysis, and network analysis (PPI, co-expression).
- **Statistical & Computational Skills:** Proficient in meta-analysis, statistical analysis, and database development. Experienced in structural analysis, molecular docking, and data visualization.
- **Scientific Communication**: Strong written and oral communication to present complex data and research findings to diverse audiences; effective in grant writing and publication preparation.
- **Project Management**: Experienced in leading research teams, directing collaborative projects, managing multiple concurrent studies, and mentoring junior scientists.
- **Data Stewardship & Organization**: Skilled in research data management, reproducible workflow practices, version control, and ensuring open data sharing in accordance with FAIR principles.
- **Problem-Solving & Collaboration:** Excellent problem-solving and critical thinking abilities. Proven ability to work both independently and collaboratively in international and interdisciplinary research teams.

Project Experiences

- **Whole Genome Sequencing & Population Genomics**: Designed and executed large-scale whole-genome sequencing projects to characterize genetic diversity and population structure in human, plants, and bacteria (Project design, leadership, data analysis, team coordination)
- **Gene Co-expression & Pathway Analysis**: Employed comparative genomics and gene co-expression analysis to identify regulatory modules linked to diseases (Project design, leadership, data analysis)
- **Biomedical Image processing**: Applied quantitative image analysis to extract features from bioimages relevant to cellular phenotyping, omics data, and disease classification (Project design, data analysis)
- **Pan-genome & Meta Analysis**: Directed comparative genomics, pan-genome, and meta-analyses identifying key genetic signals across populations and species. Organized collaborative data sharing and analysis strategies among international partners (Project design, leadership, data analysis)
- **Predictive AI Models in Humans**: Developed and validated AI-driven predictive models for genetic risk factors and biomarkers related to human health outcomes (Project design, data analysis)
- **Bioinformatics Pipeline & Database Development**: Led development of scalable NGS analysis pipelines and custom databases managing large genomic datasets; ensured reproducibility, documentation, and integration with collaborative platforms for user access and data sharing (Pipeline architecture, database design, leadership, user training, data management)

Selected Publications

🔟 Top 10% Journal　　　Q1 Top 25% Journal (Q1)　　* Corresponding author

1. **Pan-cancer analysis of SQSTM1/p62 reveals its comprehensive contribution to shaping tumor microenvironment and anti-tumor immunity**, Z Nayeri, E Tavakol, M Rahmati, <u>V Shariati</u>*, MA Moosavi (in press) Q1 Link

2. **Advanced molecular mechanisms of baicalein's neuroprotective effects in neurodegenerative disease treatments**, Z Nayeri, <u>V Shariati</u>, F Aliakbari, D Morshedi (submitted) Q1 Link

3. **Oleuropein's effects on breast cancer revealed by RNA-Sequencing and Deep Learning**, T Adel, Z Nayeri, B Jahangiri, E Tavakol, S Salesi, <u>V Shariati</u>* (submitted) Q1 Link

4. **Towards a pan-cancer atlas of endoplasmic reticulum stress network: A machine learning approach**, Z Nayeri, <u>V Shariati</u>*, M Rahmati, MA Moosavi (submitted) Q1 Link

5. **Engineered mesenchymal stem cells utilizing a BST2 Promoter for tumor-restricted IL-12 immuno-gene therapy in Triple-Negative Breast Cancer**, B Jahangiri, ZS Soheili, E Asadollahi, V Shariati, M Shamsara, A Zomorodipour (submitted) Q1 Link

6. **A comprehensive transcriptomic meta-Analysis leveraging machine learning to uncover molecular signatures and potential therapeutic targets in Triple-Negative Breast Cancers**, S Salesi, T Adel, Z Nayeri, <u>V Shariati</u>*, A Zomorodipour (Preprint) Link

7. **Decoding gastric cancer: an AI-driven transcriptomic meta-analysis**, A Asadi, T Adel, Z Nayeri, M Anisimova, <u>V Shariati</u>* (Preprint) Link

8. **Transcriptome meta-analysis of tumor-associated mesenchymal stem cells reveals differentially expressed genes driving tumor microenvironment remodeling and cancer progression**, B Jahangiri, V Shariati, E Asadollahi, ZS Soheili, M Shamsara, A Zomorodipour (Preprint) Link

9. **Population genome diversity of native Iranian and Mediterranean germplasm redefines the evolutionary history of the olive tree**, MH Pakdel, AA Asadi, E Tavakol, YF Zeng, Z Jianguo, <u>V Shariati</u>*, M Hosseini (Preprint) Link

10. **Pleiotropic effects of barley BLADE-ON-PETIOLE gene Uniculme4 on plant architecture and the jasmonic acid pathway**, E Tavakol, <u>V Shariati</u>, I M Fontana, M Binaghi, H Stellmach, B Hause, *et al.*, *Journal of Experimental Botany*, 2025 Q1 🔟

11. **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, <u>V Shariati</u>, A Zomorodipour, *Cell Journal*, 2025 Q2

12. **Whole-genome analysis of Ligilactobacillus salivarius L33, a potential probiotic strain isolated from chicken gastrointestinal tract,** SA Maniee, S Mahmoodian, JZ Amirzakaria, A Meimandipour, <u>V Shariati,</u> E Tavakol, *Microbiology Spectrum*, 2025 Q1

13. **Comprehensive in vitro and whole-genome characterization of probiotic properties in Pedio-coccus acidilactici P10 isolated from Iranian broiler chicken,** R Tabashiri, S Mahmoodian, MH Pakdel, <u>V Shariati</u>, A Meimandipour, J Zamani, *Scientific Reports*, 2025 Q1 10

14. ***de novo* transcriptome analysis and functional annotation of Silybum Marianum L. under drought stress with a focus on Silymarin synthesis and MAPK signaling pathways,** R Ghanbari Moheb Seraj, A Ahmadikhah, K Esmaeilzadeh-Salestani, <u>V Shariati</u>, Mahdi Behnamian, N Tari-verdizadeh, A Emadi, S Dezhsetan, *BMC Plant Biology*, 2025 Q1 10

15. **Unraveling the genetic basis of oil quality in olives: a comparative transcriptome analysis**, A Asadi, E Tavakol, <u>V Shariati</u>*, & M Hosseini Mazinani*, *Frontiers in Plant Science*, 2024 Q1 10

16. **Machine learning-aided microRNA discovery for olive oil quality**, M H Pakdel, A A Asadi, E Tavakol, <u>V Shariati</u>*, & M Hosseini Mazinani*, *PloS One*, 2024 Q1

17. **Genotyping-by-sequencing and weighted gene co-expression network analysis of genes responsive against Potato virus Y in commercial potato cultivars**, Z Hajibarat, A Saidi, M Zeinalabedini, A Mousapour Gorji, M R Ghaffari, <u>V Shariati</u>, & R Ahmadvand, *PloS One*, 2024 Q1

18. **Comprehensive genome analysis of Pseudomonas sp. SWRIQ11, a new growth-promoting bac-terium that alleviates salinity stress in olive,** SM Zamanzadeh-Nasrabadi, F Mohammadiapanah, S Sarikhan, <u>V Shariati</u>, K Saghafi, M Hosseini-Mazinani, *3 Biotech*, 2023 Q1

19. **Meta-analysis of transcriptome reveals key genes relating to oil quality in olive**, A Asadi, <u>V Shariati</u>*, S Mousavi, R Mariotti, & M Hosseini Mazinani, *BMC Genomics*, 2023 Q1

20. **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, <u>V Shariati</u>, *Applied Physiology, Nutrition, and Metabolism*, 2023 Q2

21. **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, <u>V Shariati</u>, *et al.*, *Scientific Reports*, 2022 Q1 10

22. **Candidate genes for anthocyanin pigmentation in rice stem revealed by GWAS and whole-genome resequencing**, R Haghi, A Ahmadikhah, A Fazeli, & <u>V Shariati</u>, *The Plant Genome*, 2022 Q1

23. **Complete chloroplast genome of Lilium ledebourii (Baker) Boiss and its comparative analysis: lights into selective pressure and adaptive evolution**, M Sheikh-Assadi, R Naderi, M Kafi, R Fatahi, S A Salami, & <u>V Shariati</u>, *Scientific Reports*, 2022 Q1 10

24. **Normalized workflow to optimize hybrid de novo transcriptome assembly for non-model species: A case study in Lilium ledebourii (Baker) Boiss**, M Sheikh-Assadi, R Naderi, S A Salami, M Kafi, R Fatahi, V Shariati, F Martinelli, A Cicatelli, M Triassi, & F Guarino, *Plants*, 2022 Q1

25. **Meta-QTL and ortho-MQTL analyses identified genomic regions controlling rice yield, yield-related traits and root architecture under water deficit conditions**, B Khahani, E Tavakol, V Shariati*, & L Rossini, *Scientific Reports*, 2021 Q1 10

26. **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 Q1

27. **Detection of genomic regions associated with tiller number in Iranian bread wheat under different water regimes using genome-wide association study,** SS Bilgrami, HD Ramandi, V Shariati*, K Razavi, *et al., Scientific Reports*, 2020 Q1 10

28. **Novel aspects on the interaction between grapevine and Plasmopara viticola: Dual-RNA-Seq analysis highlights gene expression dynamics in the pathogen and the plant,** SL Toffolatti, GD Lorenzis, M Brilli, M Moser, V Shariati, *et al.*, *Genes*, 2020 Q2

29. **Genome-wide screening and comparative genome analysis for Meta-QTLs, ortho-MQTLs and candidate genes controlling yield and yield-related traits in rice**, B Khahani, E Tavakol, V Shariati, & F Fornara, *BMC Genomics*, 2020 Q1

30. **Comprehensive genomic analysis of an indigenous Pseudomonas pseudoalcaligenes degrading phenolic compounds**, M Safari, B Yakhchali, V Shariati, *Scientific Reports*, 2019 Q1 10

31. **Transcriptional responses of wheat roots inoculated with Arthrobacter nitroguajacolicus to salt stress**, M Safdarian, H Askari, V Shariati*, G Nematzadeh, *Scientific Reports*, 2019 Q1 10

32. **Comparative transcriptome analysis to identify putative genes involved in thymol biosynthesis pathway in medicinal plant Trachyspermum ammi L.**, M Soltani Howyzeh, S A Sadat Noori, V Shariati*, & M Amiripour, *Scientific Reports*, 2018 Q1 10

33. **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 Q1 10

34. **Comprehensive genomic analysis *Pantoea agglomerans* strain P5,** V Shariati, MA Malboobi, Z Tabrizi, E Tavakol, *Scientific Reports*, 2018 Q1 10

35. **The barley Uniculme4 gene encodes a BLADE-ON-PETIOLE-like protein that controls tillering and leaf patterning**, E Tavakol, R Okagaki, G Verderio, V Shariati, A Hussien, H Bilgic, M J Scanlon, N R Todt, T J Close, & A Druka, *Plant Physiology*, 2015 Q1 10

References:

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