# Vahid Shariati



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

## **Professional Summary**

Highly accomplished Senior Bioinformatician with over 10 years of experience specializing in computational genomics. Proven expertise in developing custom pipelines and applying AI in key genetic elements and drug discovery.

### **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

- **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, including WGS, WES, RNA-seq, miRNA-seq, lncRNA-seq, and ATAC-seq at bulk and single-cell sequencing.
- 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.
- 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
- Gene Co-expression & Pathway Analysis: Employed advanced comparative genomics and gene coexpression analysis to identify key regulatory modules and pathways linked to complex human diseases, revealing novel gene-disease associations.
- **Pan-genome & Meta Analysis:** Employed comparative genomics, meta and pan analysis to identify key signals across population/types.
- **Predictive AI Modeling in Humans:** Developed predictive AI models to identify and characterize genetic risk factors and biomarkers responsible for specific human health outcomes, with applications in personalized medicine and disease prognosis prediction.
- **Bioinformatics Pipeline & Database Development:** Developed robust and scalable Next-Generation Sequencing (NGS) analysis pipelines and custom databases to manage and query large-scale genomic datasets.

### **Selected Recent Publications**

- 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
- 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</u> 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, <u>V Shariati</u>, *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, <u>V Shariati</u>, Scientific reports, 2018
- 6. **Comprehensive genomic analysis** *Pantoea agglomerans* strain P5, <u>V Shariati</u>, MA Malboobi, Z Tabrizi, E Tavakol, Scientific reports, 2018
- 7. A comprehensive transcriptomic meta-Analysis leveraging deep learning to uncover molecular signatures and potential therapeutic targets in Triple-Negative Breast Cancers, S Salesi, T Adel, Z Nayeri, V Shariati, A Zomorodipour (Preprint)
- 8. **Decoding Gastric Cancer: An Al-Drive Transcriptomic Meta-Analysis**, A Asadi, T Adel, Z Nayeri, <u>V Shariati (Preprint)</u>
- 9. Oleuropein's Effects on Breast Cancer Revealed by RNA-Sequencing and Machine Learning, T Adel, Z Nayeri, B Jahangiri, S Salesi, <u>V Shariati</u> (Preprint)
- 10. **Towards a pan-cancer atlas of endoplasmic reticulum stress network**, Z Nayeri, <u>V Shariati</u>, M Rahmati, MA Moosavi (Preprint)

# **References:**

### Laura Rossini

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### Maria Anisimova

Full professor, ZHAW Institute, Zurich, Switzerland <a href="mailto:anis@zhaw.ch">anis@zhaw.ch</a>

### Alessandra Stella

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