

Ali Hakimzadeh

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PROFESSIONAL SUMMARY

Bioinformatician with more than 6 years of experience in multi-omics data analysis, with a focus on clinical transcriptomics, WGS/WES, metagenomics, and metabarcoding. I build and deploy robust, reproducible analysis pipelines using Python, R, Snakemake, Nextflow, Docker, and Singularity on HPC (SLURM) and AWS environments. My expertise lies in applying machine learning and computational models to diverse biological questions, from identifying therapeutic targets in cancer organoids to analyzing microbiome or fungal diversity in eDNA studies.

EXPERIENCE

Junior researcher- Mycology & Microbiology center (ESTONIA) 12/2021-Present

- Executed (Meta)genomics, (meta)transcriptomics, and metabarcoding data analysis
- Collaborated on [PipeCraft2](#) pipeline development, documentation, debugged workflows, and maintained version control via Git
- Designed and built the [SnakeEuk](#) pipeline to format the [EUKARYOME](#) database for other downstream tools
- [Optimized chimera filtering of PacBio long-read sequences](#) by implementing a [new hybrid approach](#), achieving improvements of up to 32%
- Responsible for bioinformatics analysis, biodiversity, statistical analysis, and species monitoring (16S, ITS, COI) in [Funleaf](#) & [Funhome](#) projects

Bioinformatician- Azienda Ospedaliera Senese (ITALY) 11/2020 - 09/2021

- Conducted Bulk RNASeq and differential gene expression analysis, assessment of differential gene expression tools (cuffdiff, edgeR, and DeSeq2) on simulated and empirical datasets
- Developed the DEASS algorithm: a method for differential gene expression analyses on a sample-by-sample basis
- Contributed to scRNA-seq and spatial transcriptomics projects, assisting in data processing, QC, clustering, and integration with spatial data using Seurat and Scanpy
- Performed downstream analyses, including gene set enrichment and exploratory CNV and clonal structure assessment in oncological datasets
- Collaborated in pilot applications of machine learning methods for spatial mapping and cell type classification
- Applied supervised workflows for WES variant calling and annotation to support therapeutic target exploration

TEACHING

- **Lecturer**, PipeCraft2 Workshop, Department of Parasitology, University of Tartu — Mar 2025
- **Lecturer**, Metabarcoding: from Lab to Bioinformatics, Summer School, University of Tartu — Jun 2022

- **Teaching assistant**, Bioinformatics course (MSc Biotechnology), University of Tehran — 2020–2021
- **Teaching assistant**, NGS and Data Analysis course (BSc Biology), University of Tehran — 2020–2021
- **Lecturer**, RNA-Seq Analysis Workshop — May 2020
- **Lecturer**, Introduction to NCBI Workshop — Jul 2020

EDUCATION

2021-Nov2025	PhD, Ecoinformatics <i>University of Tartu</i>
2017-2019	MSc, Medical Biotechnology <i>Università degli Studi di Siena</i>
2012-2016	BSc, Zoology <i>University of Tabriz</i>

PUBLICATIONS

Complete publication list available at : [Google Scholar](#)

Ebrahimi, Nasim, Hakimzadeh Ali, et al. (2023). “Role of non-coding RNAs as new therapeutic targets in regulating the EMT and apoptosis in metastatic gastric and colorectal cancers”. In: *Cell Cycle* 22.20, pp. 2302–2323.

Hakimzadeh, Ali et al. (2024). “A pile of pipelines: An overview of the bioinformatics software for metabarcoding data analyses”. In: *Molecular Ecology Resources* 24.5, e13847.

Tedersoo, Leho et al. (2024). “EUKARYOME: the rRNA gene reference database for identification of all eukaryotes”. In: *Database* 2024, baae043.

Hagh-Doust, Niloufar, Hakimzadeh Ali, et al. (2025). “Invisible Passengers: Diversity and Risks of Fungi and Bacteria Transported via International Airport Passenger Footwear”. In: *Biological Invasions*. Manuscript submitted.

Hakimzadeh, Ali et al. (2025). “Are we throwing away good data? Evaluation of chimera detection algorithms on long-read amplicons reveals high false-positive rates across algorithms”. In: *PeerJ*. Manuscript submitted.

REFERENCES

- **Leho Tedersoo**
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