ALI HAKIMZADEH

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PROFILES

- **GitHub:** https://github.com/alihkz94
- **LinkedIn:** https://www.linkedin.com/in/alihkz94
- **ResearchGate:** https://www.researchgate.net/profile/Ali-Hakimzadeh
- **Researcher unique identifier:** https://orcid.org/0000-0003-1336-7445

EDUCATION

Ph.D.: Ecology And Botany   12/2021-Expected in10/2025
University of Tartu - Tartu, Estonia
- **Research topic**: Bioinformatics analysis of long DNA markers

Projects:
- Microbiome and fungal eDNA barcoding**,** metabarcoding, and metagenomics bioinformatics analysis
- Developing and implementing new modules for the [PipeCraft2 pipeline](#)
- Contribution to rRNA gene reference database development for eukaryotes ([EUKARYOME](#))
- Evaluation and enhancement of chimera detection algorithms on long-read amplicons
- Variant calling analysis related to fungal datasets from different sequencing platforms
- Part of the sampling team in the [TREC (Traversing European Coastlines)](#) project

Master of Science: Medical Biotechnology   11/2017-04/2020
Università Degli Studi Di Siena – Siena, Italy
- **Research topic**: Assessment of bioinformatic methods for analyzing differentially expressed genes in vaccination studies

Projects:
- **Transcriptomic data analysis** to investigate vaccine efficacy by using scripts in Bash, Python, and R and tools like: DESeq2, edgeR, HISAT2, limma, Samtools, STAR, picard, BEDtools and developing machine learning models by using Python (Pandas, Numpy, scikit-learn, TensorFlow), applying cross-validation, confusion matrix, and ROC/precision-recall curve to evaluate model performance
- **DEASS:** Differential gene expression analysis sample by sample based and optimization compared to edgeR and DESeq2

Bachelor of Science: Zoology   11/2012-06/2016
Tabriz University – Tabriz, Iran

SKILLS

- **Omics data analysis:** Transcriptomics, WGS, WES, CRISPR screening, Metabarcoding, Metagenomics, Barcoding

- **Programming:** Python, R, Bash, Git, LaTeX

- **Machine learning:** Dimensionality reduction, Hypothesis testing, Clustering

- **Workflow & Pipeline development:** Nextflow, Snakemake, Docker, Singularity

- **Cloud technologies:** HPC (SLURM), AWS

WORK EXPERIENCE

Bioinformatician   11/2020 - 09/2021
Imam Khomeini Hospital – Tehran, Iran
- Executed 10X Chromium scRNA-seq and prepared CROP-seq libraries from gastric cancer organoids for in vivo CRISPR screens.

- Applied UMI sequencing to identify enriched sgRNAs and integrate multiome data (>100k cells/donor) with spatial transcriptomic.
- Performed gene-set enrichment, somatic CNV, clonal evolution, and tissue-specific driver analyses using Seurat, Scanpy, MAST, scCN, and MOFA.
- Developed machine learning models with scVI, TensorFlow, and PyTorch for spatial mapping, cell type classification, and clone fitness prediction
- Conducted WGS and WES data analysis (JWES and Nvidia Parabricks) to identify somatic and germline mutations, structural variants, and potential therapeutic targets

Labrotary Assistant, 09/2013 - 09/2015
Tabriz University – Tabriz, Iran
- Cared for and maintained colonies of rats and mice, ensuring their well-being and adherence to ethical guidelines.
- Conducted behavioral assays, including the Morris water maze to evaluate spatial memory and the T-maze to assess decision-making processes.
- Analyzed data using Rtrack for water maze experiments and MouBeAT for T-maze studies.
- Administered substances via oral, intraperitoneal (IP), and intramuscular (IM) injections.
- Harvested brain and liver tissues for subsequent biochemical analyses.
- Performed spectrophotometric assays to assess toxicity and stress markers in collected tissues.

PUBLICATIONS

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

- **A pile of pipelines: An overview of the bioinformatics software for metabarcoding data analyses**

Molecular Ecology Resources

Ali Hakimzadeh, Alejandro Abdala Asbun, Davide Albanese, Maria Bernard, Dominik Buchner, Benjamin Callahan, J Gregory Caporaso, Emily Curd, Christophe Djemiel, Mikael Brandström Durling, Vasco Elbrecht, Zachary Gold, Hyun S Gweon, Mehrdad Hajibabaei, Falk Hildebrand, Vladimir Mikryukov, Eric Normandeau, Ezgi Özkurt, Jonathan M. Palmer, Géraldine Pascal, Teresita M Porter, Daniel Straub, Martti Vasar, Tomáš Větrovský, Haris Zafeiropoulos, Sten Anslan (https://doi.org/10.1111/1755-0998.13847)

- **EUKARYOME: the rRNA gene reference database for identification of all eukaryotes**

Oxford University Press

Leho Tedersoo, Mahdieh S Hosseyni Moghaddam, Vladimir Mikryukov, **Ali Hakimzadeh**, Mohammad Bahram, R Henrik Nilsson, Iryna Yatsiuk, Stefan Geisen, Arne Schwelm, Kasia Piwosz, Marko Prous, Sirje Sildever, Dominika Chmolowska, Sonja Rueckert, Pavel Skaloud, Peeter Laas, Marco Tines, Jae-Ho Jung, Ji Hye Choi, Saad Alkahtani, Sten Anslan (https://doi.org/10.1093/database/baae043)

- **Role of non-coding RNAs as new therapeutic targets in regulating the EMT and apoptosis in metastatic gastric and colorectal cancers**

Taylor & Francis

Nasim Ebrahimi, **Ali Hakimzadeh**, Farima Bozorgmand, Sepehr Speed, Mahdokht Sadat Manavi, Roya Khorram, Kobra Farahani, Fatemeh Rezaei-Tazangi, Atena Mansouri, Michael R. Hamblin, Amir Reza Aref (https://doi.org/10.1080/15384101.2023.2286804)

- **The Impact of Oil Palm Plantations and Pastures on Benthic Prokaryotic and Fungal Communities in Tropical Streams**

Freshwater Biology

Oscar Alberto Rojas-Castillo, **Ali Hakimzadeh**, Leho Tedersoo, Dean Jacobsen, Sebastian Kepfer-Rojas (https://doi.org/10.1111/fwb.14376)

- **Evaluation of chimera detection algorithms on long-read amplicons**

in progress

Ali Hakimzadeh, Vladimir Mikryukov, Leho Tedersoo, Sten Anslan

- **Invisible Passengers Diversity and Risks of Fungal and Bacterial Transport via International Airport Passenger Footwear**

In progress

Niloufar Hagh-Doust, **Ali Hakimzadeh**, John Yangyuoru Kupagme, Glen Dierickx, Ovidiu Copot, Leho Tedersoo

- **DNA barcoding of fungal specimens: A tripartite approach using PacBio, Oxford Nanopore, and Sanger sequencing**

In progress

John Yangyuoru Kupagme, **Ali Hakimzadeh**, Leho Tedersoo

TEACHING ACTIVITY

- PipeCraft2 Workshop - **Lecturer** March 2025

University of Tartu - Department of Parasitology

- Metabarcoding: from Lab to Bioinformatics - **Lecturer** June 2022

Summer school - University of Tartu

- Bioinformatics- **Teacher Assistant** 2020-2021

Biotechnology course (Master of science degree) - University of Tehran

- NGS and data analysis - **Teacher Assistant** 2020-2021

Biology course (Bachelor of science degree) - University of Tehran

- "RNA-Seq analysis" workshop - **Lecturer** May 2020

- "Introduction to NCBI" workshop - **Lecturer** July 2020

CONFERENCES

- "The neurotoxicity effect of cadmium in the presence or absence of vitamin C on spatial learning and memory in male rats" at the 6th International Conference Of Cognitive Science 27-29 April 2015, Tehran - Iran
- "Protective effect of vitamin C on anxiety during cadmium neurotoxicity in male rats" at the 13th Iranian International Congress of Toxicology 12-14 May 2015, Urmia - Iran
- " Effect of vitamin C on acute pain during cadmium toxicity in male rats" at the 22nd Congress of Physiology and Pharmacology 7-11 September 2015, Kashan - Iran
- "An overview of bioinformatic pipelines for metabarcoding data analyses" at Nextflow Summit 2022, Barcelona - Spain
- "Evaluation of chimera detection algorithms on long-read amplicons" at IMC12 11-15 August 2024, Maastricht – Netherlands
- " PipeCraft2: Metabarcoding data analysis pipeline" at ECCB 16- 20 September 2024, Turku – Finland

AWARDS AND HONORS

- Marie Skłodowska-Curie European Scholarship winner - Siena, Italy (2016)
- Best presentation award at the conference of the Department of Botany - Tartu, Estonia (2024)
- Ranked among the top 3 student scientific unions in the National HARAKAT FESTIVAL - Tehran, Iran (2014)
- Chan Zuckerberg Travel Grant winner (2022)
- Dora plus scholarship winner (2023)

REFERENCES

- Leho Tedersoo
  Professor of Mycology

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- Sten Anslan
  Academy Research fellow
  University of Jyväskylä, Department of Biological and Environmental Science
  Email: sten.s.anslan@jyu.fi   Phone: +358 504612239

- Simone Furini
  Associate Professor of Bioinformatics
  University of Bologna, Department of Electrical, Electronic and Information Engineering
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- Farzam Sheikhzadeh Hesari
  Associate Professor of Physiology
  Department of Animal Biology, Faculty of Natural Science
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