TAHILA ANDRIGHETTI, PH.D

Bioinformatician with expertise in scRNA-seq analysis and systems biology, focusing on transcriptomics, network-based analyses, and multi-omics integration.

CONTACT

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Tahila Andrighetti
Portfolio: tahila.work

SKILLS

Programming, Computing, and Infrastructure

Python · R · Bash · Linux · Git/GitHub · Conda/Mamba · Jupyter Notebook · High-Performance Computing (SGE/qsub) · API access and integration

Bioinformatics and Transcriptomics

RNA-seq and scRNA-seq Analysis · End-to-End Pipelines (QC, Normalization, Integration, Clustering, Annotation) · Differential Expression · Identifier Mapping and Validation

Single-Cell and Omics Toolkits

Scanpy/scverse · AnnData · Seurat · Bioconductor · CellBender · SoupX · Scrublet · MAST · Harmony · SCENIC

Systems Biology and Network Analysis

Gene Regulatory and Interaction Networks · decoupler · OmniPath · COLLECTRI · TRIs and PPIs · Cytoscape · TieDIE · Network Diffusion and Propagation

Data Visualization and Reporting

Scanpy Visualization (UMAP, MatrixPlot, DotPlot) · Matplotlib · Cytoscape Apps · Notebook-to-HTML Reporting (nbconvert)

Scientific Computing and Statistics

NumPy · pandas · SciPy · scikit-learn · statsmodels · Machine Learning (SVM)

Biological Experience and Interests

Host–Microbiome Interactions · Inflammatory Bowel Diseases (IBD) · Immunology · Microbial Virulence Factors · Immune Cell Biology · Gene Regulation in Health and Disease

PROFESSIONAL EXPERIENCE

Post-Doctoral Researcher, Bioinformatician

Jan 2025 – Current
UNICAMP, BR

- Lead bioinformatics support for scRNA-seq projects; development of reproducible, end-to-end workflows (QC, normalization, integration, clustering, annotation) primarily in **Python**, with **R/Bash** when needed.
- **Skin phototype transcriptomics (industry collaboration):** scRNA-seq characterization across skin cell populations/phototypes; pipeline development and delivery of training sessions and analysis handoffs.
- **Neutrophil programming by microbial metabolites:** SCFA- and microbiota-driven neutrophil functional programs using scRNA-seq and systems biology / network-based analyses.
- **Hcar2 in colitis:** single-cell and bulk transcriptome analyses of intestinal epithelial cells to assess inflammatory regulation and pathway-level effects.
- ***Citrobacter rodentium* transcriptomics (RNA-seq):** RNA-seq functional interpretation, integrating virulence-factor context with downstream **network-based** analyses.
- **Cross-lab contributions:** scRNA-seq troubleshooting, interpretation, reporting, and standardization of analysis practices; **Bash** support.
- **GitHub repositories:**
    - Systems biology analysis of *C. rodentium* RNA-seq
    - scRNA-seq workflows

Post-Doctoral Researcher, Bioinformatician

Sep 2020 – Apr 2022
EMBRAPA Agroenergy, BR

- Industry–academia project to develop an ecological RNAi-based biopesticide against weeds; identification and prioritization of candidate lethal target genes under predefined biological/technical criteria.
- Data mining and curation across multiple plant species/sources, ensuring integrity and scientific rigor despite data scarcity and heterogeneous protocols.
- Built scripts and pipelines in **Python/Bash/R** for dataset management, integration, and analysis; produced a structured database of candidate genes.
- NGS quality assessment (genomes and newly generated RNA-seq), including contamination screening and dataset validation; delivered results in strategic meetings with stakeholders.
- **Project Details:** https://www.tahila.work/rnai-project

Visiting PhD Candidate, Bioinformatics

Mar 2017 – May 2020
Earlham Institute, UK

Dr. Tamas Korcsmáros' Group

- **MicrobioLink:** developed a systems biology pipeline integrating multi-omics (e.g., metaproteome/metatranscriptome and host transcriptome) with host–microbe interaction networks to contextualize microbial protein effects on host signaling.
- Implementation and reproducible workflows in **Python/Bash**; applied PPIs, TRIs and diffusion-based methods for mechanistic inference.
- Publication: DOI GitHub: HMIpipeline.
- **Crohn's disease microbiome analysis:** computational analysis of metaproteomics and host–microbiome interaction networks to identify altered cellular processes and pathways. DOI

PhD Candidate, Bioinformatician

Feb 2013 – Jul 2019
UNESP, BR

- **Project:** Sequence feature evaluation for taxonomic analysis of metagenomes using Machine Learning.
- Used **Support Vector Machine (SVM)** models for taxonomic classification of reported and unknown metagenomic reads.
- Benchmarked sequence-derived feature sets to optimize classification performance.
- Implemented features such as GC content; di/tri/tetra-nucleotide entropy; 2–4-mer frequencies; dinucleotide abundance; and TETRA in **Python** and **Wolfram Language (Mathematica)**.
- Demonstrated the value of sequence features to characterize incompletely sequenced organisms and infer taxonomic composition across diverse environments.
- **Project Details:** https://www.tahila.work/metagenome-ml

Entrepreneurial Experience CEO/Director role

Aug 2022 – Feb 2024
Arbor Bio Decor, BR

- CEO/Director role (non-academic): project management plus sales/marketing operations; strengthened leadership, communication, and execution in a dynamic environment.

EDUCATION

Ph.D. – Genetics

2015 – 2019
UNESP, BR

Thesis: Influence of microbial proteins on Crohn's Disease development

- Presented research at symposiums and international conferences (oral/poster), including a *Best Oral Presentation* award.

Master's Degree – Genetics

2013 – 2015
UNESP, BR

Thesis: Computational tool for micro-organisms identification based on genomic signatures

- Presented research at symposiums and international conferences (oral/poster), including a *Best Poster Presentation* award.

Bachelor's – Biological Sciences

2008 – 2012
UCS, BR

Thesis: Analysis of organizational changes on H1N1 sequences using bioinformatics

- Presented research at symposiums and international conferences (oral/poster), including a *Best Oral Presentation* award; 4 undergraduate bioinformatics projects; co-authored 2 scientific articles.

RELEVANT PUBLICATIONS

MicrobioLink: An Integrated Computational Pipeline to Infer Functional Effects of Microbiome–Host Interactions

Andrighetti T; Bohar B, Lemke N, Sudhakar P, Korcsmaros T

2020 Cells, 9(5), 1278 DOI

Integrated Analysis of Microbe–Host Interactions in Crohn's Disease Reveals Potential Mechanisms of Microbial Proteins on Host Gene Expression

Sudhakar P; **Andrighetti T**; Verstockt S; Caenepeel C; Ferrante M; Sabino J; Verstockt B; Vermeire S

2022 iScience, 25(5), 103963 DOI

ViralLink: An Integrated Workflow to Investigate the Effect of SARS-CoV-2 on Intracellular Signalling and Regulatory Pathways

Treveil A; Bohar B; Sudhakar P; Gul L; Csabai L; Olbei M; Poletti M; Madgwick M; **Andrighetti T**; Hautefort I; Modos D; Korcsmaros T

2021 PLoS Computational Biology, 17(2), e1008685 DOI

Comparative Study of the Gut Microbiomes Between Western and Indigenous Cultures – Implications for Health and Disease

Sreenikitha K; Das S; **Andrighetti T**; Sudhakar P

2025 The Microbe, 7, 100310 DOI

DNA Duplex Stability as Discriminative Characteristic for *Escherichia coli* σ^{54}- and σ^{28}-Dependent Promoter Sequences

de Avila e Silva S; Forte F; Sartor ITS; **Andrighetti T**; Gerhardt GJL; Longaray Delamare AP; Echeverrigaray S

2014 Biologicals, 42(1), 22–28 DOI

Triplet Entropy Analysis of Hemagglutinin and Neuraminidase Sequences Measures Influenza Virus Phylodynamics

Gerhardt GJL; Takeda AAS; **Andrighetti T**; Sartor ITS; Echeverrigaray SL; de Avila e Silva S; dos Santos L; Rybarczyk-Filho JL

2013 Gene, 528(2), 277–281 DOI

RELEVANT CERTIFICATIONS

- **Systems Biology for scRNA-seq Analysis** – 15h, Columbia Uni., Jun 2025
- **Python Data Analytics** – 64h, DIO Platform, May 2024
- **Data Analysis with SQL** – 12h, DIO Platform, Apr 2024
- **Version Control with Git and GitHub** – 2h, DIO Platform, Mar 2024
- **R Scripting Applied to Bioinformatics** – 21h, CRABI-RP, Mar 2018
- **Introduction to Python and Bioinformatics** – Instructor, UNESP, Feb 2014
- **IBM Data Science Professional Certificate** – Ongoing

LANGUAGES

- **Portuguese:** Native, C2
- **English:** Fluent, C1
- **Spanish:** B1
- **Italian:** B1

FELLOWSHIPS

- **Postdoc Fellowship**

  2025-2026 EMBRAPII (Industry Partnership with Natura)

- **Postdoc Fellowship**

  2020-2022 FUNARBE (Artur Bernarder Foundation for the Federal University of Viçosa (UFV))

- **PhD Scholarships**

  2017: CAPES PhD international mobility
  2015-2019: CNPq (Brazilian National Council for Scientific and Technological Development)

- **Master's Degree Scholarship**

  2013-2015: FAPESP, São Paulo State Research Foundation

- **Undergraduate Researcher Scholarship**

  2011-2012: BIC/UCS, Universidade de Caxias do Sul Scholarship
  2010-2011: PROBIC/FAPERGS, Rio Grande do Sul State Research Foundation

  2008-2009: PIBIC - CNPq Universidade de Caxias do Sul