

Felipe Vaz Peres

[Visit my website](#) | [LinkedIn](#)

EXPERIENCE

Center for Microbial Secondary Metabolites, Technical University of Denmark

Remote

Guest Researcher

Jan 2024 - Jan 2025

- Developed metagenomic pipeline on DTU cluster (LSF) processing 100+ marine sediment samples, generating 40 high-quality MAGs (90%+ completeness) from Oxford Nanopore long-read data
- Applied ML-based contig classification to distinguish prokaryotic/eukaryotic sequences
- Standardized BGC annotation across MAGs using antiSMASH and BiG-SCAPE, functionally annotating 148 full-length BGCs and resolving cross-study labeling inconsistencies
- Reduced manual execution by developing end-to-end pipeline with benchmarking and documentation; presented findings at lab meetings

Computational, Evolutionary and Systems Biology Laboratory, University of São Paulo

Piracicaba, SP

Graduate Researcher

Jan 2022 - Jan 2025

- Applied ML models (SVMs, Random Forest, CNNs) on multi-cluster infrastructure (SGE, PBS, SLURM) to automate identification of 8.4M ncRNAs across 48 sugarcane genotypes, creating a pan-RNAome reference
- Constructed and analyzed co-expression networks (1M+ nodes) of coding/non-coding transcripts; identified 7,000+ co-expressed ncRNA modules with known protein functions using MCL clustering and complete subgraph (clique) detection
- Annotated 250K+ ncRNAs with standardized functional terms; conducted most comprehensive analysis to date on ncRNA variability in sugarcane, establishing a framework for investigating biological functions in this complex polyploid crop.
- Contributed to open-source projects across research groups, developing automated Nextflow pipelines for bacteria, microalgae, and plant genomics workflows

Genera

São Paulo, Remote

Bioinformatics Intern

Jan 2020 - Mar 2020

- Enhanced human ancestry calculator analyzing 650K+ SNPs using ADMIXTURE for maximum likelihood estimation, improving resolution across 72 diverse population groups and geographical regions
- Analyzed population structure and ancestral origins; developed documentation for Genera's ancestry calculator

Computational, Evolutionary and Systems Biology Laboratory, University of São Paulo

Piracicaba, SP

Undergraduate Researcher

May 2019 - May 2021

- Processed 3.7B NGS short reads (1.1TB+ data) from 48 sugarcane genotypes across USP/CENAPAD clusters (SGE, PBS, SLURM), identifying 16M RNAs and constructing the sugarcane pan-transcriptome
- Automated data-to-analysis workflow with Snakemake pipeline, eliminating manual execution time; revealed variability of 600K+ proteins, inferring core, accessory, and exclusive protein sets
- Presented pipeline design and findings at conferences (ISMB), emphasizing computational reproducibility

COMPUTATIONAL SKILLS

Programming: Python, Bash, R

Development: Unix/Linux, HPC cluster (SGE, PBS, LSF, SLURM), git

Pipelines: Nextflow, Snakemake

Bioinformatics: transcriptomics, genomics, metagenomics, pathway analysis, NGS (short and long reads), variant calling, gene expression, co-expression networks, functional annotation, machine learning

EDUCATION

University of São Paulo, Center of Nuclear Energy in Agriculture

Piracicaba, São Paulo

M.Sc. in Bioinformatics

Jan 2025

- Genomics and Bioinformatics, From Gene to Trait, Mobile Genetic Elements, Bioinformatics and Microbiomes

Federal University of São Carlos, Center of Agrarian Sciences

Araras, São Paulo

B.S. in Biotechnology

Jan 2022

- Statistics, Bioinformatics, Molecular Biology, Microbial Genetics, Breeding and Genetics, Genetic Engineering

HONORS AND AWARDS

- **3rd place:** Liga Brasileira de Bioinformática - The largest bioinformatics competition in Latin America *Jun 2025*
- **Graduate Research Fellowship:** National Council for Scientific and Technological Development *April 2022*
- **3rd place:** Developed an automated variant calling pipeline in under 48 hours at *Mendelics Challenge* *Nov 2021*
- **Honorable mention:** International Symposium of Undergraduate Research at University of São Paulo *Oct 2020*
- **Undergraduate Research Fellowship:** São Paulo Research Foundation *April 2019*
- **2nd place:** Synthetic Biology Hackathon at University of São Carlos *Aug 2018*

PROJECTS AND LEADERSHIP

Inteligência Não Artificial - INA (Artificial Intelligence Study Consortium)

Remote

Co-founder

Aug 2024 - Present

- Engaged in regular meetings on AI, covering ML, neural networks, and real-world applications.
- Actively contributed to hackathons and competitions, such as Liga Brasileira de Bioinformática (LBB), Genomes to Fields (G2F), applying AI techniques to complex challenges in predictive modeling and data analysis.

Study Group in Bioinformatics and Molecular Biology

Araras, São Paulo

Member

Jun 2018 - Nov 2021

- Conducted monthly meetings with 10+ bioinformatics enthusiasts, covering programming languages, computational biology concepts, and hands-on reproduction of published bioinformatics algorithms/workflows.

Sustec Junior (Junior Enterprise in Biotechnology)

Araras, São Paulo

Project Management Advisor

Jun 2018 - Jun 2021

- Implementation of new biotechnological solutions; collaboration in project planning and execution; and monitoring customer feedback.

SOFTWARE

Additional work can be seen on my GitHub profile: <https://github.com/felipevzps>

Research projects

- [KAPT](#) - Nextflow pipeline for proteome inference and annotation through de novo transcriptome assembly.
- [R2C](#) - Nextflow pipeline to build (gene) co-expression networks.
- [sugarcane RNAome](#) - Multi-genotype analyses of long-ncRNAs in sugarcane.
- [SCPT](#) - Inference and annotation of the sugarcane pan-transcriptome.
- [ContFree-NGS](#) - Open source software that removes sequences from contaminating organisms in NGS datasets.
- [YAATAP](#) - Snakemake pipeline for downloading raw RNA-seq datasets and performing transcriptome assemblies.
- [seabed-symphony](#) - Pipeline for BGCs identification in microbial community of marine sediments.

SELECTED PRESENTATIONS

2022 Python: From zero to your first software

Presented at workshop - Python Workshop for Biological Data, Online Conference - UNICAMP

An introduction to programming for bioscientists

Presented at workshop - Genetics and Molecular Biology Meeting, Online Conference - UNICAMP

2021 Removing reads from contaminating organisms in NGS datasets

Poster - Brazilian Symposium on Bioinformatics, Online Conference - Federal University of Minas Gerais

2020 Analysis of *de novo* transcriptome assemblies in sugarcane

Selected Talk (Top 15%) - International Symposium of Undergraduate Research, University of São Paulo