1. Personal Information

1.1. Last Name, First Name, Middle Name, Contact Information

Last Name: Peres
First Name: Felipe
Middle Name: Vaz

email: felipe.vzps@gmail.com
Website: felipevzps.github.io/
LinkedIn: linkedin.com/in/felipevzps/
Lattes: http://lattes.cnpq.br/7229062652523810

1.2. Academic Affiliations and Professional Experience

Jan 2024 - Jan 2025	Guest Researcher at the Center for Microbial Secondary Metabolites, Technical University of Denmark
Jan 2022 - Dez 2024	Graduate Researcher at the Computational, Evolutionary and Systems Biology Laboratory, University of São Paulo
Jan 2020 - Mar 2020	Bioinformatics Intern at Genera
May 2019 - May 2021	Undergraduate Researcher at the Computational, Evolutionary and Systems Biology Laboratory, University of São Paulo

1.3. Educational Background

2022 - 2024	**MSc.** in Bioinformatics at University of São Paulo Thesis*: Multi-genotype analyses of long-ncRNAs in sugarcane* Supervised by Dr. rer. nat. Diego Mauricio Riaño-Pachón
2018 - 2021	**BSc.** in Biotechnology at University of São Carlos

1.4. Memberships

2020 - 2021	International Society for Computational Biology (ISCB)
2020 - 2021	Brazilian Association of Bioinformatics and Computational Biology (AB3C)

2. Research, Scholarly, Creative and/or Professional Activities

2.2. Published Conference Proceedings

2.2.1. Refereed Conference Proceedings

PERES, **F.V**, RIAÑO-PACHÓN, DIEGO. M. (2021). ContFree-NGS: Removing Reads from Contaminating Organisms in Next Generation Sequencing Data. In: Stadler, P.F., Walter, M.E.M.T., Hernandez-Rosales, M., Brigido, M.M. (eds) Advances in Bioinformatics and Computational Biology. BSB 2021. Lecture Notes in Computer Science, vol 13063. Springer, Cham. https://doi.org/10.1007/978-3-030-91814-9_6

2.3. Conferences, Workshops and Talks

2.3.1. Invited Talks

PERES, **F.V**. Python: From zero to your first software. Python Workshop for Biological Data, State University of Campinas. 2022.

PERES, **F.V**. An introduction to programming for bioscientists. Genetics and Molecular Biology Meeting, State University of Campinas. 2022.

2.3.2. Refereed Presentations

I include below both the refereed presentations which I have given and those presented by a co-author

SILVA, H. R. S.; MUNOZ-PEREZ, J. M.; **PERES**, **F.V**.; RIAÑO-PACHÓN, DIEGO. M. Análises do pan-transcriptoma da cana-de-açúcar. International Symposium of Undergraduate Research, University of São Paulo. 2024

PERES, **F.V**.; RIAÑO-PACHÓN, DIEGO. M. Inferência e anotação do pan-transcriptoma da cana-de-açúcar. International Symposium of Undergraduate Research, University of São Paulo. 2022.

PERES, **F.V**.; RIAÑO-PACHÓN, DIEGO. M. Inference and annotation of the sugarcane pan-transcriptome. Intelligent Systems For Molecular Biology. 2022.

PERES, **F.V**.; RIAÑO-PACHÓN, DIEGO. M. Analysis of de novo transcriptome assemblies in sugarcane. International Symposium of Undergraduate Research, University of São Paulo. 2020. (**received honorable mention**)

PERES, **F.V**.; ROSSI, V. S.; RIAÑO-PACHÓN, DIEGO. M. Analysis of de novo transcriptome assemblies in sugarcane. Intelligent Systems for Molecular Biology. 2020.

ROSSI, V. S.; **PERES**, **F.V.**; RIAÑO-PACHÓN, DIEGO. M. In silico analysis of sugarcane SP80-3280 genes involved in transcriptional regulation and the metabolism of carbohydrates. Intelligent Systems for Molecular Biology. 2020.

2.3.3. Refereed Posters

HURTADO-LOPEZ, N.; SCHOSTAG, M. D.; LOLLE, S.; **PERES**, **F.V.**; KHODJAYAN, K.; GONZALEZ, H. M. E.; OTTO, D. J.; GRAM, L.; STRUBE, M. L. Exploring the biosynthetic potential of marine sediment microbiomes across Denmark: A multiomics approach. Danish Microbiological Society Congress, University of Copenhagen. 2024.

MUNOZ-PEREZ, J. M.; **PERES**, **F.V.**; RIAÑO-PACHÓN, DIEGO. M. Sorghum Pan-transcriptome: A new tool for bioenergy crop improvement. XIV Simpósio Científico dos Pós-Graduandos no CENA, University of São Paulo. 2023.

PERES, **F.V.**; RIAÑO-PACHÓN, DIEGO. M. Inferência e anotação funcional do pan-transcriptoma da cana-de-açúcar. XIII simpósio dos pós-graduandos no CENA, University of São Paulo. 2022.

SANTOS, R. A. C.; CARDOSO, A. S. O.; **PERES**, **F.V.**; MUNOZ-PEREZ, J. M.; RIAÑO-PACHÓN, DIEGO. M. Desenvolvimento do CoNekT Bioenergy, uma plataforma para mineração de dados transcriptômicos de plantas com importância em bioenergia. XIII simpósio dos pós-graduandos no CENA. 2022.

PERES, **F.V.**; ROSSI, V. S.; MUNOZ-PEREZ, J. M.; RIAÑO-PACHÓN, DIEGO. M. Sugarcane genomics and transcriptomics resources. XVIII Brazilian Congress of Plant Physiology and I Ibero-latinamerica of Plant Biology, Global Plant Council. 2022.

PERES, **F.V.**; RIAÑO-PACHÓN, DIEGO. M. ContFree-NGS: Removing reads from contaminating organisms in next generation sequencing datasets. Brazilian Symposium on Bioinformatics, Federal University of Minas Gerais. 2021.

ROSSI, V. S.; **PERES**, **F.V.**; RIAÑO-PACHÓN, DIEGO. M. A computational study of genes involved in transcriptional regulation and the metabolism of carbohydrates in Sugarcane (Saccharum sp.) cultivar SP80-3280. 2020.

2.4. Completed Creative Works and Scholarship

2.4.1. Software and Applications

Sugarcane pan-RNAome: Multi-genotype analyses of long-ncRNAs in sugarcane
Code available at: https://github.com/labbces/sugarcane_RNAome

Sugarcane pan-transcriptome: Inference and annotation of the sugarcane pan-transcriptome
Code available at: https://github.com/labbces/SCPT

seabed-symphony: Metagenomics pipeline designed for BGCs identification.
Code available at: https://github.com/felipevzps/seabed-symphony

YAATAP: Fully automated pipeline for *de novo* transcriptome assembly
Software available at: https://github.com/labbces/YAATAP

ContFree-NGS: Tool designed to remove contaminant sequences from NGS datasets
Software available at: https://github.com/labbces/ContFree-NGS

paper-trackr: Tired of missing out on cool papers? stay up to date with paper-trackr!
Software available at: https://github.com/felipevzps/paper-trackr

fun-MNIST: A simple neural network built from scratch.
Code available at: https://github.com/felipevzps/fun-MNIST

Indeed jobs: Automated web scraping to extract job listings from Indeed.com
Software available at: https://github.com/felipevzps/indeed_jobs

2.5. Research Fellowships and Awards

Received Graduate Research Fellowship from National Council for Scientific and Technological Development (2022)

Mendelics Challenge 2021 - Developed an automated variant calling pipeline in under 48 hours. (**awarded third place**)

International Symposium of Undergraduate Research 2020 - “Analysis of de novo transcriptome assemblies in sugarcane”. (**received honorable mention**)

Received Undergraduate Research Fellowship from São Paulo Research Foundation (2019)

Synthetic Biology Hackathon 2018 (BIOHACK) - Developed the project “BIOREMEDYATOR”, at the largest biotechnology conference in Brazil, the “IV Encontro Nacional dos Estudantes de Biotecnologia”. (**awarded second place**)

2.6. Projects and Leadership

Aug 2024 - Present	**Inteligência Não Artificial - INA** (Artificial Intelligence Study Consortium) **Co-founder**: Engaged in regular meetings on AI, covering ML, neural networks and real-world applications. Actively contributed to hackathons and competitions, such as the Genomes to Fields (G2F), applying AI techniques to complex challenges in predictive modeling and data analysis.
Jun 2018 - Nov 2021	**Study Group in Bioinformatics and Molecular Biology** **Member**: Conducted monthly meetings with 10+ bioinformatics enthusiasts, emphasizing programming languages, computational biology, and the replication of scientific paper pipelines.

Jun 2018 - Jun 2021	**Sustec Junior** (Junior Enterprise in Biotechnology) **Project Management Advisor**: Implementation of new biotechnological solutions; collaboration in project planning and execution; and monitoring customer feedback.