WENDELL JACINTO PEREIRA
RESEARCH ASSISTANT PROFESSOR
UNIVERSITY OF FLORIDA

+1 352 871-1367
wendelljpereira@gmail.com
LinkedIn: www.linkedin.com/in/wendelljpereira/
GitHub: https://github.com/wendelljpereira/ &
https://github.com/KirstLab/asc_seurat (main maintainer)
Gainesville, Florida

PROFILE

Highly motivated and results-oriented Biotechnologist and Bioinformatician with a Ph.D. in Molecular Biology and extensive experience as a Researcher and Professor. Proven expertise in applying cutting-edge genomics, transcriptomics (including single-cell technologies), and epigenomics to investigate complex plant traits relevant to agricultural improvement. Adept at developing and implementing robust computational pipelines and software tools (R/Shiny, Python, Snakemake) for biological data analysis, interpretation, and visualization. A collaborative researcher and effective communicator with a passion for translating scientific discoveries into practical solutions and a track record of mentoring and teaching. Co-founder with experience in directing data services.

SKILLS

- Expert in R (including Shiny).
- Competent in Python and Shell scripting.
- Proficient in executing and interpreting results of software commonly deployed in bioinformatics.
- Experienced in generating high-quality and informative reports using Markdown, Asciidoctor, and tools such as Jupyter Notebook and R Notebook.
- Experienced with workflow management systems, such as Snakemake.
- Adept with reproducible data analysis using version control, Git, and GitHub, and reproducible computational environments such as Docker and Conda environments.
- Advanced beginner in machine learning and deep learning.

LANGUAGES

Portuguese – Native.

English – Full professional proficiency.

Spanish – Elementary proficiency.

WORK EXPERIENCE

2024 – present **Research Assistant Professor, University of Florida, Gainesville, Florida**

2021 – 2024 **Post-Doctoral Associate, University of Florida, Gainesville, Florida**

Responsibilities:

• Developed a novel web application to facilitate single-cell RNA sequencing data analysis aimed at biologists with low bioinformatics skills, resulting in dozens of students and scientists conducting their investigations using this platform (Asc-Seurat; https://github.com/KirstLab/asc_seurat).

• Analysis of single-cell RNA sequencing data of different plant species, investigating the developmental processes governing wood formation in Populus and nitrogen fixation in *Medicago truncatula.*

• Provide data analysis support (developing and executing analytical workflow; consultation and supervision) for students, staff, and professors of different research teams and collaborators at the University of Florida and pattern institutions.

• Teaching assistant for a genomics and bioinformatics course, including lecturing, facilitation, and developing training material for hands-on sections.

• Communicating research results to the scientific community via conference presentations and publication of scientific papers.

2019 – 2020 **Laboratory technician, University of Florida, Gainesville, Florida**

Responsibilities:

• Genome assembly of plant species aiming at the identification of structural variants among genotypes.

• Development of computational pipeline for comparative genomics of plant species aiming to identify conserved coding and non-coding sequences among nitrogen-fixing species.

EDUCATION

2016-2020 **Ph.D. in Molecular Biology, University of Brasilia, Brazil.**

Note 1: Related research conducted in partnership with the Brazilian Agricultural Research Corporation ("Embrapa") Genetic Resources and Biotechnology.

Note 2: Includes an exchange program at the University of Florida, Gainesville, Florida, from August 2018 to August 2019.

Responsibilities:

• Developed an easy-to-use computation workflow for detecting DNA methylation via analysis of DNA sequencing data originated by Methyl-sensitive genome reduction. https://github.com/wendelljpereira/DArTseqMet/

• Identified DNA methylation marks in *Eucalyptus* and conducted comparative analyses of epigenetic profiles among multiple clones, investigating the environmental effects on DNA methylation and revealing a strong genetic effect on the sampled methylome.

2014-2016 **MSc in Biological Sciences, Federal University of Goiás, Brazil.**

Note 1: Related research conducted in partnership with Embrapa Rice and Beans

Responsibilities:

• Analyzed RNA sequencing data of *Phaseolus vulgaris,* investigating the transcriptional regulation in response to drought.

• Participated in the genomic characterization of a common bean core collection using single nucleotide polymorphisms.

2010-2014 **BSc in Biotechnology, Federal University of Goiás, Brazil.**

Note 1: Includes internship at Embrapa Rice and Beans, Brazil, from 2012 to 2014.

Note 2: Includes internship at the Laboratory of Protein Chemistry, Federal University of Goiás, Brazil, from 2011 to 2012.

Responsibilities:

• Optimized protocol for RNA extraction from common bean seeds.

• Conducted expression analysis (via qPCR) of genes of interest in common beans.

• Participated in genomic characterization of a common bean core collection using single nucleotide polymorphism.

• Physic-chemical characterization of proteins and polysaccharides of plants native to the Brazilian Savanna (Cerrado).

PATENTS AND COPYRIGHTS

M. Kirst, D. Conde, **W. Pereira**, P. Triozzi, C. Dervinis, J.-M. Ane. Transgenic plant and methods of stimulating spontaneous nodule formation in non-legume plants (Patent No. 20,240,384,283; Date of Patent: November 21, 2024). The patent describes methods to generate the development of pseudo-nodules in Populus.

PUBLICATIONS

Pereira, W. J., Conde, D., Perron, N., Schmidt, H. W., Dervinis, C., Venado, R. E., ... & Kirst, M. (2024). Investigating biological nitrogen fixation via single-cell transcriptomics. *Journal of Experimental Botany*, erae454. https://doi.org/10.1093/jxb/erae454

Pereira, W. J., Boyd, J., Conde, D., Triozzi, P. M., Balmant, K. M., Dervinis, C., ... & Kirst, M. (2024). The single-cell transcriptome program of nodule development cellular lineages in Medicago truncatula. *Cell Reports*, *43*(2).

Pereira, W. J., de Castro Rodrigues Pappas, M., & Pappas Jr, G. J. (2023). Computational Protocol for DNA Methylation Profiling in Plants Using Restriction Enzyme-Based Genome Reduction. In *Plant Genotyping: Methods and Protocols* (pp. 23-36). New York, NY: Springer US. https://doi.org/10.1007/978-1-0716-3024-2_3.

Knaack, S. A., Conde, D., Chakraborty, S., Balmant, K. M., Irving, T. B., Maia, L. G. S., ... & Roy, S. (2022). Temporal change in chromatin accessibility predicts regulators of nodulation in Medicago truncatula. *BMC biology*, *20*(1), 252. https://doi.org/10.1186/s12915-022-01450-9.

Conde, D., Triozzi, P. M., **Pereira, W. J.,** Schmidt, H. W., Balmant, K. M., Knaack, S. A., ... & Kirst, M. (2022). Single-nuclei transcriptome analysis of the shoot apex vascular system differentiation in Populus. *Development*, *149*(21), dev200632. https://doi.org/10.1242/dev.200632.

Pereira, W. J., Knaack, S., Chakraborty, S., Conde, D., Folk, R. A., Triozzi, P. M., ... & Kirst, M. (2022). Functional and comparative genomics reveals conserved non-coding sequences in the nitrogen-fixing clade. *New Phytologist*, *234*(2), 634-649. https://doi.org/10.1111/nph.18006.

Triozzi, P. M., Irving, T. B., Schmidt, H. W., Keyser, Z. P., Chakraborty, S., Balmant, K., ... & Conde, D. (2022). Spatiotemporal cytokinin response imaging and ISOPENTENYLTRANSFERASE 3 function in Medicago nodule development. *Plant Physiology*, *188*(1), 560-575. https://doi.org/10.1093/plphys/kiab447.

Pereira, W. J., Almeida, F. M., Conde, D., Balmant, K. M., Triozzi, P. M., Schmidt, H. W., ... & Kirst, M. (2021). Asc-Seurat: analytical single-cell Seurat-based web application. *BMC bioinformatics*, *22*, 1-14. https://doi.org/10.1186/s12859-021-04472-2.

Conde, D., Triozzi, P. M., Balmant, K. M., Doty, A. L., Miranda, M., Boullosa, A., ... & Kirst, M. (2021). A robust method of nuclei isolation for single-cell RNA sequencing of solid tissues from the plant genus Populus. *PLoS One*, *16*(5), e0251149. https://doi.org/10.1371/journal.pone.0251149.

Pereira, W. J., Pappas, M. D. C. R., Campoe, O. C., Stape, J. L., Grattapaglia, D., & Pappas Jr, G. J. (2020). Patterns of DNA methylation changes in elite Eucalyptus clones across contrasting environments. *Forest Ecology and Management*, *474*, 118319. https://doi.org/10.1016/j.foreco.2020.118319

Pereira, W. J., Pappas, M. D. C. R., Grattapaglia, D., & Pappas Jr, G. J. (2020). A cost-effective approach to DNA methylation detection by Methyl Sensitive DArT sequencing. *PLoS One*, *15*(6), e0233800. https://doi.org/10.1371/journal.pone.0233800.

Batista, K. A., **Pereira, W. J.,** Moreira, B. R., Silva, C. N., & Fernandes, K. F. (2020). Effect of autoclaving on the nutritional quality of hard-to-cook common beans (Phaseolus vulgaris). *Int. J. Environ. Agric. Biotechnol*, *5*(1), 22. https://dx.doi.org/10.22161/ijeab.51.4.

Pereira, W. J., Melo, A. T. D. O., Coelho, A. S. G., Rodrigues, F. A., Mamidi, S., Alencar, S. A. D., ... & Vianello, R. P. (2020). Genome-wide analysis of the transcriptional response to drought stress in root and leaf of common bean. *Genetics and Molecular Biology*, *43*. https://doi.org/10.1590/1678-4685-GMB-2018-0259.

Valdisser, P. A., **Pereira, W. J.,** Almeida Filho, J. E., Müller, B. S., Coelho, G. R., de Menezes, I. P., ... & Vianello, R. P. (2017). In-depth genome characterization of a Brazilian common bean core collection using DArTseq high-density SNP genotyping. *BMC genomics*, *18*, 1-19. https://doi.org/10.1186/s12864-017-3805-4.

Pereira, W. J., Bassinello, P. Z., Brondani, C., & Vianello, R. P. (2017). An improved method for RNA extraction from common bean seeds and validation of reference genes for qPCR. *Crop Breeding and Applied Biotechnology*, *17*, 150-158. https://doi.org/10.1590/1984-70332017v17n2a22.

Pereira, W. J., Alves, G. L., Purcena, L. L., Bataus, L. A. M., Fernandes, K. F., & Batista, K. A. Statistical optimization of α-amylase production by Escherichia coliusing extruded bean as nitrogen and carbon source (2017). *International Journal of Environment, Agriculture and Biotechnology*, *2*(4), 238886.

Abreu, F. R. M., de Deus, K. E., **Pereira, W. J.,** Dias Silveira, R. D., Pereira Vianello, R., & Brondani, C. (2016). Expression of rice genes homologous of Arabidopsis genes previously related to drought tolerance. *Australian Journal of Crop Science*, *10*(9), 1266-1272. https://doi.org/10.21475/ajcs.2016.10.09.p7652.

Valdisser, P. A. M., Pappas, G. J., de Menezes, I. P., Müller, B. S., **Pereira, W. J.,** Narciso, M. G., ... & Vianello, R. P. (2016). SNP discovery in common bean by restriction-associated DNA (RAD) sequencing for genetic diversity and population structure analysis. *Molecular Genetics and Genomics*, *291*, 1277-1291. https://doi.org/10.1007/s00438-016-1182-3.

Siqueira, B. S., Bassinello, P. Z., Malgaresi, G., **Pereira, W. J.,** & Fernandes, K. F. (2016). Analyses of technological and biochemical parameters related to the HTC phenomenon in carioca bean genotypes by the use of PCA. *LWT-Food Science and Technology*, *65*, 939-945. https://doi.org/10.1016/j.lwt.2015.09.030.

Evaristo de Deus, K., Lanna, A. C., Abreu, F. R. M., Dias Silveira, R. D., **Jacinto Pereira, W.,** Brondani, C., & Pereira Vianello, R. (2015). Molecular and biochemical characterization of superoxide dismutase (SOD) in upland rice under drought. *Australian Journal of Crop Science*, *9*(8).

Silva Filho, V., **Pereira, W. J.,** Fernandes, K. F., & Batista, K. D. A. (2014). Extração, purificação parcial e caracterização de lectinas de sementes de Crotalaria juncea. *Revista de Biotecnologia & Ciência (ISSN 2238-6629)*, *2*(2).

Mueller, B. S. D. F., Sakamoto, T., Silveira, R. D. D., Zambussi-Carvalho, P. F., Pereira, M., Pappas, G. J., ... & Vianello-Brondani, R. P. (2014). Differentially expressed genes during flowering and grain filling in common bean (Phaseolus vulgaris) grown under drought stress conditions. *Plant molecular biology reporter*, *32*, 438-451. https://doi.org/10.1007/s11105-013-0651-7.

Siqueira, B. D. S., **Pereira, W. J.,** Batista, K. D. A., Oomah, B. D., Fernandes, K. F., & Bassinello, P. Z. (2014). Influence of storage on darkening and hardening of slow-and regular-darkening carioca bean (Phaseolus vulgaris L.) genotypes. https://doi.org/10.5296/jas.v2i2.5859.

Pereira, W. J., Silva Filho, R. R., Pereira Junior, M. A., Batista, K. D. A., & Fernandes, K. F. (2012). Uso de goma de cajueiro em substituição ao ágar em meio de cultura. *Revista de Biotecnologia & Ciência (ISSN 2238-6629)*, *1*(2).

Pereira, W. J., Silva Filho, R. R., Pereira Junior, M. A., Di-Medeiros, M. C., Batista, K. D. A., & Fernandes, K. F. (2012). Uso de goma de angico em substituição ao ágar em meio de cultura. *Revista de Biotecnologia & Ciência (ISSN 2238-6629)*, *2*(2).

PRE-PRINTS

Gomez-Soto, D., **Pereira, W. J**., Piedrabuena-Diaz, A., Dervinis, C., Kirst, M., Allona, I., ... & Conde, D. (2025). Single-nuclei transcriptomics revealed auxin-driven mechanisms of wood plasticity and severe drought tolerance in poplar. *bioRxiv*, 2025-01.

Perron, N., Dervinis, C., **Pereira, W.**, Barbazuk, B., & Kirst, M. (2024). Mesophyll-specific circadian dynamics of CAM induction in the ice plant unveiled by single-cell transcriptomics. *bioRxiv*, 2024-01.

SCHOLARSHIPS

2023 - Awarded a Corteva New Frontiers scholarship to present my work on the Corteva New Frontiers workshop.

2018 - Awarded a scholarship from the Coordination of Superior Level Staff Improvement (CAPES), Brazil, to spend a year of my Ph.D. in an exchange program abroad as part of the Sandwich Doctorate Abroad Program.

PRESENTATIONS

Pereira, W. J. (2023) – Cell Lineage Transitions During Initial Phases of Nodule Development of *Medicago truncatula*. Oral presentation at the American Society of Plant Biologists meeting, Savannah, GA.

Pereira, W. J. (2023) – The Single-Cell Transcriptome Program of Nodule Development in *Medicago truncatula.* Oral presentation at the Corteva New Frontiers workshop, Johnson, IA.

Pereira, W. J. (2023) – Single-Cell Genomics of Poplar Wood Development. Poster presentation at the 2023 Genomic Sciences Program Annual PI Meeting, Washington, DC.

Pereira, W. J. (2022) – The Single-Cell Revolution in Genomics. Online workshop taught to graduate students in Biological Sciences, Federal University of Goiás, Brazil.

Pereira, W. J. (2022) – Characterization of the expression profile of *Medicago truncatula* roots during the first 96 hours of the root nodule symbiosis at the single-cell level. Oral presentation at the 25th North American Symbiotic Nitrogen Fixation Conference, Madison, WI.

Pereira, W. J. (2021) – Functional and comparative genomics reveals conserved non-coding sequences in the nitrogen-fixing clade. Online oral presentation at the 14th European Nitrogen Fixation Conference.

Pereira, W. J. (2020) – Snakemake workflows. Online workshop taught to graduate students participating in the Bioinformatics Workshop organized by the University of Florida Plant Science Council.