

FABRÍCIO ALMEIDA-SILVA

I am a computational biologist interested in developing and applying algorithms to understand how evolution shaped plant genomes and gene networks. I am an active software developer in the fields of plant genomics and systems, with a special focus on gene network reconstruction, candidate gene mining, and evolutionary genomics.



EDUCATION

- Current
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2022
- **PhD, Bioinformatics**
Ghent University 📍 Ghent, Belgium
 - **Master's, Plant Biotechnology**
State University of Northern Rio de Janeiro 📍 RJ, Brazil
 - Thesis: Identification and prioritization of biotic stress-related genes in soybean by integrating GWAS and gene coexpression networks
 - **Undergraduate, Biological Sciences**
State University of Northern Rio de Janeiro 📍 RJ, Brazil
 - Thesis: Analysis of soybean transcriptional regulation using gene coexpression networks
- 2022
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2020
- 2019
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2016



PUBLICATIONS

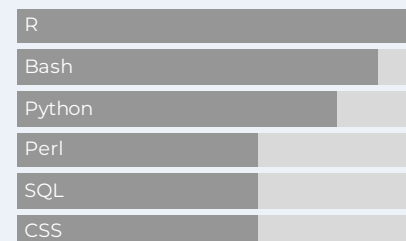
- 1 **F Almeida-Silva**, TM Venancio (2022). *BioNERO: an all-in-one R/Bioconductor package for comprehensive and easy biological network reconstruction. Functional & Integrative Genomics*. 22 (1), 131-136
- 2 **F Almeida-Silva**, TM Venancio (2022). *Pathogenesis-related protein 1 (PR-1) genes in soybean: Genome-wide identification, structural analysis and expression profiling under multiple biotic and abiotic stresses. Gene*. 809, 146013
- 3 DK Turquetti-Moraes, KC Moharana, **F Almeida-Silva**, F Pedrosa-Silva et al. (2022). *Integrating omics approaches to discover and prioritize candidate genes involved in oil biosynthesis in soybean. Gene*. 808, 145976
- 4 **F Almeida-Silva**, TM Venancio (2021). *Integration of genome-wide association studies and gene coexpression networks unveils promising soybean resistance genes against five common fungal pathogens. Scientific Reports*. 11 (1), 1-10
- 5 **F Almeida-Silva**, TM Venancio (2021). *cageminer: an R/Bioconductor package to prioritize candidate genes by integrating GWAS and gene coexpression networks. bioRxiv*.
- 6 **F Almeida-Silva**, KC Moharana, TM Venancio (2021). *The state of the art in soybean transcriptomics resources and gene coexpression networks. in silico Plants*. 3 (1), diab005
- 7 S Sangi, PM Araújo, FS Coelho, RK Gazara, **F Almeida-Silva** et al. (2021). *Genome-Wide*



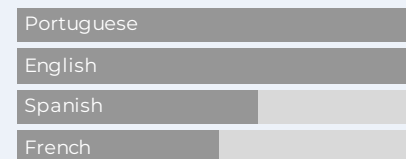
CONTACT

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PROGRAMMING SKILLS



LANGUAGES



Last updated on 2022-03-25.

Analysis of the COBRA-Like Gene Family Supports Gene Expansion through Whole-Genome Duplication in Soybean (Glycine max). **Plants.** 10 (1), 167

8 **F Almeida-Silva**, KC Moharana, FB Machado, TM Venancio (2020). *Exploring the complexity of soybean (Glycine max) transcriptional regulation using global gene co-expression networks*. **Planta.** 252 (6), 1-12

9 KC Moharana, **F Almeida-Silva**, RK Gazara, F Pedrosa-Silva, FS Coelho et al. (2020). *Systematic analysis of 1,298 RNA-Seq samples and construction of a comprehensive soybean (Glycine max) expression atlas.* **The Plant Journal: for Cell and Molecular Biology.**