FABRÍCIO ALMEIDA-SILVA

I am a computational biologist interested in developing and applying algorithms to understand how evolution shaped plant genomes and gene networks. Additionally, I am interested in developing biometrical and biostatistical frameworks to identify genes associated with quantitative traits of agronomical relevance in crop species, especially legumes.

🎓 EDUCATION

Current | 2020

Master's Candidate, Plant Biotechnology
State University of Northern Rio de Janeiro
📍 RJ, Brazil

2019 | 2016

Undergraduate, Biological Sciences
State University of Northern Rio de Janeiro
📍 RJ, Brazil

· Thesis: Analysis of soybean transcriptional regulation using gene coexpression networks

💻 RESEARCH EXPERIENCE

Current | 2020

Graduate Researcher
Venancio Lab 📍 State University of Northern Rio de Janeiro

· Development of an R package to infer and compare biological networks
· Development of an R package to integrate GWAS and RNA-seq data to mine candidate genes associated with agronomically important traits
· Development and optimization of pipeline to process and analyze large-scale RNA-seq data
· Genomic analysis of stress-related gene families in soybean

2019 | 2017

Undergraduate Researcher
Venancio Lab 📍 State University of Northern Rio de Janeiro

· Analysis of large-scale RNA-seq data
· Construction of the largest soybean expression atlas

📖 PUBLICATIONS

1 **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

2 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

3 **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
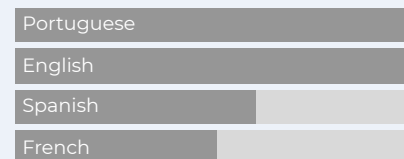
CONTACT

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🔗 almeidasilvaf.github.io
🐦 almeidasilvaf
🐱 almeidasilvaf

PROGRAMMING SKILLS

R	
Bash	
Python	
Perl	
SQL	
CSS	

LANGUAGES

Portuguese	
English	
Spanish	
French	
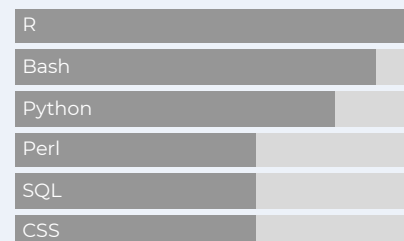
Last updated on 2022-01-10.

④ **F Almeida-Silva**, TM Venancio (2021). *BioNERO: an all-in-one R/Bioconductor package for comprehensive and easy biological network reconstruction.* **Functional and Integrative Genomics**.

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 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**.

▰ R PACKAGES AND DATA PRODUCTS

F Almeida-Silva, TM Venancio (2021). *BioNERO: Biological Network Reconstruction Omnibus.* DOI: 10.18129/B9.bioc.BioNERO

F Almeida-Silva, TM Venancio (2021). *cageminer: Candidate Gene Miner.* DOI: 10.18129/B9.bioc.cageminer

F Almeida-Silva, TM Venancio (2021). *SoyFungiGCN: R/Shiny package to explore a gene coexpression network of soybean infected with pathogenic fungi.*
   Package: github.com/almeidasilvaf/SoyFungiGCN
   Web app: soyfungigcn.venanciogroup.uenf.br

ꙮ AWARDS AND DISTINCTIONS

2021 — **Best oral presentation**
6th Fluminense Graduate Congress ⚲ Brazil

2020 — **Honorable mention**
3rd Symposium on Plant Biotechnology ⚲ Brazil

2020 — **Best poster presentation**
5th Fluminense Graduate Congress ⚲ Brazil

2020 — **Undergraduate Honors**
State University of Northern Rio de Janeiro ⚲ Brazil

2015 **Honorable mention**
Brazilian Maths Olympiad for Public Schools

◉ Brazil

📖 COMPLEMENTARY EDUCATION

2021 **Building Web Applications in Django**
University of Michigan

◉ Michigan, USA

2021 **Using Databases with Python**
University of Michigan

◉ Michigan, USA

2021 **Using Python to Access Web Data**
University of Michigan

◉ Michigan, USA

2020 **Integrated Analysis in Systems Biology**
Icahn School of Medicine at Mount Sinai

◉ New York, USA

2020 **Dynamical Modeling Methods for Systems Biology**
Icahn School of Medicine at Mount Sinai

◉ New York, USA

2020 **Network Analysis in Systems Biology**
Icahn School of Medicine at Mount Sinai

◉ New York, USA

2020 **Statistics for Genomic Data Science**
Johns Hopkins University

◉ Baltimore, USA

2020 **Developing Data Products**
Johns Hopkins University

◉ Baltimore, USA

2020 **Building Data Visualization Tools**
Johns Hopkins University

◉ Baltimore, USA

2020 **Regression Models**
Johns Hopkins University

◉ Baltimore, USA

2020 **Advanced R Programming**
Johns Hopkins University

◉ Baltimore, USA

2020 **Algorithms for DNA sequencing**
Johns Hopkins University

◉ Baltimore, USA

2020 **Python for Genomic Data Science**
Johns Hopkins University

◉ Baltimore, USA

2020 **Practical Machine Learning**
Johns Hopkins University

◉ Baltimore, USA

2020	**Statistical Inference**	
	Johns Hopkins University	📍 Baltimore, USA
2019	**Plant Bioinformatics**	
	Johns Hopkins University	📍 Baltimore, USA
2019	**Bioinformatic Methods**	
	Johns Hopkins University	📍 Baltimore, USA

▣ SELECTED TALKS AND POSTERS

1. **F Almeida-Silva**. *cageminer: mining candidate genes by integrating GWAS and gene coexpression networks*. **BioC2021**. Virtual. (2021)

2. **F Almeida-Silva**, TM Venancio. *Prioritizing biotic stress-related genes in soybean by integrating GWAS and gene coexpression network analysis*. **5th Meeting on Genetics and Plant Breeding**. Viçosa, Brazil. (2020)

3. **F Almeida-Silva**, KC Moharana, FB Machado, RK Gazara, TM Venancio. *Global coexpression network analysis unveils important aspects of evolution and transcriptional regulation in soybean (Glycine max)*. **15th International Conference of the Brazilian Society for Bioinformatics and Computational Biology**. Campos do Jordão, Brazil. (2019)

4. **F Almeida-Silva**, FB Machado, KC Moharana, TM Venancio. *Gene coexpression networks uncover transcription factors that probably shape the transcriptional landscape during soybean germination*. **47th Annual Meeting of the Brazilian Society for Biochemistry and Molecular Biology**. Joinville, Brazil. (2018)

🔖 SERVICE

REVIEWER

· 2021 - current **Scientific Reports**
· 2021 - current **BMC Plant Biology**