

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
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2020
- **Master's Candidate, Plant Biotechnology**
State University of Northern Rio de Janeiro 📍 RJ, Brazil
 - **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
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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
 - **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

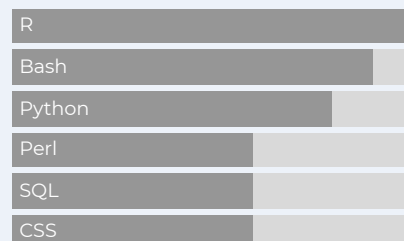
- 1 **F Almeida-Silva**, TM Venancio (2022). *Pathogenesis-related protein 1 (PR-1) genes in soybean: Genome-wide identification, structural analysis and expression profiling under multiple biotic and abiotic stresses*. **Gene**. 809, 146013
- 2 DK Turquetti-Moraes, KC Moharana, **F Almeida-Silva**, 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*. **bioRxiv**.



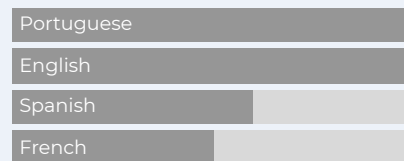
CONTACT

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🐦 [almeidasilvaf](https://twitter.com/almeidasilvaf)
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PROGRAMMING SKILLS



LANGUAGES



Last updated on 2021-11-29.

- 4 **F Almeida-Silva**, TM Venancio (2021). *cageminer: an R/Bioconductor package to prioritize candidate genes by integrating GWAS and gene coexpression networks*. **bioRxiv**.
- 5 **F Almeida-Silva**, TM Venancio (2021). *BioNERO: an all-in-one R/Bioconductor package for comprehensive and easy biological network reconstruction*. **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](https://doi.org/10.18129/B9.bioc.BioNERO)



F Almeida-Silva, TM Venancio (2021). *cageminer: Candidate Gene Miner*. DOI: [10.18129/B9.bioc.cageminer](https://doi.org/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/almeidasilva/SoyFungiGCN

Web app: soyfungigcn.venanciogroup.uenf.br



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**