

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

- PhD, Bioinformatics**
Ghent University 📍 Ghent, Belgium
Current | 2022
- Master's, Plant Biotechnology**
State University of Northern Rio de Janeiro 📍 RJ, Brazil
2022 | 2020
 - 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
2019 | 2016
 - Thesis: Analysis of soybean transcriptional regulation using gene coexpression networks

RESEARCH EXPERIENCE

- Graduate Researcher**
Venancio Lab 📍 State University of Northern Rio de Janeiro
Current | 2020
 - 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
2019 | 2017
 - Analysis of large-scale RNA-seq data
 - Construction of the largest soybean expression atlas

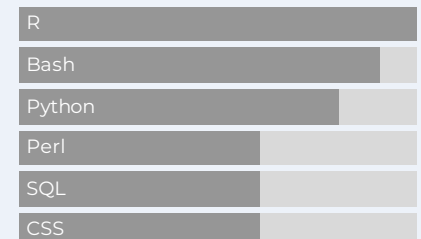
PUBLICATIONS

- 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

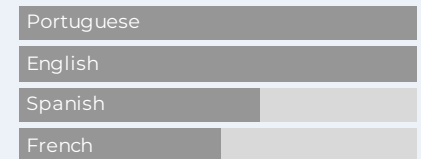
CONTACT

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- 🐦 [almeidasilvaf](https://twitter.com/almeidasilvaf)
- 📷 [almeidasilvaf](https://www.instagram.com/almeidasilvaf)

PROGRAMMING SKILLS



LANGUAGES



Last updated on 2022-03-25.

- 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 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/almeidasilvaf/SoyFungiGCN
Web app: soyfungigcn.venanciogroup.uenf.br



AWARDS AND DISTINCTIONS

- | | | |
|------|---|----------|
| 2021 | <ul style="list-style-type: none"> ● Best oral presentation 6th Fluminense Graduate Congress | 📍 Brazil |
| 2020 | <ul style="list-style-type: none"> ● 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**
- 2022 - current **Frontiers in Plant Science**