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.

CONTACT

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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

PROGRAMMING SKILLS

- R
- Bash
- Python
- Perl
- SQL
- CSS

PUBLICATIONS

1. **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**.

2. DK Turquetti-Moraes, KC Moharana, **F Almeida-Silva**, F Pedrosa-Silva et al. (2021). *Integrating omics approaches to discover and prioritize candidate genes involved in oil biosynthesis in soybean*. **bioRxiv**.

3. **F Almeida-Silva**, TM Venancio (2021). *cageminer: an R/Bioconductor package to prioritize candidate genes by integrating GWAS and gene coexpression networks*. **bioRxiv**.

Last updated on 2021-09-10.

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

5 **F Almeida-Silva**, TM Venancio (2021). *Pathogenesis-related protein 1 (PR-1) genes in soybean: genome-wide identification, structural analysis and expression profiling under multiple biotic and abiotic stresses*. **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

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

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

Almeida-Silva F, Venancio T (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 — **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

SERVICE

REVIEWER

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