# 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

Master's Candidate, Plant Biotechnology

State University of Northern Rio de Janeiro

Q RJ. Brazil

2020 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 largescale 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 (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. hioPxiv



#### CONTACT

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### PROGRAMMING SKILLS

R
Bash
Python
Perl
SQL
CSS

- 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**.





**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

**Q** AWARDS AND DISTINCTIONS Best oral presentation 2021 Brazil 6th Fluminense Graduate Congress Honorable mention 2020 Brazil 3rd Symposium on Plant Biotechnology 2020 Best poster presentation Brazil 5th Fluminense Graduate Congress **Undergraduate Honors** 2020 Brazil State University of Northern Rio de Janeiro Honorable mention 2015 Brazil Brazilian Maths Olympiad for Public Schools

		COMPLEMENTARY EDUCATION	
2021		Building Web Applications in Django University of Michigan	<b>♥</b> Michigan, USA
2021	•	Using Databases with Python University of Michigan	<b>♥</b> Michigan, USA
2021		Using Python to Access Web Data University of Michigan	<b>♥</b> 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	<b>♥</b> Baltimore, USA
2020	•	Developing Data Products Johns Hopkins University	<b>♥</b> Baltimore, USA
2020		Building Data Visualization Tools Johns Hopkins University	<b>♥</b> Baltimore, USA
2020	•	Regression Models Johns Hopkins University	<b>♥</b> Baltimore, USA
2020		Advanced R Programming Johns Hopkins University	<b>♥</b> Baltimore, USA
2020		Algorithms for DNA sequencing Johns Hopkins University	Paltimore, USA
2020	•	Python for Genomic Data Science Johns Hopkins University	<b>♥</b> Baltimore, USA
2020		Practical Machine Learning Johns Hopkins University	<b>♥</b> Baltimore, USA
2020	•	Statistical Inference Johns Hopkins University	<b>♥</b> Baltimore, USA

Plant Bioinformatics
Johns Hopkins University

■ Bioinformatic Methods
Johns Hopkins University

■ SERVICE

#### **REVIEWER**

- · 2021 current **Scientific Reports**
- $\cdot$  2021 current **BMC Plant Biology**