Jacqueline Salvi de Mattos

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I have a BSc in Biological Sciences and I am currently pursuing my PhD degree, having my research focus on genomics and bioinformatics for an evolutionary biology approach. For research purposes, I have had training in both R and Python, and I am also skilled in Linux command line, bash scripting, SQL, High Performance Computing (HPC), GitHub and Git version control, and many genomic/bioinformatics frameworks and tools for analyses of NGS data. I have experience with *de-novo* genome assembly, chromosome-level assembly, and transcriptomic assembly as well. In addition, I have skills with many programming languages and web/software development tools, such as JavaScript, PHP, HTML, CSS.

Education

2022	**Visiting PhD Researcher (current)**
	Ecology and Evolutionary Biology Department - EBIO - University of Colorado Boulder
	Colorado/USA - The Kane Lab
	Co-advisor: Prof. Nolan Kane
2021	**PhD in Plant Sciences (current)**
	Department of Plant Sciences, Campinas State University – Brazil
	Supervisor: Prof. Fabio Pinheiro
	Co-supervisor: Profa. Clarisse Palma da Silva; Prof. Diego Riaño Pachon.
	Research funded by CNPq.
2019	**MSc in Environmental Sciences**
	Department of Environmental Sciences, Federal University of São Carlos, São Carlos/ São Paulo - Brazil
	Supervisor: Prof. Marco Antônio Batalha – Department of Plant Sciences
	Funded research by CAPES.
2015	**BSc in Biological Sciences**
	Department of Ecology, São Paulo State University, Rio Claro/São Paulo - Brazil
	Supervisor: Prof. Mauro Galetti – Department of Ecology – São Paulo State University, Brazil

Research

2021	Graduate Researcher (PhD); University of Campinas, Brazil; University of Colorado Boulder, USA;
2019	Graduate Researcher (MSc); University of São Carlos, Brazil
2016	Research Intern; School of Earth, Ocean and Ecological Sciences University of Liverpool, UK

Publications

<u>Peer-reviewed</u>

1. GALETTI, MAURO ; MOLEÓN, MARCOS ; JORDANO, PEDRO ; PIRES, MATHIAS M.; GUIMARÃES, PAULO R. ; PAPE, THOMAS ; NICHOLS, ELIZABETH ; HANSEN, DENNIS; OLESEN, JENS, M.; MUNK, MICHAEL ; **DE MATTOS, JACQUELINE S.** ; SCHWEIGER, ANDREAS H.; OWEN-SMITH, NORMAN ; JOHNSON, CHRISTOPHER N.; MARQUIS, ROBERT J.;SVENNING, JENS-CHRISTIAN. 2018.Ecological and evolutionary legacy of megafauna extinctions. *Biological Reviews*, vol. 93, issue 2. DOI: HTTPS://DOI.ORG/10.1111/BRV.12374

2. **MATTOS, J.S.**, MORELLATO, L.P.C., CAMARGO, M.G.G., BATALHA, M.A. 2019. Plant phylogenetic diversity of tropical mountaintop rocky grasslands: local and regional constraints. *Plant Ecology. DOI:* HTTPS://DOI.ORG/10.1007/S11258-019-00982-5

3. **MATTOS, J.S.**, MORELLATO, L.P.C., BATALHA, M.A. 2021. Plant communities in tropical ancient mountains: how are they spatially and evolutionary structured? *Botanical Journal of the Linnean Society*. January 2021.

Workshops & Courses

2022   **Bioinformatics and Genomics for Biodiversity**
University of Lima, Peru - Extension International Course.

2021   **Bioinformatics Algorithms** – Federal University of Minas Gerais, Brazil.

2021   **Bioinformatics for Biologists: an introduction to Linux, Bash and R**
Wellcome Genome Campus Advanced Courses and Scientific Conferences, UK.

2017   **Complete Web Developer Course** - Udemy
Certification fromCambridge Certification Authority.
Main skills learned: PHP, JavaScript, MySQL, Bootstrap, Python.

Work experience

2019-2021 *Supersoft Sistemas de Gestão – Rio Claro/SP – Brazil*
Full-Stack Software Developer. Main skills: development of websites, applications and softwares. Maintenance of websites and applications/services. Also participating in the leadership of projects. Main programming languages and frameworks: PHP, JavaScript, Angular, TypeScript, HTML, CSS, MySQL.

2017-2018 *Supersoft Sistemas de Gestão – Rio Claro/SP - Brazil*
Web and Software Development Intern. Main skills: Developing websites using all the available technologies and programming languages for the web, such as PHP, JavaScript, HTML, CSS, MySQL.

Computational Tools and Programming Languages

Bash, Linux Command Line, High Performance Computing (HPC), GitHub and Git version control, R, SQL Databases, Javascript, Html.

Computational Research Methods

Reproducible bioinformatics workflows to work with NGS sequence data, align sequence reads to a reference genome, call variants; de novo genome assembly, including chromosome-level assembly with chromatin conformation capture analyses, genome and transcriptome annotation, de-novo transcriptome assembly. Writing bash scripts for bioinformatic pipelines. Currently studying Python for genome data science.