

Cristiane Hayumi Taniguti | CV

I'm a geneticist with focus in statistical genetics, bioinformatics and plant breeding. My eight years of academic experience provided my opportunities to interact with researchers and plant breeders from private and public organizations, understand their needs and develop statistical methods, computational tools, and graphical interfaces to attend them. I'm enthusiast to understand and solve complex issues such as polyploid species genetics. I'm a extrovert person with great communication skills. I enjoy to disseminate new methods and technologies through talks and courses. For more information about me, please, visit my personal website: <https://cristianetaniguti.github.io/>

»»» Technical Skills

- » **Genetics:** Studies in meiosis heritage properties, reconstruction of diploid and polyploid population haplotypes, phenotypes and genotypes association, identification of candidate genes.
- » **Bioinformatics:** Development of bioinformatic workflows to compare and perform SNP and dosage calling with different combinations of software.
- » **Statistics:** Agricultural experimental designs, linear mixed models, and graphical models.
- » **R Packages:** Development and maintenance of `OneMap` R package to build linkage maps in diploid outcrossing species. Development and maintenance of `VIEWpoly` package and shiny app to integrate and visualize results from polyploid species genetic analysis.
- » **HPC Servers and Cloud Computing:** I have experience working with high-performance computers at the University of São Paulo and Texas A&M. Also using the Google Cloud platform.

Software and Language Skills

- » **Programming skills:** R, Bash, WDL
- » **Computational programs:** GitHub, L^AT_EX, Markdown, RStudio, Docker, Emacs, Office 365, Inkscape, Shiny
- » **Operational systems:** Unix|Linux, Mac, Windows
- » **Languages:** Portuguese (native), English

»»» Education

2017-2021 (4 years)	Ph.D. in Genetics and Plant Breeding	University of São Paulo – ESALQ/USP
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- » Title: Building highly saturated genetic maps with OneMap 3.0: new approaches using workflows
- » Advisor: Prof. Antonio Augusto Franco Garcia
- » Statistical Genetics Laboratory

2015-2017 (2 years)	Master Degree in Genetics and Plant Breeding	University of São Paulo – ESALQ/USP
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- » Title: Development of an integrated genetic map for a full-sib progeny from crossing between *Eucalyptus grandis* and *Eucalyptus urophylla*
- » Advisor: Prof. Antonio Augusto Franco Garcia
- » Statistical Genetics Laboratory

2009 – 2014 Bachelor's Degree in Biotechnology Federal University of São Carlos
(5 years) – UFSCar

- » Title: Gene expression of *Anastrepha obliqua* male tissue libraries
- » Advisor: Prof. Reinaldo Alvarenga Alves de Brito
- » Population Genetics and Evolution Laboratory

»»» Professional Experience

2021 - present	Postdoctoral Research Associate	Texas A&M University, Department of Horticultural Sciences
	<ul style="list-style-type: none"> » Funded by USDA SCRI grant: "Tools for Genomic-Assisted Breeding in Polyploids" Grant No. 2020-51181-32156 » Supervisor: Oscar Riera-Lizarazu and David Byrne 	
2014	Intern	Sugarcane Technology Center – CTC
	<ul style="list-style-type: none"> » Topic: SNP calling in sugarcane GBS dataset » Supervisor: Sabrina Chabregas 	
2012 (3 months)	Summer student	McGill University MCGILL
	<ul style="list-style-type: none"> » Title: Cellular regulation of CNC transcription factors » Advisor: Prof. Volker Blank » Division of Experimental Medicine 	

»»» Most relevant publications

Article	TANIGUTI, C. H. , TANIGUTI, L. M.; AMADEU, R. R.; LAU, J.; DE SIQUEIRA GESTEIRA, G.; OLIVEIRA, T. D. P.; FERREIRA, G. C.; Pereira, G. D. S.; BYRNE, D.; MOLLINARI, M.; RIERA-LIZARAZU, O.; & GARCIA, A. A. F. Developing best practices for genotyping-by-sequencing analysis using linkage maps as benchmarks. BioRxiv .doi: 10.1101/2022.11.24.517847, 2022.
Article	TANIGUTI, C. H. ; GESTEIRA, G. S.; LAU, J.; PEREIRA, G. S.; ZENG, Z. B.; BYRNE, D. H.; RIERA-LIZARAZU, O.; MOLLINARI, M. . VIEWpoly: a visualization tool to integrate and explore results of polyploid genetic analysis. Journal of Open Source Software . doi: 10.21105/joss.04242, 2022.
Article	CONSON, A. R. O.; TANIGUTI, C. H. ; AMADEU, R. R.; ANDREOTTI, I. A. A.; DE SOUZA, L. M.; DO SANTOS, L. H. B.; DE SOUZA, A. P. . High-resolution genetic map and QTL analysis of growth-related traits of <i>Hevea brasiliensis</i> cultivated under suboptimal temperature and humidity conditions. Frontiers in Plant Science , doi: 10.3389/fpls.2018.01255, 2018.

»»» Awards

2023	Postdoctoral Scholar Travel Award - Texas A&M University
2021	Market Ready Prize - Cornell Institute Digital Agriculture Hackathon 2021
2018	WikiProject Computational Biology/ISCB award 2018 - International Society for Computational Biology (ISCB) and WikiProject Computational Biology
2017	Best Poster Award - Brazilian Association for Bioinformatics and Computational Biology