Genomics Coordinator with Breeding Insight at Cornell University· Ithaca, New York · **cht47@cornell.edu**

Cristiane Hayumi Taniguti | CV

Email:	cht47@cornell.edu | chaytaniguti@gmail.com
Website:	cristianetaniguti.github.io
Programming Languages:	R (expert), Bash (advanced), WDL (advanced), Nextflow (intermediate), Python (intermediate)
Languages:	Portuguese (native), English (fluent)
Operating Systems:	Unix|Linux, Mac, Windows
Technical Skills:	Git/GitHub, LaTeX, Markdown, RStudio, VS Code, Docker, Emacs, Office 365, Inkscape, Shiny

I currently serve as the Genomics Coordinator for the Breeding Insight Program at Cornell University, which supports ARS-USDA plant breeders across the United States by providing comprehensive assistance in modern plant breeding, including genomics, phenomics, and data management. In my role, I lead and assist with genomic analyses for a wide range of specialty crops and coordinate communication between the Breeding Insight team and breeders, particularly for coffee and hydrangea. The program supports breeding programs across over 23 species, including hydrangea, coffee, red clover, potato, blackberry, raspberry, sugar beet, hops, alfalfa, blueberry, cranberry, cucumber, grape, hemp, honeybee, lettuce, oat, pecan, salmon, trout, sorghum, strawberry, and sweetpotato.

I also work as a developer and maintainer of several software tools that support genetic analysis. These include OneMap, for building linkage maps in diploid inbred and outcrossing species; Reads2Map,a suite of workflows that guide best practices for SNP calling, dosage calling, and linkage map construction; VIEWpoly, a Shiny app designed to facilitate the visualization and integration of genetic analysis results in polyploid species; and Qploidy, a tool for identifying ploidy levels and aneuploidy using molecular marker data. I also contribute to the development of other impactful tools in the field, including MAPpoly, for linkage map construction in polyploids, and BIGapp, user-friendly R Shiny app to analyze diploids and polyploids genomic data. I regularly assist users with genetic analysis across diverse species and continuously enhance these tools based on user feedback and evolving research needs.

Previously, I worked as a Postdoctoral Research Associate in the TexasA&M University Rose Breeding and Genetics Program within the Horticultural Sciences Department, where I focused on developing computational tools for genetic analysis in polyploid species as part of the Tools for Polyploids Project.

For my Ph.D., I focused on developing novel methods and algorithms to construct genetic maps in highly heterozygous diploid species using markers generated by modern sequencing technologies. This work contributed to the advancement of the *OneMap* software and led to the development of *Reads2Map*. During my master's studies, I specialized in SNP and genotype calling methods and developed an integrated genetic map for an outcrossing population derived from a *Eucalyptus grandis* × *Eucalyptus urophylla* cross.

During my undergraduate studies, I participated in various scientific initiation projects, including the organic chemistry of fungal mycotoxins, cellular regulation of CNC transcription factors, QTL mapping for fat deposition in mice, differential expression studies in *Anastrepha obliqua*, and SNP calling in a sugarcane Genotyping-by-Sequencing (GBS) dataset. These projects gave me a solid foundation in laboratory techniques such as chromatography, cell culture, western blotting, RNA interference (RNAi), and RT-PCR.

My current research interests include biallelic and haplotype-based marker–trait association studies, encompassing QTL mapping, genomic selection (GS), and genome-wide association studies (GWAS). I am particularly interested in polyploid genetics, structural variations such as aneuploidy, and the integration of cytogenetics to better understand genome organization and inheritance patterns in complex plant species.

Education

2017-2021 (4 years)
Ph.D. in Genetics and Plant Breeding
University of São Paulo – ESALQ/USP

- 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

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

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

Experience

2024 - present
Genomics Coordinator
Breeding Insight
Cornell University

- Funded by USDA through Cornell University
- Supervisor: Dongyan Zhao

2021 - 2024
Postdoctoral Research Associate
Texas A&M University
Department of Horticultural Sciences

- 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

- Topic: SNP calling in sugarcane GBS dataset
- Supervisor: Sabrina Chabregas

2012 (3 months)
Summer student
McGill University
MCGILL

- Title: Cellular regulation of CNC transcription factors
- Advisor: Prof. Volker Blank
- Division of Experimental Medicine

2009-2010	Technical training	Accert! Chemistry and Biotechnology

- Topic: Studies in commercial important mycotoxin production by *Fusarium sp.*
- Supervisor: Rodrigo Facchini Magnani

Publications

Refereed articles for which reprints are available:

Article	SANDERCOCK, A. M.; PEEL, M. D.; **TANIGUTI, C. H.**; CHINCHILLA-VARGAS, J.; CHEN, S;, SAPKOTA, M;, LIN, M.; ZHAO, D.; BEIL, C.T.; SHEEHAN, M.J. BIGapp: A User-Friendly Genomic Tool Kit Identified Quantitative Trait Loci for Creeping Rootedness in Alfalfa (Medicago sativa L.). **The Plant Genome**, doi: 10.1002/tpg2.70067, 2025.
Article	**TANIGUTI, C. H.**; LAU, J.; HOCHHAUS, T.; ARIAS LOPEZ, D. C.; HOKANSON, S. C.; ZLESAK, D. C.; BYRNE, D. H.; KLEIN, P. E.; RIERA-LIZARAZU, O. Exploring Chromosomal Variations in Garden Roses: Insights from High-density SNP Array Data and a New Tool, Qploidy. **The Plant Genome**. doi: https://doi.org/10.1002/tpg2.70044, 2025.
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 in the construction of linkage maps. **GigaScience**. doi: https://doi.org/10.1093/gigascience/giad092, 2023.
Article	LAU, J.; GILL, H.; **TANIGUTI, C. H.**; YOUNG, E.; KLEIN, P. E.; BYRNE D. H.; RIERA-LIZARAZU, O. QTL discovery for resistance to black spot and cercospora leaf spot, and defoliation in two interconnected F1 bi-parental tetraploid garden rose populations. **Frontiers in Plant Science**. doi:10.3389/fpls.2023.1209445, 2023.
Article	HOCHHAUS, T.; LAU, J.; **TANIGUTI, C. H.**; YOUNG, E. L.; BYRNE, D. H.; RIERA-LIZARAZU, O. Meta-Analysis of Rose Rosette Disease-Resistant Quantitative Trait Loci and a Search for Candidate Genes. **Pathogens**. doi: 10.3390/pathogens12040575. 2023.
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	RAVERDY, R.; LOURGANT, K.; MIGNOT, E.; ARNOULT, S.; BODINEAU, G.; GRIVEAU, Y.; **TANIGUTI, C. H.**; BRANCOURT-HULMEL, M. Linkage Mapping of Biomass Production and Composition Traits in a *Miscanthus sinensis* Population. **BioEnergy Research**, doi: 10.1007/s12155-022-10402-8, 2022.
Article	ALMEIDA, C. P.; PAULINO, J. F. de C. ; BONFANTE, G. F. J. ; PERSEGUINI, J. M. K. C. ; SANTOS, I. L. ; GONÇALVES, J. G. R. ; PATRÍCIO, F. R. A. ; **TANIGUTI, C. H.**; GESTEIRA, G. de S. G.; GARCIA, A. A. F. ; SONG, Q. ; CARBONELL, S. A. M. ; CHIORATO, A. F.; BENCHIMOL-REIS, L. L. Angular Leaf Spot Resistance *Loci* Associated With Different Plant Growth Stages in Common Bean. **Frontiers in Plant Science**, doi: 10.3389/fpls.2021.647043, 2021.
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 *Hevea brasiliensis* cultivated under suboptimal temperature and humidity conditions. **Frontiers in Plant Science**, doi: 10.3389/fpls.2018.01255, 2018.
Article	NAKAMURA, A. M.; CHAHAD-EHLERS, S.; LIMA, A. L. A.; **TANIGUTI, C. H.**; SOBRINHO Jr, I.; TORRES, F. R.; DE BRITO, R. A. Reference genes for accessing differential expression among developmental stages and analysis of differential expression of OBP genes in *Anastrepha obliqua*. **Scientific Reports**, doi: 10.1038/srep17480, 2016.

Under peer-review:

Article CHEN, S. ; LIN, M.; **TANIGUTI, C. H.**; TANG, X.; TORRE, F.; SIDELI, G.; IORIZZO, M.; EDGER, P.; NEYHART, J.; ZALAPA, J.; HELLER-USZYNSKA, K.; BASSIL, N.; ZHAO, D.; BEIL, C.; SHEEHAN, M.J. A Public Mid-Density Genotyping Platform For Cultivated Cranberry (Vaccinium macrocarpon Aiton). Submitted June 2025.

Article ZHAO, D; CHINCHILLA-VARGAS, J.; SANDERCOCK, A. M.; **TANIGUTI, C. T.**; LONG, R.; PALTI, Y.; GAO, G.; PIETRAK, M.; MAY, S. A.; HELLER-USZYNSKA, K.; BEIL, C. T.; SHEEHAN, M. J. A Public Mid-density Genotyping Platform for North American Atlantic Salmon (Salmo salar L.) . Submitted April 2025.

Available as pre-print:

Article GAZAFFI, R.; AMADEU, R. R.; MOLLINARI, M.; ROSA, J. R. B. F.; **TANIGUTI, C. H.**; MARGARIDO, G. R. A.; GARCIA, A. A. F. . fullsibQTL: an R package for QTL mapping in biparental populations of outcrossing species. **BioRxiv**, doi: 10.1101/2020.12.04.412262, 2020.

Software

As principal developer:

2025 **TANIGUTI, C. H.**; LAU, J. **Qploidy**: ploidy and aneuploidy estimation using genotyping platform data. Available on CRAN and GitHub: `https://github.com/Cristianetaniguti/Qploidy` - 427 CRAN downloads by July 2025

2023 **TANIGUTI, C. H.**; TANIGUTI, L. M. **Reads2Map**: WDL workflows to build genetic maps from sequencing reads. Available on GitHub: `https://github.com/Cristianetaniguti/Reads2Map`

2023 **TANIGUTI, C. H.**. **Reads2MapApp**: Shiny app to evaluate Reads2Map workflows results. Available on GitHub: `https://github.com/Cristianetaniguti/Reads2MapApp`

2022 **TANIGUTI, C. H.**; LAU, J. ; ANGELIN-BONNET, O.; GESTEIRA, G. S. ; PEREIRA, G. S. ; BYRNE, D. ; ZENG, Z. B. ; THOMSON, S.; MOLLINARI, M.; RIERA-LIZARAZU, O. **VIEWpoly**: R package to visualize genetic maps and QTL analysis. Available on CRAN and GitHub: `https://github.com/mmollina/viewpoly` - 11k CRAN downloads by July 2025

2017 MARGARIDO, G. R. A; MOLLINARI, M.; **TANIGUTI, C. H.**; FERREIRA, G.; AMADEU, R. R.; LAU, J.; BROMAN, K.; PREEDY, K.; SCHIFFTHALER, B.; GARCIA, A. A. F. **OneMap**: Construction of Genetic Maps in Experimental Crosses. Responsible for maintaining and update the package since 2017. Package available on CRAN and GitHub: `https://github.com/Cristianetaniguti/onemap` - 65k CRAN downloads by July 2025

As collaborator:

2025 SANDERCOCK, A. M.; **TANIGUTI, C. H.**; CHINCHILLA-VARGAS, J.; CHEN, S;, SAPKOTA, M; LIN, M.; ZHAO, D. **BIGapp**: Breeding Insight Genomics Shiny Application. Available on GitHub: `https://github.com/Breeding-Insight/BIGapp`

2025 SANDERCOCK, A. M.; **TANIGUTI, C. H.**; CHINCHILLA-VARGAS, J.; CHEN, S;, SAPKOTA, M; LIN, M.; ZHAO, D.**BIGr**: Breeding Insight Genomics Functions for Polyploid and Diploid Species. Available on CRAN and GitHub: `https://github.com/Breeding-Insight/BIGr` - 540 CRAN downloads by July 2025

2025 CHINCHILLA-VARGAS, J.;**TANIGUTI, C. H.**; SANDERCOCK, A. M.; ZHAO, D.**BIGf90**: R face front for running K-fold crossvalidation, estimating ebvs and variance componenet estimation with Blupf90 modules. Available on GitHub: `https://github.com/josuechinchilla/BIGf90`

2024 MOLLINARI, M.; GESTEIRA, G.; **TANIGUTI, C. H.**; LAU, J.; PEREIRA, G. S.; GARCIA, A. A. F.; ZENG, Z. B.; PREEDY, K.; GENTLEMEN, R.; IHAKA, R. **MAPpoly**: Genetic Linkage Maps in Autopolyploids v2.0. Available on GitHub: `https://github.com/mmollina/mappoly2`

2023	MOLLINARI, M.; GESTEIRA, G.; **TANIGUTI, C. H.**; LAU, J.; PEREIRA, G. S.; GARCIA, A. A. F.; ZENG, Z. B.; PREEDY, K.; GENTLEMEN, R.; IHAKA, R. **MAPpoly**: Genetic Linkage Maps in Autopolyploids. Available on CRAN and GitHub: `https://github.com/mmollina/MAPpoly` - 40k CRAN downloads by July 2025
2020	GAZAFFI, R.; AMADEU, R; **TANIGUTI, C. H.**; MOLLINARI, M.; MARGARIDO, G.; ROSA, J.; BROMAN, K.; GARCIA, A. A. F. **fullsibQTL**: Software for QTL Mapping using a Full-Sib Progeny. Available on GitHub: `https://github.com/augusto-garcia/fullsibQTL`

Awards & Distinctions

Selected awards recognizing academic contributions and participation during graduate and postdoctoral training.

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

Oral presentation in events

2024	**TANIGUTI, C. H.**; ZHAO, D.; BEIL,C.T.; SHEEHAN, M.J. Enhancing Genetic Insights with Polyploid Tools and User-Friendly Interfaces. **Plant Science Symposium - University of Florida**. Gainesville (FL), United States.
2024	**TANIGUTI, C. H.**; LAU, J.; MOLLINARI, M.; BYRNE, D.; RIERA-LIZARAZU, O. Computational Tools for Genetic Analysis of Polyploid Crops. **Texas A&M Plant Pathology and Microbiology Department Seminar**. College Station (TX), United States.
2024	**TANIGUTI, C. H.**; TANIGUTI, L. M.; LAU, J.; GARCIA, A. A.; MOLLINARI, M.; BYRNE, D.; RIERA-LIZARAZU, O. Benchmarking Genotyping-by-Sequencing Pipelines with Linkage Maps. **XXXI Plant & Animal Genome Conference, Linkage and Deletion Mapping Workshop**. San Diego (CA), United States.
2024	**TANIGUTI, C. H.**; LAU, J.; BYRNE, D.; RIERA-LIZARAZU, O. Investigating Ploidy and Aneuploidy Patterns Among Rosa spp. and the Effect on Linkage Analysis. **XXXI Plant & Animal Genome Conference, Landscape Trees and Shrubs Workshop**. San Diego (CA), United States.
2024	**TANIGUTI, C. H.**; TANIGUTI, L. M.; LAU, J.; GARCIA, A. A.; MOLLINARI, M.; BYRNE, D.; RIERA-LIZARAZU, O. Reads2Map updates: Benchmarking Genotyping-by-Sequencing Pipelines for Polyploids Using Linkage Maps. **Tools for Polyploids Workshop**. San Diego (CA), United States.
2024	**TANIGUTI, C. H.**; LAU, J.; BYRNE, D.; RIERA-LIZARAZU, O. Ploidy and Aneuploidy Determination in a Collection of Rosa spp. Accessions and the Impact of Aneuploidy on Linkage Analysis. **Tools for Polyploids Workshop**. San Diego (CA), United States.
2024	**TANIGUTI, C. H.**; GESTEIRA, G. S.; LAU, J.; PEREIRA, G,; BYRNE, D.; ZENG, ZB.; MOLLINARI, M.; RIERA-LIZARAZU, O. VIEWpoly updates: An Interactive Visualization Tool for Linkage Analysis Results of Diploid and Polyploid Species. **Tools for Polyploids Workshop**. San Diego (CA), United States.
2023	**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. Selecting best bioinformatic pipeline for evaluating diploid and auto-tetraploid garden roses genotyping-by-sequence data. **XXX Plant & Animal Genome Conference**. San Diego (CA), United States.

2023 **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. Reads2map: Practical and Reproducible Workflows to Build Polyploid Linkage Maps from Sequencing Data. **Tools for Polyploids Workshop**. San Diego (CA), United States.

2022 **TANIGUTI, C. H.**, DE SIQUEIRA G. G.; MOLLINARI, M. Genetic data analysis in polyploids: from allelic dosage to QTL mapping. **GVENCK workshop**. Remote, hosted in Piracicaba (SP), Brazil.

2022 **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. Reads2map: Practical and Reproducible Workflows to Build Linkage Maps from Sequencing Data. **Tools for Polyploids Workshop**. Remote, hosted in College Station (TX), United States.

2022 **TANIGUTI, C. H.**; GESTEIRA, G. S.; LAU, J.; PEREIRA, G. S.; ZENG, Z. B.; BYRNE, D. H.; RIERA-LIZARAZU, O.; MOLLINARI, M. VIEWpoly: An Interactive Tool to Visualize, Explore and Integrate Genetic Maps and QTL Analysis with Genomic Information. **XXIX Plant & Animal Genome Conference**. Remote, hosted in San Diego (CA), United States.

2020 **TANIGUTI, C. H.**; CORRER, F. H. Plant Biotechnology: from domestication to modern plant breeding. **BiotecLives**. Remote, hosted in Santa Cruz do Sul (RS), Brazil.

2019 **TANIGUTI, C. H.**; DIAS, K. O. Talk “Statistical Genetics in Breeding 4.0”. **Workshop in Genetics and Plant Breeding (ESALQ/USP)**. Piracicaba (SP), Brazil.

Teaching and Training Courses

2025 **TANIGUTI, C. H.**; CHINCHILLA-VARGAS, J.. Introduction to R Programming. 16 hours course. Presented to **Instituto Nacional de Innovación y Transferencia en Tecnología Agropecuaria**. Remote, hosted in Ithaca (NY), United States.

2023 MOLLINARI, M.; **TANIGUTI, C. H.**. Building Linkage Map for Inbred Diploid Populations with OneMap. 1 hour course. Part of the course "Theoretical and Practical Aspects of Linkage Analysis in Diploids and Polyploids" presented to **USDA/Breeding Insight group**. Remote, hosted in Ithaca (NY), United States.

2023 CORRER, F. H; **TANIGUTI, C. H.**. Linkage and Recombination. 2 hour course. Part of the summer course in Genetics of **Montana State University**. Remote, hosted in Bozeman (MT), United States.

2023 **TANIGUTI, C. H.**; ANGELIN-BONNET, O.; GESTEIRA, G. S.; LAU, J.; PEREIRA, G. S.; ZENG, Z. B.; THOMSON, S.; BYRNE, D. H.; MOLLINARI, M.; RIERA-LIZARAZU, O. VIEWpoly + HIDECAN: Usage demonstration of VIEWpoly updates and the integration with HIDECAN package. 1 hour course. **Tools for Polyploids Training Workshop**. Nelson, New Zealand.

2023 **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. Reads2Map: Usage demonstration in a High-Performance Computing environment. 1 hour course. **Tools for Polyploids Training Workshop**. Nelson, New Zealand.

2022 CORRER, F. H; **TANIGUTI, C. H.**. Linkage and Recombination. 2 hour course. Part of the summer course in Genetics of **Montana State University**. Remote, hosted in Bozeman (MT), United States.

2022 **TANIGUTI, C. H.**; LAU, J.; GESTEIRA, G. S.; CARAZA-HARTER, M. Computational Support session for SNP and Dosage calling. 2 hours sessions. **Tools for Polyploids Project**. Remote, hosted in College Station (TX), United States.

2021 **TANIGUTI, C. H.**; ARAUJO, W.; GODOY, C.; DIAS, K. O. Update on Statistical Tools Applied to Plant Breeding. 8 hours course. **Epagri - Research Center for Family Agriculture**. Remote, hosted in Piracicaba (SP), Brazil.

2021 **TANIGUTI, C. H.**; CORRER, F. H; HOSAKA, G. Short course “R introduction and applications in genetics”. 4 hours course. **11 Integrated Undergraduate and Graduate Week, São Carlos Institute of Physics**. Remote, hosted in São Carlos (SP), Brazil.

2021 **TANIGUTI, C. H.**; CORRER, F. H; HOSAKA, G. Short course “R introduction”. 4 hours course. Part of the course for graduate students “Biometrics of Genetic Markers”, **Department of genetics, ESALQ/USP**. Remote, hosted in Piracicaba (SP), Brazil.

2020 **TANIGUTI, C. H.**; CORRER, F. H. Short course “R introduction and applications in genetics”. 4 hours course. **X Four Biotec, Federal University of São Carlos**. Remote, hosted in São Carlos (SP), Brazil.

2020 **TANIGUTI, C. H.**. SNP and genotype calling in GBS data - A practical guide. 2 hours course. **Conservation Genetics and Genomics Group, ESALQ/USP**. Remote, hosted in Piracicaba (SP), Brazil.

2020 **TANIGUTI, C. H.**; GARCIA, A. L.; PESSOA, V. H. M. Short course “R programming training”. 12 hours course. Trainning organized by extension group **GENt, Department of Genetics, ESALQ/USP**. Piracicaba (SP), Brazil.

2019 **TANIGUTI, C. H.**; GARCIA, A. A. F. Teaching assistant in the Genetic Marker Biometry course for graduate students. 4 hours course weekly during one semester. **ESALQ/USP**. Piracicaba (SP), Brazil.

2018 **TANIGUTI, C. H.**; CORRER, F. H; BATISTA, L.; GARCIA, A. L. “R Introduction Short Course”. 6 hours course. **XII Genetics and Plant Breeding Workshop, Department of Genetics, ESALQ/USP**. Piracicaba (SP), Brazil.

2018 **TANIGUTI, C. H.**; CORRER, F. H; GESTEIRA, G. S.; GARCIA, A. L.; AVELAR, A.; HOSAKA, G. “Introduction to R data analysis”. 12 hours course. Trainning organized by the extension group **GVENCK, Department of Genetics, ESALQ/USP**. Piracicaba (SP), Brazil.

2018 **TANIGUTI, C. H.**; GARCIA, A. A. F. Lecture in the discipline Molecular Biology Applied to Plant Breeding with the talk “Building genetic maps, QTL mapping and applications in Plant Breeding” for graduate students. 4 hours course. **Agronomic Institute of Campinas (IAC)**. Campinas (SP), Brazil.

2017 **TANIGUTI, C. H.**; CORRER, F. H. “R Introduction Short Course”. 4 hours course. **Plant Ecological Genetics Lab, Department of Genetics, ESALQ/USP**. Piracicaba (SP), Brazil.

2017 **TANIGUTI, C. H.**; KRAUSE, M. “R Introduction and Applications to Genetics and Plant Breeding”. 6 hours course. **XI Genetics and Plant Breeding Winter Workshop, Department of Genetics, ESALQ/USP**. Piracicaba (SP), Brazil.

2017 **TANIGUTI, C. H.**; GARCIA, A. A. F. Teaching assistant of the Genetic course for undergrad students. 4 hours course weekly during one semester. **ESALQ/USP**. Piracicaba (SP), Brazil.

2016 **TANIGUTI, C. H.**; AMADEU, R. R.; CORRER, F. H.; LARA, L.; QUEZADA, M. “Introduction to the R platform”. 4 hours course. **X Genetics and Plant Breeding Workshop, Department of Genetics, ESALQ/USP**. Piracicaba (SP), Brazil.

2015 **TANIGUTI, C. H.**; LARA, L.; QUEZADA, M. “Introduction to R and Genetic Mapping”. 4 hours course. **IX Genetics and Plant Breeding Workshop, Department of Genetics, ESALQ/USP**. Piracicaba (SP), Brazil.

Poster Presentations

Abstract **TANIGUTI, C. H.**; LAU, J.; BYRNE, D. & RIERA-LIZARAZU. Qploidy: ploidy and aneuploidy determination for polyploids species. **The Allied Genetics Conference**. Washington DC, United States. Year: 2024.

Abstract **TANIGUTI, C. H.**; LAU, J.; BYRNE, D. & RIERA-LIZARAZU. A survey of ploidy and aneuploidy in a collection of Rosa spp. accessions and the impact of aneuploidy on linkage analysis. **XXXI Plant and Animal Genome Conference**. San Diego (CA), United States. Year: 2024.

Abstract **TANIGUTI, C. H.**; GESTEIRA, G. S. ; LAU, J. ; PEREIRA, G. S. ; BYRNE, D. ; ZENG, Z. B. ; RIERA-LIZARAZU O. & MOLLINARI, M. . VIEWpoly: An interactive tool for mining results from genetic mapping analysis in autopolyploid species. **Advances in Genome Biology and Technology Conference**. San Antonio (TX), United States. Year: 2023.

Abstract **TANIGUTI, C. H.**; TANIGUTI, L. M. ; GESTEIRA, G. S. ; OLIVEIRA, T. P. ; LAU, J. ; FERREIRA, G. C. ; AMADEU, R. R. ; BYRNE, D. ; RIERA-LIZARAZU O. ; PEREIRA, G. S. ; MOLLINARI, M. & GARCIA, A. A. F.. Comparing genotype calling software performance in Genotyping-by-Sequencing data of outcrossing population based on genetic maps quality. **30th Conference on Intelligent Systems for Molecular Biology**. Madison (WI), United States. Year: 2022.

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Peer Review & Evaluation Roles

2025 Theoretical and Applied Genetics — Manuscript Reviewer (1 time)

- ISSN: 0040-5752
- IF: 4.2 (2024), Q1 in Plant Science

2023 Bioinformatics Advances — Manuscript Reviewer (1 time)

- ISSN: 2635-0041
- IF: 2.8 (2024), Q1 in Bioinformatics

2023 Annals of Applied Biology — Manuscript Reviewer (1 time)

- ISSN: 1744-7348
- IF: 1.8 (2024), Q2 in Agricultural and Biological Sciences

2025 Journal of Pure and Applied Microbiology — Manuscript Reviewer (1 time)

- ISSN: 0973-7510
- IF: 0.882 (2024), Q3 in Microbiology

2025 F1000Research Manuscript Reviewer (1 time)

- ISSN: —
- SJR: 0.537 (2024), Q1 in multiple categories

2021 PhD Qualification Exam – State University of Campinas Committee Member

- Molecular-genetics studies in *Urochloa humidicola*: building a high-density linkage map
- Candidate: Aline da Costa Lima Moraes

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