

curriculum vitae of
Murillo F. Rodrigues

PHD CANDIDATE · INSTITUTE OF ECOLOGY AND EVOLUTION · UNIVERSITY OF OREGON

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EDUCATION

2018 – 2024	Ph.D. in Biology Dissertation title: “Understanding evolution with simulations: Three tales about trees”.	UNIVERSITY OF OREGON, UNITED STATES
2016 – 2018	M.Sc. in Genetics and Evolutionary Biology Thesis title: “Adaptive or neutral clines? Integrating genome-wide clinal and seasonal variation to infer natural selection in <i>Drosophila melanogaster</i> ”.	UNIVERSIDADE DE SÃO PAULO, BRASIL
2012 – 2015	B.Sc. in Biology Thesis title: “Diversity and phylogenetic positioning of freshwater lineages of <i>Rhinebotrhium</i> Linton, 1890 from Lake Maracaibo and Orinoco basin, Venezuela”.	UNIVERSIDADE DE SÃO PAULO, BRASIL

SKILLS

Coding	Python, R, Bash, C++.
Computing	Unix, HPC, SLURM, Snakemake (workflow management), Git.
Bioinformatics	Next-gen sequencing data quality control and preprocessing, genome and transcriptome alignment, SNP calling, differential expression analysis.
Statistics	Frequentist and bayesian statistics (using R and Stan), simulation-based inference, machine learning (mostly using PyTorch – CNN, RNN and GNN).

PUBLICATIONS

- [7] Estevez-Castro, C. F., **Rodrigues, M. F.**, Babarit, A., Ferreira, F. V., Andrade, E. G., Marois, E., Cogni, R., Aguiar, E. R., Marques, J. T., Olmo, R. P.
“Neofunctionalization driven by positive selection led to the retention of the loqs2 gene encoding an Aedes specific dsRNA binding protein”. In: *BMC biology* 22.1 (2024), p. 14.
- [6] **Rodrigues, M. F.**, Kern, A. D., Ralph, P. L. “Shared evolutionary processes shape landscapes of genomic variation in the great apes”. In: *Genetics* (Jan. 2024), iyae006. ISSN: 1943-2631. DOI: [10.1093/genetics/iyae006](https://doi.org/10.1093/genetics/iyae006).
- [5] Lauterbur, M. E., Cavassim, M. I. A., Gladstein, A. L., Gower, G., Pope, N. S., Tsambos, G., Adrion, J., Belsare, S., Biddanda, A., Caudill, V., Cury, J., Echevarria, I., Haller, B. C., Hasan, A. R., Huang, X., Iasi, L. N. M., Noskova, E., Obsteter, J., Pavinato, V. A. C., Pearson, A., Peede, D., Perez, M. F., **Rodrigues, M. F.**, Smith, C. C., Spence, J. P., Teterina, A., Tittes, S., Unneberg, P., Vazquez, J. M., Waples, R. K., Wohns, A. W., Wong, Y., Baumdicker, F., Cartwright, R. A., Gorjanc, G., Gutenkunst, R. N., Kelleher, J., Kern, A. D., Ragsdale, A. P., Ralph, P. L., Schrider, D. R., Gronau, I. “Expanding the stdpopsim species catalog, and lessons learned for realistic genome simulations”. In: *eLife* 12 (June 2023). Ed. by Ziyue Gao and Molly Przeworski.

- [4] Baumdicker, F., Bisschop, G., Goldstein, D., Gower, G., Ragsdale, A. P., Tsambos, G., Zhu, S., Eldon, B., Ellerman, E. C., Galloway, J. G., Gladstein, A. L., Gorjanc, G., Guo, B., Jeffery, B., Kretzschmar, W. W., Lohse, K., Matschiner, M., Nelson, D., Pope, N. S., Quinto-Cortés, C. D., **Rodrigues, M. F.**, Saunack, K., Sellinger, T., Thornton, K., Kemenade, H., Wohns, A. W., Wong, Y., Gravel, S., Kern, A. D., Koskela, J., Ralph, P. L., Kelleher, J. "Efficient ancestry and mutation simulation with msprime 1.0". In: *Genetics* 220.3 (Dec. 2021), iyab229.
- [3] **Rodrigues, M. F.**, Cogni, R. "Genomic Responses to Climate Change: Making the Most of the *Drosophila* Model". In: *Frontiers in Genetics* 12 (2021), p. 676218.
- [2] **Rodrigues, M. F.**, Vibranovski, M. D., Cogni, R. "Clinal and seasonal changes are correlated in *Drosophila melanogaster* natural populations". In: *Evolution* 75.8 (2021), pp. 2042–2054.
- [1] Stankowski, S., Chase, M. A., Fuiten, A. M., **Rodrigues, M. F.**, Ralph, P. L., Streisfeld, M. A. "Widespread selection and gene flow shape the genomic landscape during a radiation of monkeyflowers". In: *PLoS biology* 17.7 (2019), e3000391.

RESEARCH EXPERIENCE

2018 – present

PhD Student

UNIVERSITY OF OREGON, UNITED STATES

- Developed open source population genetics simulation tools within the *tskit* and *stdpopsim* communities (mostly in Python and C++).
- Analyzed population genomic data and used simulations to tease apart the role of natural selection in shaping genetic variation in the great apes
- Developed a machine learning framework based on graph neural networks that takes tree sequences as input to infer evolutionary processes.

Advised by Drs. Andrew Kern and Peter Ralph.

2017 – 2018

Visiting Researcher

UNIVERSITY OF WISCONSIN, UNITED STATES

- Identified differences in immunity phenotypes between *D. melanogaster* populations.
- Analyzed population genomic data to find unusually differentiated immunity genes.

Advised by Dr. John Pool.

2016 – 2018

Master's Student

UNIVERSIDADE DE SÃO PAULO, BRASIL

- Analyzed a Pool-seq dataset of geographically and temporally distributed samples.
- Modelled the association between spatial and temporal variation in allele frequencies to understand the importance of selection in structuring clinal patterns.

Advised by Drs. Rodrigo Cogni and Maria Vibranovski.

2013 – 2014

Undergraduate Researcher

UNIVERSIDADE DE SÃO PAULO, BRASIL

- Performed DNA extraction and Sanger sequencing of animal samples.
- Analyzed DNA sequence data to build a new phylogeny for *Rhinebothrium*, a genus of tapeworms found in freshwater stingrays.

Advised by Dr. Fernando Portella de Luna Marques.

TEACHING

2019	Introduction to Programming for Biologists Teaching assistant for consecutive terms (12h/week for 10 weeks).	UNIVERSITY OF OREGON, UNITED STATES
2018	General Biology III: Populations Teaching assistant (12h/week for 10 weeks).	UNIVERSITY OF OREGON, UNITED STATES
2017	Molecular Ecology Teaching assistant (6h/week for 16 weeks).	UNIVERSIDADE DE SÃO PAULO, BRASIL
2016	Evolutionary Processes Teaching assistant (6h/week for 16 weeks).	UNIVERSIDADE DE SÃO PAULO, BRASIL
2015	Introduction to Biotatistics Invited to give a short course on Biostatistics in Semana Temática da Biologia – IB/USP (12h)	UNIVERSIDADE DE SÃO PAULO, BRASIL
2015	Introduction to Statistics Undergraduate teaching assistant (6h/week for 16 weeks).	UNIVERSIDADE DE SÃO PAULO, BRASIL
2013	Introduction to Systematics and Biogeography Undergraduate teaching assistant (6h/week for 16 weeks).	UNIVERSIDADE DE SÃO PAULO, BRASIL

SCHOLARSHIPS AND AWARDS

2022 – 2023	Harvey E Lee Graduate Scholarship	UNIVERSITY OF OREGON
2022 – 2023	Marthe E. Smith Memorial Science Scholarship	CAS, UNIVERSITY OF OREGON
2019 – 2020	Hill Fund Award	CAS, UNIVERSITY OF OREGON
2019 – 2021	Genetics Training Grant	CAS, UNIVERSITY OF OREGON
2017 – 2018	Research Internship Abroad Fellowship	THE SÃO PAULO RESEARCH FOUNDATION
2016 – 2018	Master's Fellowship	THE SÃO PAULO RESEARCH FOUNDATION
2013 – 2014	Undergraduate Research Fellowship	THE SÃO PAULO RESEARCH FOUNDATION

PRESENTATIONS AND POSTERS

2023	<p>SMBE2023 ORGANIZED BY THE SOCIETY FOR MOLECULAR BIOLOGY AND EVOLUTION, HELD IN FERRARA, ITALY.</p> <p>Talk title: Shared evolutionary processes shape genomic variation in the great apes. See slides here.</p>
2022	<p>Population, Evolutionary, and Quantitative Genetics Conference ORGANIZED BY THE GENETICS SOCIETY OF AMERICA, HELD IN CALIFORNIA, UNITED STATES.</p> <p>Poster title: Why are landscapes of diversity correlated in the great apes? See poster here.</p>

2021	<p>SMBE_{v2021} ORGANIZED BY THE SOCIETY FOR MOLECULAR BIOLOGY AND EVOLUTION, HELD VIRTUALLY. Poster title: Natural selection and landscapes of diversity in the great apes.</p>
2021	<p>Probabilistic Modeling in Genomics ORGANIZED BY COLD SPRING HARBOR LABORATORIES, HELD VIRTUALLY. Poster title: Natural selection and landscapes of diversity in the great apes. See poster here.</p>
2020	<p>The Allied Genetics Conference ORGANIZED BY THE GENETICS SOCIETY OF AMERICA, HELD VIRTUALLY.</p>
2014	<p>8th Workshop on Cestode Systematics and Phylogeny UNIVERSIDADE DE SÃO PAULO, BRASIL</p>

SERVICE

Reviewing	<p>GENETICS, Molecular Ecology Resources, G₃, Proceedings of the Royal Society B: Biological Sciences</p>
Treasurer	<p>Graduate Evolutionary Biology and Ecology Students A student led organization that aims to provide career-building activities to graduate students and to promote outreach programs to the general community.</p>
Developer	<p>tskit Part of a community of developers that maintain different population genetics open-source software.</p>