curriculum vitæ of

Murillo F. Rodrigues

PhD Candidate · Institute of Ecology and Evolution · University of Oregon

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Education

Sep 2018 – Mar 2024

Ph.D. in Biology   University of Oregon, United States
Dissertation title: "Understanding evolution with simulations: Three tales about trees".

Jan 2016 – Aug 2018

M.Sc. in Genetics and Evolutionary Biology   Universidade de São Paulo, Brasil
Thesis title: "Adaptive or neutral clines? Integrating genome-wide clinal and seasonal variation to infer natural selection in *Drosophila melanogaster*".

Feb 2012 – Dec 2015

B.Sc. in Biology   Universidade de São Paulo, Brasil
Thesis title: "Diversity and phylogenetic positioning of freshwater lineages of *Rhinebotrhium* Linton, 1890 from Lake Maracaibo and Orinoco basin, Venezuela".

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.

[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., Kretzschumar, 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

Sep 2018 – Mar 2024

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.

Aug 2017 – Feb 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.

Jan 2016 – Aug 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.

Jan 2013 – Jan 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

Jan 2019 – Mar 2020	Introduction to Programming for Biologists Teaching assistant for consecutive terms (12h/week for 10 weeks).	University of Oregon, United States
Sep 2018 – Dec 2018	General Biology III: Populations Teaching assistant (12h/week for 10 weeks).	University of Oregon, United States
Feb 2017 – Jun 2017	Molecular Ecology Teaching assistant (6h/week for 16 weeks).	Universidade de São Paulo, Brasil
Feb 2016 – Jun 2016	Evolutionary Processes Teaching assistant (6h/week for 16 weeks).	Universidade de São Paulo, Brasil
Oct 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
Aug 2015 – Dec 2015	Introduction to Statistics Undergraduate teaching assistant (6h/week for 16 weeks).	Universidade de São Paulo, Brasil
Feb 2013 – Jun 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	SMBE2023 organized by the Society for Molecular Biology and Evolution, held in Ferrara, Italy. Talk title: Shared evolutionary processes shape genomic variation in the great apes. See slides here.
2022	Population, Evolutionary, and Quantitative Genetics Conference organized by the Genetics Society of America, held in Californa, United States. Poster title: Why are landscapes of diversity correlated in the great apes? See poster here.

2021 SMBEv2021   organized by the Society for Molecular Biology and Evolution, held virtually.
Poster title: Natural selection and landscapes of diversity in the great apes.

2021 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.

2020 The Allied Genetics Conference   organized by the Genetics Society of America, held virtually.

2014 8th Workshop on Cestode Systematics and Phylogeny   Universidade de São Paulo, Brasil

Service

Reviewing GENETICS, Molecular Ecology Resources, G3, Proceedings of the Royal Society B: Biological Sciences

Treasurer 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.

Developer tskit
Part of a community of developers that maintain different population genetics open-source software.