Denis Jacob Machado

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- **Computational biologist** integrating molecular biology, bioinformatics, and evolutionary genomics to study health-relevant organisms and emerging infectious diseases.
- Expertise in **genomics**, **phylogenetics**, and **machine learning** for large-scale biological data analysis, including **genomic epidemiology** and **AI-driven discovery**.
- 15+ years of experience in **molecular biology**, **high-throughput sequencing** (Illumina, PacBio, RNA-Seq, Hi-C), genome assembly, and transcriptomic analysis.
- 7+ years applying **predictive modeling**, **data mining**, and **AI/ML frameworks** (PyTorch, TensorFlow) to biological and public-health problems.
- Proven record of **peer-reviewed publications**, leadership in **computational phylogenetics**, and mentoring of multidisciplinary research teams.

Positions Held

2022–Current	**Assistant Professor in Bioinformatics**, *University of North Carolina at Charlotte*, Charlotte–NC, USA
2019–2022	**Postdoctoral Researcher**, *University of North Carolina at Charlotte*, Charlotte–NC, USA
2018–2019	**Research Collaborator**, *University of São Paulo*, São Paulo–SP, Brazil
2018–2019	**Invited Lecturer**, *University of São Paulo*, São Paulo–SP, Brazil
2017, 2025	**Invited Lecturer**, *University of Magdalena*, Santa Marta D.T.C.H., Colombia

Education

2013–2018	**Ph.D. in Bioinformatics**, *University of São Paulo (USP)*, São Paulo–SP, Brazil
2010–2012	**Master's in Zoology (Parasitology)**, *University of São Paulo (USP)*, São Paulo–SP, Brazil
2006–2009	**Bachelor's in Biological Sciences (Marine Biology)**, *São Paulo State University (UNESP)*, São Vicente–SP, Brazil

Selected Publications

Márquez, R., **Jacob Machado, D.**, Nouri, R., Gendreau, K. L., Janies, D., Saporito, R. A., Kronforst, M. R., & Grant, T. (2025). A draft genome assembly for the dart-poison frog *Phyllobates terribilis*. *Gigabyte*. 10.46471/gigabyte.157.

Alves, P. V., da Silva, R. J., Scholz, T., de Chambrier, A., Luque, J. L., Duchenko, A., Janies, D., & **Jacob Machado, D.** (2025). Machine learning models accurately predict clades of proteocephalidean tapeworms (Onchoproteocephalidea) based on host and biogeographical data. *Cladistics*. 10.1111/cla.12610.

Nouri, R., Mashanov, V., Harris, A., New, G., Taylor, W., Janies, D., Reid, R. W., & **Jacob Machado, D.** (2024). Unveiling putative modulators of mutable collagenous tissue in the brittle star *Ophiomastix wendtii*: an RNA-Seq analysis. *BMC Genomics*. 10.1186/s12864-024-10926-7.

Jacob Machado, D., Marques, F. P. L., Jiménez-Ferbans, L., & Grant, T. (2022). An empirical test of the relationship between the bootstrap and likelihood ratio support in maximum likelihood phylogenetic analysis. *Cladistics*. 10.1111/cla.12496.

Jacob Machado, D., Scott, R., Guirales, S., & Janies, D. A. (2021). Fundamental evolution of all Orthocoronavirinae including three deadly lineages descendent from Chiroptera-hosted coronaviruses: SARS-CoV, MERS-CoV and SARS-CoV-2. *Cladistics*. 10.1111/cla.12454.

Grant, T., Rada, M., Anganoy-Criollo, M., Batista, A., Dias, P. H., Jeckel, A. M., **Jacob Machado, D.**, & Rueda-Almonacid, J. V. (2017). Phylogenetic systematics of dart-poison frogs and their relatives revisited (Anura: Dendrobatoidea). *South American Journal of Herpetology*, 12(s1), S1–S90. 10.2994/sajh-d-17-00017.1.

Trevisan, B., Alcantara, D. M. C., **Machado, D. J.**, Marques, F. P. L., & Lahr, D. J. G. (2019). Genome skimming is a low-cost and robust strategy to assemble complete mitochondrial genomes from ethanol-preserved specimens in biodiversity studies. *PeerJ*, 7, e7543. 10.7717/peerj.7543.

Orrico, V. G. D., Grant, T., Faivovich, J., Rivera-Correa, M., Rada, M. A., Lyra, M. L., Cassini, C. S., Valdujo, P. H., Schargel, W. E., **Machado, D. J.**, Wheeler, W. C., Barrio-Amorós, C., Loebmann, D., Moravec, J., Zina, J., Solé, M., Sturaro, M. J., Peloso, P. L. V., Suarez, P., & Haddad, C. F. B. (2021). The phylogeny of Dendropsophini (Anura: Hylidae: Hylinae). *Cladistics*. 10.1111/cla.12429.

Ford, C. T., **Jacob Machado, D.**, & Janies, D. A. (2022). Predictions of the SARS-CoV-2 Omicron variant (B.1.1.529) spike protein receptor-binding domain structure and neutralizing antibody interactions. *Frontiers in Virology*, 2. 10.3389/fviro.2022.830202.

Machado, D. J. (2015). YBYRÁ facilitates comparison of large phylogenetic trees. *BMC Bioinformatics*. 10.1186/s12859-015-0642-9.

Links

○ **ORCiD:** https://orcid.org/my-orcid?orcid=0000-0001-9858-4515
○ **Google Scholar:** https://scholar.google.com/citations?user=TK6Ms80AAAAJ&hl=pt-BR
○ **LinkedIn:** https://www.linkedin.com/in/machadodj
○ **Phyloinformatics Lab:** https://phyloinformatics.com
○ **UNC Charlotte's CCI:** https://cci.charlotte.edu/directory/denis-jacob-machado
○ **Web of Science:** https://www.webofscience.com/wos/author/record/I-1452-2015
○ **Loop:** https://loop.frontiersin.org/people/1352271/overview
○ **SciProfiles:** https://sciprofiles.com/profile/machadodj
○ **GitHub:** https://github.com/machadodj
○ **GitLab:** https://gitlab.com/MachadoDJc