

**IDENTIFYING INFORMATION:**

NAME: Jacob Machado, Denis

ORCID iD: <https://orcid.org/0000-0001-9858-4515>

POSITION TITLE: Assistant Profesor

**PRIMARY ORGANIZATION AND LOCATION:** University of North Carolina at Charlotte, Charlotte, North Carolina, United States**Professional Preparation:**

ORGANIZATION AND LOCATION	DEGREE (if applicable)	RECEIPT DATE	FIELD OF STUDY
Universidade de São Paulo, São Paulo, Not Applicable, N/A, Brazil	PHD	04/2018	Bioinformatics
Universidade de São PAulo, São Paulo, Not Applicable, N/A, Brazil	MS	07/2012	Zoology
Universidade Estadual Paulista "Júlio de Mesquita Filho", São Vicente, Not Applicable, N/A, Brazil	BS	12/2009	Biological Sciences

**Appointments and Positions**

2022 - present Assistant Profesor, University of North Carolina at Charlotte, Charlotte, North Carolina, United States

2019 - 2022 Postdoctoral Fellow, University of North Carolina at Charlotte, Charlotte, North Carolina, United States

**Products****Products Most Closely Related to the Proposed Project**

1. Roberto Márquez, Denis Jacob Machado, Reyhaneh Nouri, Kerry L. Gendreau, Daniel Janies, Ralph A. Saporito, Marcus R. Kronforst, Taran Grant. A draft genome assembly for the dart-poison frog *Phylllobates terribilis*. Gigabyte. 2025 June. DOI: 10.46471/gigabyte.157
2. Philippe Vieira Alves, Reinaldo José da Silva, Tomáš Scholz, Alain de Chambrier, José Luis Luque, Anastasiia Duchenko, Daniel Janies, Denis Jacob Machado. Machine learning models accurately predict clades of proteocephalidean tapeworms (Onchoproteocephalidea) based on host and biogeographical data. Cladistics. 2025 June. DOI: 10.1111/cla.12610
3. Reyhaneh Nouri, Vladimir Mashanov, April Harris, Gari New, William Taylor, Daniel Janies, Robert W. Reid, Denis Jacob Machado. Unveiling putative modulators of mutable collagenous tissue in the brittle star *Ophiomastix wendtii*: an RNA-Seq analysis. BMC Genomics. 2024 October. DOI: 10.1186/s12864-024-10926-7
4. Denis Jacob Machado, Fernando Portella de Luna Marques, Larry Jiménez-Ferbans, Taran Grant. An empirical test of the relationship between the bootstrap and likelihood ratio support in maximum likelihood phylogenetic analysis. Cladistics. 2022 June. Available from: <https://doi.org/10.1111%2Fcla.12496> DOI: 10.1111/cla.12496

5. Denis Jacob Machado, Rachel Scott, Sayal Guirales, Daniel A. Janies. Fundamental evolution of all Orthocoronavirinae including three deadly lineages descendent from Chiroptera-hosted coronaviruses: SARS-CoV, MERS-CoV and SARS-CoV-2. *Cladistics*. 2021 October. DOI: 10.1111/cla.12454

*Other Significant Products. Whether or Not Related to the Proposed Project*

1. Taran Grant, Marco Rada, Marvin Anganoy-Criollo, Abel Batista, Pedro Henrique Dias, Adriana Moriguchi Jeckel, Denis Jacob Machado, José Vicente Rueda-Almonacid. Phylogenetic systematics of dart-poison frogs and their relatives revisited (Anura: Dendrobatoidea). *South American Journal of Herpetology*. 2017 September; 12(s1):S1--S90. Available from: <https://doi.org/10.2994/sajh-d-17-00017.1> DOI: 10.2994/sajh-d-17-00017.1
2. Trevisan B, Alcantara DMC, Machado DJ, Marques FPL, Lahr DJG. Genome skimming is a low-cost and robust strategy to assemble complete mitochondrial genomes from ethanol preserved specimens in biodiversity studies. *PeerJ*. 2019;7:e7543. PubMed Central PMCID: [PMC6746217](https://pubmed.ncbi.nlm.nih.gov/PMC6746217/).
3. Victor G.D. Orrico, Taran Grant, Julian Faivovich, Mauricio Rivera-Correa, Marco A. Rada, Mariana L. Lyra, Carla S. Cassini, Paula H. Valdujo, Walter E. Schargel, Denis J. Machado, Ward C. Wheeler, Cesar Barrio-Amorós, Daniel Loebmann, Jiří Moravec, Juliana Zina, Mirco Solé, Marcelo J. Sturaro, Pedro L.V. Peloso, Pablo Suarez, Célio F.B. Haddad. The phylogeny of Dendropsophini (Anura: Hylidae: Hylinae). *Cladistics*. 2021 February. DOI: 10.1111/cla.12429
4. Colby T. Ford, Denis Jacob Machado, Daniel A. Janies. 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*. 2022 February; 2. Available from: <https://doi.org/10.3389/fviro.2022.830202> DOI: 10.3389/fviro.2022.830202
5. Machado D.J.. YBYRÁ facilitates comparison of large phylogenetic trees. *BMC Bioinformatics*. 2015. DOI: 10.1186/s12859-015-0642-9

**Certification:**

I certify that the information provided is current, accurate, and complete. This includes but is not limited to information related to domestic and foreign appointments and positions.

I also certify that, at the time of submission, I am not a party to a malign foreign talent recruitment program.

Misrepresentations and/or omissions may be subject to prosecution and liability pursuant to, but not limited to, 18 U.S.C. §§ 287, 1001, 1031 and 31 U.S.C. §§ 3729-3733 and 3802.

Certified by Jacob Machado, Denis in SciENCv on 2025-10-07 21:58:25