

# Denis Jacob Machado, Ph.D.

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🌐 phyloinformatics.com

- **Bioinformaticist** with strong biology, biostatistics, and programming background.
- Peer-reviewed publications on topics including **genomics**, **evolution**, **parasitology**, **regeneration**, **emerging infectious diseases**, and **genomic epidemiology**.
- 3+ years of experience using **machine learning** (e.g., PyTorch, TensorFlow), **predictive modeling**, **high-throughput data processing**, and **data mining** algorithms to solve practical problems.
- 10+ years of experience in **molecular biology**, **high-throughput sequencing** (e.g., Illumina, PacBio, Hi-C, GWAS, and RNA-Seq), and sequence assembly, and differential gene expression analyses.

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## Work Experience

Aug/15/22–  
Current **Assistant Professor in Bioinformatics**, *University of North Carolina at Charlotte*, Charlotte–NC, USA

- First line of research: Investigate new pathogens' emergence, evolution, and spread, focusing on preventing and treating infectious diseases.
- Second line of research: Create computational and molecular solutions to make data from biorepositories more readily available to biomedical research.
- For more information, please visit [phyloinformatics.com](http://phyloinformatics.com).

2019–2022 **Postdoctoral Researcher**, *University of North Carolina at Charlotte*, Charlotte–NC, USA

- I studied the origins, evolution, and zoonotic events of coronaviruses. I also employed big data analysis to categorize different variants of SARS-CoV-2 and applied deep learning techniques to produce highly accurate structure predictions of their proteins.
- I predict how structural changes in the receptor-binding domain of the spike protein of different variants of SARS-CoV-2 may reduce antibody interaction without completely evading existing neutralizing antibodies.
- I created the first programs for gene prediction and annotation of *Orthocoronavirinae* (including SARS-CoV-2) and *Flaviviridae* (including Hepatitis C, yellow fever, dengue, and Zika virus).
- Produced draft genomes of highly regenerative echinoderms such as brittle stars and sea cucumbers for comparative genomics and tissue regeneration research.

2018–2019 **Research Collaborator**, *University of São Paulo*, São Paulo–SP, Brazil

- I built and administered the first computer clusters at the Museum of Zoology of the University of São Paulo (MUZUSP).
- I participated in the planning, funding acquisition, and implementation of the first laboratory to sequence historical DNA at the Department of Zoology of the University of São Paulo (USP).
- I developed new genome skimming techniques to retrieve genomic data of non-model organisms when samples were small or degraded. I also created the necessary software to facilitate the analysis of organelle genomes.

2018–2019 **Invited Lecturer**, *University of São Paulo*, São Paulo–SP, Brazil

- I created and taught the first graduate-level courses in bioinformatics and computer programming for biologists at USP's Graduate Program in Zoology.

Jul–Aug 2017 **Invited Lecturer**, *University of Magdalena*, Santa Marta D.T.C.H., Colombia

- I designed and taught the first course in bioinformatics at the University of Magdalena. Classes included practical and theoretical lessons on DNA extraction and isolation, high-throughput sequencing, sequence alignment, reference, and *de novo* genome assembly, and gene prediction and annotation.
- I also offered consultation to faculty members involved in animal research who needed web and dry lab solutions for next-generation sequence analyses.

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## 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

You will find my *curriculum vitae* and other professional information at [phyloinformatics.com](http://phyloinformatics.com).