

DEISE JP GONÇALVES

BIOINFORMATICS | GENOMICS DATA SCIENCE

CONTACT

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PROFILE

Bioinformatics scientist with 4+ years of experience developing high-performance workflows for NGS analysis, including data processing, curation, annotation, and statistical modelling. Experience in evolutionary phylogenomics, genome evolution, and SNV, CNV, and Fusion annotation R&D. Excels working independently and collaborating with cross-disciplinary teams. Experience mentoring academic and non-academic scientists.

EDUCATION

PhD in Computational Biology, 2019
The University of Texas at Austin [TX]

Masters in Plant Biology, 2013
State University of Campinas [Brazil]

Bachelor of Science, 2009
Federal University of Uberlandia [Brazil]

TECHNICAL SKILLS

- System agnostic (Python, R, Bash, SQL Windows PowerShell)
- Expertise in standard bioinformatics tools
- Cloud computing (AWS SageMaker studio, Azure)
- HPC (SLURM executor, batch processing)
- Nextflow (SNV/CNV/Fusion variant call)
- Generative AI prompting, RAG, embeddings
- Statistical modeling and probability
- Code documentation, version control (Git)
- Team collab (Slack/Discord/Teams)
- General data visualization (PowerBI)
- Scientific communication and writing

EXPERIENCE

Bioinformatics Scientist at BioIVT, 2022-present

Company's data person leading the local bioinformatics team and participating in global initiatives. Bridges the communication of data-driven biological insights between the company's leadership and departments such as clinical data, lab operations, quality assurance and compliance, and global sales teams.

Current Projects

- Implementing and deploying a data product that explores NGS, slide images, and clinical data assets
- Proposing a new NGS biomarker annotation portfolio for FFPE and ctDNA samples
- Exploring Generative AI to extract relevant information from free text in large clinical datasets
- Collaborated on research exploring the use of FFPE blocks from lab-generated FNAs for molecular annotation (to be presented at Molecular TriCon, March 2025)

Past Projects

- Developed an NGS pipeline that significantly reduced variant detection error, processing time, and ensured reproducibility of biospecimen biospecimen annotation

Postdoctoral Researcher, University of Michigan, 2020-2022

Conducted analyses to detect structural variants for evolutionary genomics ([NSF project](#), [publication](#)).

Past Projects

- Developed and implemented [various pipelines](#) to assemble and analyze various NGS datasets, including transcriptomes, nuclear target capture, and organelle genomes
- Collaborated on projects analyzing venom evolution in [snakes](#) and developing an [analytical tool](#) for NGS data processing
- Developed a [method](#) to explore organelle genome variants

Leadership and service

- Received multiple awards and grants that resulted in various [publications](#)
- Instructed advanced bioinformatics at the [Workshop on Molecular Evolution](#) at [MBL](#) (2018-2022)
- Dean's Council Student leader at the UT Austin College of Natural Sciences and the Dept. of Integrative Biology
- Co-organized the Austin Chapter of PyLadies (Python meetup, 2018)

** Links can be accessed for additional information*