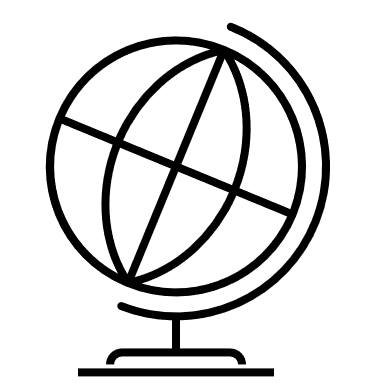
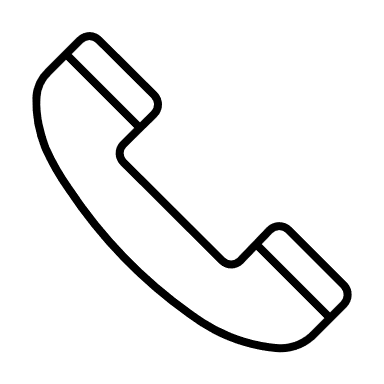
**DEISE JP GONÇALVES**

BIOINFORMATICS | GENOMICS DATA SCIENCE

Free Github Logo Icon of Glyph style - Available in SVG, PNG, EPS, AI &  Icon fontsLinkedIn Icon – Free Download, PNG and Vector**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](https://www.nsf.gov/awardsearch/showAward?AWD_ID=1917146&HistoricalAwards=false), [publication](https://nph.onlinelibrary.wiley.com/doi/10.1111/nph.20200)).

Past Projects

* Developed and implemented [various pipelines](https://github.com/deisejpg/manipulating_fastas.git) to assemble and analyze various NGS datasets, including transcriptomes, nuclear target capture, and organelle genomes
* Collaborated on projects analyzing venom evolution in [snakes](https://github.com/deisejpg/mito-genes_from_transcriptome) and developing an [analytical tool](https://github.com/edgardomortiz/sam2consensus) for NGS data processing
* Developed a [method](https://github.com/deisejpg/rosids) to explore organelle genome variants

Leadership and service

* Received multiple awards and grants that resulted in various [publications](https://scholar.google.com/citations?user=l0q5YpsAAAAJ&hl=en)
* Instructed advanced bioinformatics at the [Workshop on Molecular Evolution](https://molevolworkshop.github.io/about/) at [MBL](https://molevolworkshop.github.io/?_ga=2.119272586.2013273605.1651511791-1963788801.1650375037) (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)