

# DEISE JP GONÇALVES

## GENOMICS DATA SCIENCE

### CONTACT



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### PROFILE

Bioinformatics scientist with four years of experience developing advanced algorithms for data analysis, specializing in NGS pipelines and variant detection. Experience designing and implementing algorithms to extract meaningful signals from biological datasets, including NGS data processing, curation, annotation, and statistical modeling. Excels in collaborative teams with opportunities for independent work and multi-directional mentorship.

### 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

- Python, R, Bash, PowerShell, SQL (SSMS)
- Algorithms for NGS analysis and variant detection (classic and custom software)
- Azure (data processing, analytics, storage)
- High-Performance Computing on-prem, TACC (Stampede, Lonestar)
- Generative AI prompting, RAG, embeddings, and LLM training
- Statistical modeling and probability
- Git, Slack/Discord, PowerBI
- Scientific communication and writing

### EXPERIENCE

#### Bioinformatics Scientist at BioIVT, 2022-present

Bridges the communication of data-driven biological findings and business strategy insights between the company's leadership and departments such as clinical data, lab operations, quality assurance and compliance, and global sales teams.

#### Current Projects

- Proposing and implementing an innovative NGS biomarker portfolio, integrating custom pipelines optimized for QC and structural variant detection
- Working with leadership to explore NGS, slide images, and clinical data assets as a product
- Exploring Generative AI for data wrangling focusing on extracting and grouping relevant tests, treatments, and medications from free text in large clinical datasets
- Developed an NGS pipeline that significantly reduced variant detection and annotation processing time and ensured reproducibility of biospecimen molecular 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](#) for assembling and analyzing diverse NGS datasets, including transcriptomes, nuclear target capture data, and organelle genomes
- Collaborated on projects analyzing venom evolution in [snakes](#) and developing an [analytical tool](#) to optimize NGS data processing
- Developed a [method](#) to explore organelle genome variants

#### Leadership and service

- Received multiple awards and grants that funded research that resulted in various [publications](#)
- Instructed advanced bioinformatics in one of the most prestigious workshops in the field, the [Workshop on Molecular Evolution](#) at [MBL](#) (2018-2022, except during pandemic years)
- 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); member of [WoC|code](#) (2022)

*\* Links can be accessed for additional information*