

Samuel Chagas de Assis

BIOTECHNOLOGIST - COMPUTATIONAL BIOLOGIST

Campinas, São Paulo - Brazil

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About me

I'm a computational biologist fascinated by understanding the molecular biodiversity and mechanisms. I have experience with workflow development in Python and R, molecular dynamics simulations data analysis, and immunogenetics. Currently, my work focuses on workflow development through documentation, automation, and reproducibility. I'm an intern researcher at the Computational Biocatalysis Group at LNBR/CNPEN in Brazil, where I work with specific Carbohydrate-Active Enzymes for microbiome and structural biology research projects using biomolecular modeling data and biochemical interpretation. When I have some time, I enjoy to draw molecular scientific illustrations and cooking plant-based recipes.

Education

Federal University of Latin-American Integration (UNILA)

BACHELOR IN BIOTECHNOLOGY

Foz do Iguaçu, Brazil

2018-2024

Liberato Salzano Vieira da Cunha Foudation

ELECTRICAL TECHNICIAN

Novo Hamburgo, Brazil

2013-2017

Experience

Brazilian Center for Research in Energy and Materials (CNPEN)

COMPUTATIONAL BIOCATALYSIS INTERN

Campinas, São Paulo

Feb 2023 - Present

- I have performed data analysis of several molecular dynamics simulations, primarily using Python and Shell scripting compatible with SLURM HPC environment. The main goal are new insights about molecular mechanisms from new Carbohydrate-Active enzyme families.
- | Gromacs | SLURM/HPC | Python/MDAnalysis | Python/Autodock Vina | Conda/Bioconda | Pymol/VMD |

SporeData Inc.

FREELANCER - JR DATA ANALYST

Remote

Oct 2022 - Feb 2023

- Worked as a freelancer on healthcare data projects, performing ETL, cohort generation, data visualization, clinical study reports, and statistical analyses.
- | R/Tidyverse | RStats | RMarkdown | Cloud/N3C |

Medical Genetics Lab - UNILA

UNDERGRADUATE RESEARCHER

Foz do Iguaçu, Paraná

Aug 2020 - Mar 2023

- I have performed DNA sequencing and HLA-B analysis of COVID-19 patients, gathering clinical and genomic data, along with HLA-epitopes binding affinities from computational predictions, to study the mutational landscape of SARS-CoV-2 variants in Foz do Iguaçu. I worked in a Nextflow pipeline to collect, transform and visualize missense mutations affecting HLA-apitopes.
- | Missense mutation analyses | GISAID | Nextflow | Bash | Python | R | Sanger Sequencing/Wet Lab | netMHCpan4.1 |

International Genetically Engineered Machine Competition (iGEM)

DRYLAB COORDINATOR

Foz do Iguaçu, Paraná

Jan 2020 - Dez 2021

- | system biology modeling | Python/Scipy | Python/NUPACK | R/ggplot2 | ODEs/Modeling |

Microbiology and Biochemical Lab - UNILA

UNDERGRADUATE RESEARCHER

Foz do Iguaçu, Paraná

Jun 2018 - Dez 2019

- | |

Habilidades e Qualificações

- Linguagens de Programação: R, Python e Bash
- Markup: RMarkdown e HTML

- Gerenciamento: Git/GitHub, GitHub Actions, Slurm
- Sistemas UNIX/Linux

Microbiology and Biochemical Lab - UNILA

UNDERGRADUATE RESEARCHER

Foz do Iguaçu, Paraná

Jun 2018 - Dez 2019

Prêmios

- 2022 Primeiro Lugar. Menção Honrosa na área de Ciências da Saúde no XI EICTI - UNILA
- 2021 Medalha de Ouro e Nomeação de Melhor Projeto de Nova Aplicação e Práticas Humanas na *International Genetically Engineering Machine Competition* (iGEM)
- 2020 Melhor Projeto de Escolha do Público no V Curso de Verão de Engenharia de Máquinas Biológicas - UFMG
- 2020 Melhor Apresentação no V Curso de Verão de Engenharia de Máquinas Biológicas - UFMG
- 2019 Primeiro Lugar. Menção Honrosa na área de Tecnologia e Produção no VII SEUNI - UNILA
- 2016 Menção Honrosa UNESCO pelo Projeto de Relevância Social na Conferência Internacional de Ciência e Tecnologia de Nível Médio - MOSTRATEC/UNESCO

Publicações

- **De Assis**, S.C., Morgado, D.L., Scheidt, D.T., De Souza, S.S., Cavallari, M.R., Ando, O.H.J., Carrilho, E. (2023). Review of Bacterial Nanocellulose-Based Electrochemical Biosensors: Functionalization, Challenges, and Future Perspectives. *MDPI Biosensors*, 13. <https://doi.org/10.3390/bios13010142>