Gabriel Bianchin de Oliveira

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Education

Florida International University (FIU) Aug. 2025 – Present
Postdoctoral Fellow in Computer Science *Miami, Florida, United States of America*

University of Campinas (Unicamp) Mar. 2021 – Jul. 2025
Ph.D. in Computer Science *Campinas, São Paulo, Brazil*

University of Campinas (Unicamp) Mar. 2019 – Mar. 2021
M.Sc. in Computer Science *Campinas, São Paulo, Brazil*

Federal Institute of Southern Minas Gerais (IFSULDEMINAS) Jan. 2015 – Dec. 2018
B.Sc. in Computer Science *Muzambinho, Minas Gerais, Brazil*

Experience

Complex Data Mining Extension Course at Unicamp Apr. 2020 – Dec. 2025
Teaching Assistant *Campinas, São Paulo, Brazil*

- Assisted the professor during lectures by presenting code demonstrations and offering assistance outside class hours.
- Served as a teaching assistant for courses in Information Retrieval, Unsupervised Machine Learning, and Capstone Project.
- Served as a tutor, assisting students with course materials across various subjects.

Major Projects

Protein Function Prediction Mar. 2021 – Jul. 2025
A classifier leveraging Transformer embeddings and BLASTp *Campinas, São Paulo, Brazil*

- Currently being developed as part of my doctoral thesis.
- Developed a classifier utilizing the ESM2 and ProtT5 architectures available on Hugging Face, combined with BLASTp.
- Implemented the model using TensorFlow and PyTorch frameworks.
- Achieved best performance compared to state-of-the-art approaches in evaluations.
- Published findings in peer-reviewed conference proceedings and journals.

Protein Secondary Structure Prediction Mar. 2019 – Mar. 2021
An ensemble-based classifier combining Transformers, deep learning, machine learning, and BLASTp *Campinas, São Paulo, Brazil*

- Developed as part of my Master’s thesis.
- Implemented a classifier employing an ensemble of seven models.
- Incorporated BERT, custom deep learning architectures, classical machine learning classifiers, and BLASTp.
- Outperformed state-of-the-art methods during evaluations.
- Published results in peer-reviewed conference proceedings and journals.

COVID-19 Classification Jun. 2020 – Mar. 2021
Diagnosis of COVID-19 from X-ray and CT images *Campinas, São Paulo, Brazil*

- Developed a model leveraging pretrained convolutional neural networks.
- Achieved promising results in distinguishing between COVID-19 and non-COVID images.
- Published findings in peer-reviewed conference proceedings.

Awards

- Best Master’s Thesis Award, Institute of Computing, University of Campinas (2021).
- Best Paper Award, XIII Brazilian Symposium on Bioinformatics (BSB), 2020.

Technical Skills, Language Skills, and Interests

Operating Systems: Windows and Linux
Programming Languages: Python
Libraries: TensorFlow, PyTorch, transformers, scikit-learn, NumPy, pandas, Matplotlib, and Seaborn
Version Control: Git
Languages: Portuguese (native) and English (advanced)
Interests: Machine Learning, Deep Learning, Natural Language Processing, and Bioinformatics

Publications

Journal Papers

1. **Gabriel Bianchin de Oliveira**; Helio Pedrini; Zanoni Dias. SUPERMAGOv2: Protein Function Prediction via Transformer Embeddings and Bitscore-Weighted Features. IEEE Access. 2025. v. 13, p. 139743-139757. DOI: https://doi.org/10.1109/ACCESS.2025.3596851.
2. **Gabriel Bianchin de Oliveira**; Helio Pedrini; Zanoni Dias. SUPERMAGO: Protein Function Prediction Based on Transformer Embeddings. PROTEINS: Structure, Function, and Bioinformatics. 2025. v. 93, 5, p. 981-996. DOI: https://doi.org/10.1002/prot.26782.
3. **Gabriel Bianchin de Oliveira**; Helio Pedrini; Zanoni Dias. TEMPROT: protein function annotation using transformers embeddings and homology search. BMC Bioinformatics. 2023. v. 24, 242, p. 1-16. DOI: https://doi.org/10.1186/s12859-023-05375-0.
4. **Gabriel Bianchin de Oliveira**; Helio Pedrini; Zanoni Dias. Ensemble of Template-Free and Template-Based Classifiers for Protein Secondary Structure Prediction. International Journal of Molecular Sciences. 2021. v. 22, n. 21, 11449, p. 1-24. DOI: https://doi.org/10.3390/ijms222111449.

Conference Papers

1. **Gabriel Bianchin de Oliveira**; Helio Pedrini; Zanoni Dias. Scaling Up ESM2 Architectures for Long Protein Sequences Analysis: Long and Quantized Approaches. Brazilian Symposium on Bioinformatics 2024 (BSB' 2024). p. 1-11. DOI: https://doi.org/10.5753/bsb.2024.244804.
2. **Gabriel Bianchin de Oliveira**; Helio Pedrini; Zanoni Dias. Integrating Transformers and AutoML for Protein Function Prediction. 46th Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBC 2024). p. 1-5. DOI: https://doi.org/10.1109/EMBC53108.2024.10782139.
3. Ana Paula S. Dantas; **Gabriel Bianchin de Oliveira**; Helio Pedrini; Cid C. de Souza; Zanoni Dias. The Multi-attribute Fairer Cover Problem. 12th Brazilian Conference on Intelligent Systems (BRACIS 2023). p. 163-177. DOI: https://doi.org/10.1007/978-3-031-45368-7_11.
4. Ana Paula S. Dantas; **Gabriel Bianchin de Oliveira**; Daiane Mendes de Oliveira; Helio Pedrini; Cid C. de Souza; Zanoni Dias. Algorithmic Fairness Applied to the Multi-Label Classification Problem. 18th International Joint Conference on Computer Vision, Imaging and Computer Graphics Theory and Applications (VISAPP 2023). p. 737-744. DOI: https://doi.org/10.5220/0011746400003417.
5. **Gabriel Bianchin de Oliveira**; Helio Pedrini; Zanoni Dias. Protein Molecular Function Annotation Based on Transformer Embeddings. 11th Brazilian Conference on Intelligent Systems (BRACIS 2022). p. 210-220. DOI: https://doi.org/10.1007/978-3-031-21689-3_16.
6. Felipe Lopes Mello; **Gabriel Bianchin de Oliveira**; Helio Pedrini; Zanoni Dias. Prediction of Protein Molecular Functions Using Transformers. 21st International Conference on Artificial Intelligence and Soft Computing (ICAISC 2022). p. 379-387. DOI: https://doi.org/10.1007/978-3-031-23480-4_32.
7. Thiago Dong Chen; **Gabriel Bianchin de Oliveira**; Zanoni Dias. Ensemble of Patches for COVID-19 X-Ray Image Classification. 14th International Conference on Agents and Artificial Intelligence (ICAART 2022). p. 561-567. DOI: https://doi.org/10.5220/0010864500003116.
8. **Gabriel Oliveira**; Lucas David; Rafael Padilha; Ana Paula da Silva; Francine de Paula; Lucas Infante; Lucio Jorge; Patricia Xavier; Zanoni Dias. Bias Assessment in Medical Imaging Analysis: A Case Study on Retinal OCT Image Classification. 14th International Conference on Agents and Artificial Intelligence (ICAART 2022). p. 574-580. DOI: https://doi.org/10.5220/0010867400003116.
9. Daniel Ferber; Felipe Vieira; João Dalben; Mariana Ferraz; Nicholas Sato; **Gabriel Oliveira**; Rafael Padilha; Zanoni Dias. Deep Learning-Based COVID-19 Diagnostics of Low-Quality CT Images. Brazilian Symposium on Bioinformatics 2021 (BSB' 2021). p. 69-80. DOI: https://doi.org/10.1007/978-3-030-91814-9_7.
10. **Gabriel Bianchin de Oliveira**; Helio Pedrini; Zanoni Dias. MMEC: Multi-Modal Ensemble Classifier for Protein Secondary Structure Prediction. 19th International Conference on Computer Analysis of Images and Patterns (CAIP 2021). p. 175-187. DOI: https://doi.org/10.1007/978-3-030-89128-2_17.
11. **Gabriel Oliveira**; Rafael Padilha; André Dorte; Luis Cereda; Luiz Miyazaki; Maurício Lopes; Zanoni Dias. COVID-19 X-ray Image Diagnostic with Deep Neural Networks. Brazilian Symposium on Bioinformatics 2020 (BSB' 2020). p. 57-68. DOI: https://doi.org/10.1007/978-3-030-65775-8_6.
12. **Gabriel Bianchin de Oliveira**; Helio Pedrini; Zanoni Dias. Fusion of BLAST and Ensemble of Classifiers for Protein Secondary Structure Prediction. 33rd Conference on Graphics, Patterns and Images (SIBGRAPI 2020). p. 308-315. DOI: https://doi.org/10.1109/SIBGRAPI51738.2020.00049.
13. **Gabriel Bianchin de Oliveira**; Helio Pedrini; Zanoni Dias. Ensemble of Bidirectional Recurrent Networks and Random Forests for Protein Secondary Structure Prediction. 27th International Conference on Systems, Signals and Image Processing (IWSSIP 2020). p. 311-316. DOI: https://doi.org/10.1109/IWSSIP48289.2020.9145437.

Short Papers

1. **Gabriel Bianchin de Oliveira**; Helio Pedrini; Zanoni Dias. Protein secondary structure prediction based on fusion of machine learning classifiers. 36th Symposium on Applied Computing – Track Bioinformatics (ACM SAC BIO 2021). p. 26-29. DOI: https://doi.org/10.1145/3412841.3442067.

Peer-Review Activities

- Reviewer for Bioinformatics (2025).
- Reviewer for Computational and Structural Biotechnology Journal (2024).