Curriculum Vitae for Paulo Cilas M Lyra-Jr, Ph.D.

Current Position: Postdoctoral Fellow
Division of Population Science
Department of Cancer Epidemiology
H. Lee Moffitt Cancer Center & Research Institute
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Education, Work Experience and Fellowship Appointments:

2022-Current	Postdoctoral Fellow, Moffitt Cancer Center & Research Institute, Tampa, FL.
2022-2022	Back-end developer (Cybersecurity), ISH Technology, Remote, Brazil.
2020-2022	Course coordinator, University FAEMA, Ariquemes, Brazil.
2019-2022	Full Stack Developer, ENIGMA international consortium data, Remote.
2018-2019	Postdoctoral Fellow, Federal University of Espirito Santo, ES, Brazil.
2014-2018	Ph.D. in Biotechnology, Federal University of Espirito Santo, ES, Brazil.
2011-2013	M.Sc. in Biotechnology, Federal University of Espirito Santo, ES, Brazil.
2007-2011	B.Sc. in Pharmacy, Escola Superior de Ciências, Espirito Santo, Brazil

Projects

Digital Risk Protection (DRP):

Roles**:**

- Implemented an ETL solution that continuously analyzes large and combined datasets to detect specific events in the dark web and deep web, while maintaining a high level of customer service.
- Developed complex queries in response to client requirements, enabling the feeding of a dashboard through an API for real-time viewing of status updates for captured data elements.
- Took responsibility for improving the query efficiency and indexing performance of the warehouse database.

Architecture: REST API; Web Crawler; Microservice

Database: MongoDB; ElasticSearch; MySQL

Programming language: Python

Tools and Technologies: Git; Unix/bash; Docker; Apache Airflow

Cloud: AWS

Frameworks and libraries: Flask; FastAPI; Alembic; SQLAlchemy; Scrapy; Selenium; Beautifulsoup

Data analysis Script:

Roles**:**

- Script generated as part of the article entitled: "Integration of functional assay data results provides strong evidence for classification of hundreds of BRCA1 variants of uncertain significance".
- Developed to perform data mining, aggregation, wrangling, and classification of BRCA1 variants.

Programming language: R

Scientific Data Management WebApp Tool:

<u>Roles</u>**:**

- Designed and implemented a user-friendly interface for effectively conveying data-driven insights to cancer investigators.
- Utilized a robust technology stack to query, tidy, and summarize research data, facilitating effortless manipulation and visualization.
- Database modeling and data processing (aggregation, wrangling)

Architecture: MVC

Database: SQL

Programming language: C#; JavaScript; SQL

Tools and Technologies: Git; ASP.NET; MS SQL Server Management Studio

Cloud: Azure

Frameworks and libraries: .NET; Entity Framework; jQuery; Bootstrap

Miscellaneous:

<u>Roles</u>**:**

- Designed and implemented a user interface that seamlessly integrates the Iterative Rank-Order Normalization of Gene Expression Microarray Data (IRON) pipeline, enhancing usability and efficiency for researchers and scientists as part of the Bio-Data Club's 4th Annual Hackathon at Moffitt Cancer Center.
- Developed a Python-based tool to retrieve patient data for validating and correcting variant nomenclatures inputted by clinicians, ensuring the accuracy and reliability of clinical data.
- Generated circular layout figures, ideal for exploring relationships between objects or positions, using Circos software to enhance data visualization.

Certificates	
Microsoft – Data Scientist Associate	Databricks – Generative AI Fundamentals
Microsoft – AI Fundamentals	Databricks – Lakehouse Fundamentals
Microsoft – Security, Compliance, and Identity	
Microsoft – Azure Fundamentals	
Microsoft – Data Fundamentals	

Peer-Reviewed Publications

1. Zipinotti Dos Santos D, de Souza JC, Pimenta TM, Martins BS, Ribeiro Junior RS, Butzene SMS, Tessarolo NG, **<u>Lyra-Jr PC</u>** et al. The impact of lipid metabolism on breast cancer: a review about its role in tumorigenesis and immune escape. Cell Commun Signal. 2023 Jun. DOI: 10.1186/s12964-023-01178-1.
2. Fasching PA, Liu D, Scully S, Ingle JN, **<u>Lyra-Jr PC</u>**, Rack B, Hein A, Ekici A B, Reis A, Schneeweiss A, Tesch H, Fehm TN, Heinrich G, Beckmann MW, Ruebner M, Huebner H, Lambrechts D, Madden E, Shen J, Room J, Doheny K, Jenkins GD, Carlson EE, Li I, Fridley BL et al. Identification of two genetic loci associated with leukopenia after chemotherapy in Breast Cancer Patients. Clin Can Res. 2022 Aug. DOI: 10.1158/1078-0432.CCR-20-4774.
3. Mendoza-Fandiño G, **<u>Lyra-Jr PC</u>**, Nepomuceno TC, Harro CM, Woods NT, Li X, Rangel LB, Carvalho MA, Couch FJ, Monteiro ANA. Two distinct mechanisms underlie estrogen-receptor-negative breast

cancer susceptibility at the 2p23.2 locus. Eur J Hum Genet. 2021 Nov. DOI: 10.1038/s41431-021-01005-6.

4. Henriques TB, dos Santos DZ, Guimarães IS, Tessarollo NG, **Lyra-Jr PC**, Mesquita P, Pádua D, Amaral AL, Cavadas B, Pereira L, Silva IV, Almeida RMSG, Rangel LBA. Inhibition of CXCR2 plays a pivotal role in re-sensitizing ovarian cancer to cisplatin treatment. Aging. 2021 May. DOI: 10.18632/aging.203074.

5. **Lyra-Jr PC**, Nepomuceno TC, de Souza MLM, Machado GF, Veloso MF, Henriques TB, dos Santos DZ, Ribeiro IG, Ribeiro-Jr RSR, Rangel LBA, Richardson M, Iversen ES, Goldgar D, Couch FJ, Carvalho MA, Monteiro ANA. Integration of functional assay data results provides strong evidence for classification of hundreds of BRCA1 variants of uncertain significance. Genet Med. 2020 Oct. DOI: 10.1038/s41436-020-00991-0.

6. **Lyra-Jr PC**, Rangel LBA, Monteiro ANA. Functional landscape of common variants associated with susceptibility to epithelial ovarian cancer. Curr Epidemiol Rep. 2020 Jan. DOI: 10.1007/s40471-020-00227-4.

7. Gusev A, Lawrenson K, Lin X, **Lyra-Jr PC**, Kar S, Vavra KC, Segato F, Fonseca MAS, Lee JM, Pejovic T, Liu G, Ovarian Cancer Association Consortium, Karlan BY, Freedman ML, Noushmehr H, Monteiro ANA, Pharoah PDP, Pasaniuc B, Gayther SA. A transcriptome-wide association study of high grade serous epithelial ovarian cancer identifies new susceptibility genes and splice variants. Nat Genet. 2019 May. DOI: 10.1038/s41588-019-0395-x.

8. Buckley MA, Woods NT, Tyrer JP, Mendoza-Fandiño G, Lawrenson K, Hazelett DJ, Najafabadi HS, Gjyshi A, Carvalho RS, **Lyra-Jr PC**, Coetzee SG, Shen HC, Yang AW, Earp MA, Yoder SJ, Risch H, Chenevix-Trench G, Ramus SJ, Phelan CM, Coetzee GA, Noushmehr H, Hughes TR, Sellers TA, Goode EL, Pharoah PDP, Gayther SA, Monteiro ANA. Functional analysis and fine mapping of the 9p22.2 ovarian cancer susceptibility locus. Cancer Res. 2019 Feb 1. DOI: 10.1158/0008-5472.CAN-17-3864.

9. Phelan CM, Kuchenbaecker KB, Tyrer JP, Kar SP, Lawrenson K, Winham SJ, Dennis J, Pirie A, Riggan MJ, Chornokur G, Earp MA, **Lyra-Jr PC** … Gayther SA, Antoniou AC, Pharoah PDP. Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nat Genet. 2017 May. DOI: 10.1038/ng.3826.