Internacional fellowship call CAPES PEC-PG

Open position 1 – Master`s degree opportunity

Researcher/Professor: Dr. Matias Eliseo Melendez

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Project: Development of an Oncolytic Virus Derived from HSV-1 Expressing Bispecific T-Cell Engagers (BiTEs) for the Treatment of Solid Tumors

Number of positions in this project: 1

Abstract: This project focuses on the development of a genetically engineered oncolytic herpes simplex virus type 1 (HSV-1) designed to enhance anti-tumor immune responses. The virus is will express a bispecific T-cell engagers (BiTEs). By combining direct oncolysis induced by HSV-1 with BiTE-mediated recruitment and activation of T-cells, this approach seeks to overcome immune evasion mechanisms characteristic of solid tumors. The strategy aims to achieve a synergistic therapeutic effect: selective viral replication and tumor cell lysis, together with robust and localized T-cell–mediated cytotoxicity.

Open position 2 – Master`s degree opportunity

Researcher/Professor: Dr. Matias Eliseo Melendez

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Project: Development of an Oncolytic Virus Derived from HSV-1 Expressing Bispecific T-Cell Engagers (BiTEs) Conjugated to the Proapoptotic Molecule sfTRAIL for the Treatment of Solid Tumors

Number of positions in this project: 1

Abstract: This project proposes the engineering of a herpes simplex virus type 1 (HSV-1)-based oncolytic virus to enhance the therapeutic potential against solid tumors. The virus will be designed to express bispecific T-cell engagers (BiTEs) conjugated to sfTRAIL (soluble, trimeric TNF-related apoptosis-inducing ligand), a molecule capable of inducing apoptosis selectively in cancer cells via death receptor signaling. The combination of HSV-1–mediated oncolysis, T-cell redirection by BiTEs, and apoptosis induction through sfTRAIL represents a multimodal strategy aimed at overcoming resistance mechanisms in the tumor microenvironment.

Open position 3 – Master`s degree opportunity

Researcher/Professor: Dr Barbara da Costa Reis Monte Mor

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Project: Study of germline variants in the pathogenesis of myeloproliferative neoplasms

Number of positions in this project: 1

Abstract: Myeloproliferative neoplasms (MPNs) are clonal diseases characterized by the abnormal expansion of one or more myeloid lineages. Classic BCR-ABL-negative MPNs include polycythemia vera (PV), essential thrombocythemia (ET), and primary myelofibrosis (PMF). These diseases are driven by somatic activating mutations in the JAK/STAT pathway, which promote the increased production of one or more myeloid lineages, including platelets, erythrocytes, and neutrophils. Although most MPNs occur sporadically, hereditary factors can contribute to their development. Among these factors, recent studies have identified many common germline genetic variants that may be associated with an increased risk of developing MPN, with low penetrance. Conversely, some rare germline genetic variants have been found in familial clusters of MPN. Next-Generation Sequencing (NGS), whether using targeted panels, exome, or genome sequencing, enables in-depth characterization of the genomic landscape of myeloproliferative neoplasms, which can lead to the identification of both somatic and germline mutations. This project aims to study germline variants in Brazilian MPN patients, evaluating their potential role as susceptibility factors for these conditions. To this end, genomic data from MPN patients will be analyzed, and in vitro cellular models will be used to study their role. The discovery of new germline variants associated with hematologic malignancies has the potential to elucidate the molecular mechanisms of susceptibility and expand our understanding of the pathophysiology of these diseases.

Open position 4 – Master`s degree opportunity

Researcher/Professor: Dr Paula Sabbo

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Project: Exploring the relationship between TP53 and miR-210 in radiotherapy response of glioblastoma cells lines

Number of positions in this project: 1

Abstract: Cancer is one of the main public health problems worldwide. Central nervous system (CNS) malignant tumors are aggressive and heterogenous tumors with growing incidence. Glioblastoma (GBM) is the most frequent malignant brain tumor and only 6.8% of patients survive five years. Treatment resistance represents one of the leading causes of disease progression. In recent years, our group has observed that the presence of TP53 mutations is associated with a better response to radiotherapy, both in vitro and in patient samples. Additionally, we have identified a potential correlation with miR-210 expression. In this context, our goal is to understand the relationship between the mutational status of TP53 and the expression of miR-210 in radiotherapy response by modulating miR-210 expression in isogenic cell lines with TP53 wildtype and mutated forms.

Open position 5 – Master`s degree opportunity

Researcher/Professor: Dr Mario Jorge Sobreira da Silva

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Project: REAL-WORLD DATA ANALYSIS ON CANCER PHARMACOTHERAPY

Number of positions in this project: 1

Abstract: Cancer remains a major public health concern worldwide. Over recent decades, both incidence and mortality rates have risen significantly across the globe. Nonetheless, disparities in cancer survival estimates persist, largely influenced by a country's level of economic development, which directly affects access to timely and effective treatment. Anticancer drugs constitute the leading category of innovative health technologies approved globally. However, many of these therapies receive market authorization through expedited regulatory pathways, often based on limited evidence and without meeting thresholds for clinically meaningful benefit. In oncology, Real-World Data (RWD) are increasingly employed to inform both clinical and policy-relevant decision-making. Data obtained from electronic health records, cancer registries, and other real-world sources can yield valuable insights into therapeutic utilization and outcomes in routine clinical settings. This project aims to analyze RWD related to cancer pharmacotherapy, focusing on its incorporation and availability within health systems. The methodological framework comprises: (i) retrospective analyses of publicly available health system databases to characterize treatment patterns; (ii) comparative effectiveness research on biosimilars; (iii) retrospective chart reviews from cancer care facilities to evaluate clinical effectiveness and safety; and (iv) prospective collection of patient-reported outcomes, including quality-of-life metrics. The studies will target high-incidence cancer types—breast, lung, and colorectal cancers—and are designed to facilitate cross-national comparisons. This comprehensive methodological strategy offers a robust platform for generating actionable insights to inform healthcare policy and clinical practice.

Open position 6 – PhD degree opportunity

Researcher/Professor: Dr. Matias Eliseo Melendez

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Project: Development of an Oncolytic Virus Derived from HSV-1 for Targeted Therapy of BRAF-Mutated Tumors

Number of positions in this project: 1

Abstract: This project aims to develop a herpes simplex virus type 1 (HSV-1)-based oncolytic virus tailored to target tumors harboring mutations in the BRAF oncogene, a driver alteration frequently associated with aggressive growth and therapy resistance in several cancers, such as melanoma, colorectal, and thyroid carcinomas. The engineered HSV-1 will be optimized for selective replication in BRAF-mutated tumor cells, promoting direct oncolysis while simultaneously stimulating antitumor immune responses.

Open position 7 – PhD degree opportunity

Researcher/Professor: Dr. Matias Eliseo Melendez

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Project: Development of a Colorimetric Sensing System for the Identification of Gene Fusions in the Early Diagnosis of Prostate Cancer

Number of positions in this project: 1

Abstract: This project focuses on creating a low-cost, rapid, and accessible colorimetric biosensing platform to detect gene fusions associated with prostate cancer, such as TMPRSS2:ERG, which are highly prevalent and clinically relevant biomarkers. The system will be designed to generate a visible color change upon recognition of specific nucleic acid sequences, allowing direct interpretation without the need for complex instrumentation. By enabling early and accurate detection of prostate cancer through a simple molecular assay, the technology aims to improve diagnostic accuracy, expand access to precision oncology, and support timely therapeutic decision-making, particularly in resource-limited settings.

Open position 8 – PhD degree opportunity

Researcher/Professor: Dr Mariana Emerenciano Cavalcanti de Sa

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Project: Genomic Determinants of Treatment-Related Toxicity in Pediatric Acute Lymphoblastic Leukemia

Number of positions in this project: 1 for PhD and 1 for Sandwich PhD

Abstract: Acute lymphoblastic leukemia (ALL) is the most common pediatric cancer, and its development is associated with underlying genetic alterations. They not only drive leukemogenesis but also impact the therapeutic response and toxicity events observed in individual patients. Understanding the genetic determinants of treatment-related toxicity is essential to improve clinical outcomes and guide precision medicine in pediatric ALL. Therefore, this project aims to identify and characterize pharmacogenomic variants associated with treatment-related toxicities in pediatric ALL patients enrolled in a unique therapeutic protocol. The research will focus on large-scale data analysis and bioinformatics to integrate genomic information with clinical outcomes, offering opportunities to contribute to translational discoveries with direct clinical relevance. We invite applications from motivated researchers with a background in genetics or related fields. Familiarity with programming languages is highly desirable, as computational analysis will be a central component of the work. Candidates should demonstrate strong analytical skills, curiosity, and a commitment to collaborative research. The project will be supervised by Dr. Mariana Emerenciano and Dr. Bruno A. Lopes, who have extensive expertise in leukemia genetics and translational oncology. This is an excellent opportunity for researchers eager to advance precision oncology and contribute to the improvement of pediatric cancer care.

Open position 9 – PhD degree opportunity

Researcher/Professor: Dr Luis Felipe Ribeiro Pinto

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Project: The role of ZNF281 in esophageal squamous cell carcinoma

Number of positions in this project: 1

Abstract: Esophageal squamous cell carcinomas (ESCC) is a highly incident tumor in South America. Recently, a transcriptome study of Brazilian ESCC subjects revealed 1,328 differentially expressed genes (DEGs) in this tumor. We carried out a master regulator analysis and showed that among transcription factors responsible for these DEGs, ZNF281 was the most enriched transcription factor. ZNF281 is not only involved in the DNA damage response, which is fundamental to resistance to chemotherapy treatment, but also orchestrates various characteristics of tumor cells, including epithelial-mesenchymal transition and cell differentiation, among others. Although the involvement of ZNF281 has been shown in cervical and colorectal tumors, there is no data regarding the importance of this gene in ESCC. Therefore, the objective of this study is to characterize the role of ZNF281 in ESCC. We will analyze its expression in ESCC samples from patients, both by real-time PCR and immunohistochemistry, and correlate its expression with prognosis endpoints, such as overall survival and pathological response to chemoradiotherapy treatment. Furthermore, we will modulate its expression by overexpressing or silencing ZNF281 in esophageal non-tumor and tumor cell lineages and organoids, aiming to observe the outcomes on cellular endpoints, such as cell viability, proliferation, migration, and others. Additionally, we plan to evaluate ZNF281-mediated transcriptomic reprogramming through RNA-seq analysis. After selecting specific genes, we will examine their roles as effectors of ZNF281 overexpression.

Open position 10 – PhD degree opportunity

Researcher/Professor: Dr Edenir Inez Palmero

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Project: Genomic Landscape of Germline Alterations in Prostate Cancer: A Whole-Exome Sequencing Study

Number of positions in this project: 1

Abstract: Prostate cancer (CaP) is one of the most common types of cancer worldwide and represents a major public health concern. The diversity in its clinical presentation underscores the need for a precision medicine approach to guide appropriate screening and oncological treatment. The present project aims to identify patients with hereditary cancer predisposition syndromes and perform a wide genomic chatacterization through germline whole exome sequencing. Data from WES will be also correlated with genetic ancestry and clinico-pathological information. Clinical and molecular data and family histories will be included in a RedCap database. The study cohort will consist of 500 men ≥40–45 years of age, with or without prostate cancer, who meet at least one of the following criteria: (i) African ancestry (self-reported); (ii) personal and/or family history suggestive of a hereditary cancer predisposition syndrome. In summary, this proposal brings innovative and comprehensive strategies, in order to promote scientific, technological and social advances that will position the country as a global reference in applied oncogenetics. The expected impacts encompass crucial dimensions: subsidy for public policies, advancements in scientific research, and social and economic development.

Open position 11 – PhD degree opportunity

Researcher/Professor: Dr Mariana Boroni

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Project: Análise das alterações moleculares em tumores de câncer de colo de útero através de dados múltiomicos

Number of positions in this project: 1

Abstract: O câncer do colo do útero é uma das principais causas de mortalidade por neoplasias em mulheres no Brasil e no mundo, estando fortemente associado à infecção persistente pelo papilomavírus humano (HPV). Apesar dos avanços em prevenção e tratamento, muitos aspectos biológicos relacionados à progressão tumoral, heterogeneidade molecular e resposta terapêutica permanecem pouco compreendidos. Nesse contexto, o presente projeto tem como objetivo realizar uma análise integrada das alterações moleculares em tumores de câncer de colo de útero por meio de abordagens multiômicas, incluindo transcriptômica, epigenômica e genômica. A utilização desses diferentes níveis de informação permitirá caracterizar assinaturas moleculares associadas a processos críticos, como evasão imune, instabilidade genômica e alterações epigenéticas, que contribuem para a agressividade e evolução da doença. Além disso, a integração desses dados possibilitará a identificação de potenciais biomarcadores de diagnóstico e prognóstico, bem como alvos terapêuticos de interesse clínico. A análise será conduzida com metodologias de bioinformática e inteligência artificial, capazes de lidar com a complexidade e a alta dimensionalidade dos dados multiômicos. Espera-se que os resultados obtidos ampliem o conhecimento sobre os mecanismos biológicos que sustentam o câncer do colo do útero e forneçam subsídios para estratégias mais precisas de manejo clínico, contribuindo para a medicina de precisão no contexto do Sistema Único de Saúde (SUS).