Leveraging Microbiome Data and Machine Learning for the Identification of Novel Biomarkers in Early Detection and Classification of Pancreatic Cancer

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Pancreatic cancer remains one of the most lethal diseases, primarily due to its asymptomatic progression and late-stage diagnosis, which severely limits treatment options and reduces survival rates. Current diagnostic methods, including imaging and biomarker-based approaches, lack the sensitivity and specificity required for early detection, highlighting the urgent need for reliable biomarkers. This project aims to address this challenge by developing a machine learning-based framework that integrates microbiome and multi-omics data to identify early-stage biomarkers for pancreatic cancer. Advanced neural network architectures, specifically convolutional neural networks (CNNs) and recurrent neural networks (RNNs), were employed to process and classify high-dimensional clinical genomic datasets. Feature selection techniques such as LASSO regression and Principal Component Analysis were utilized to extract key microbial markers associated with early-stage pancreatic cancer. Identified biomarkers underwent pathway enrichment analysis, revealing their functional roles in pancreatic tumorigenesis and classifying cancer development. Building on these findings, this research develops synthetic inhibitors that target cancer-promoting metabolic pathways within the microbiome. The ultimate goal of this research is to translate these findings into a non-invasive saliva diagnostic test using lateral flow assays, allowing for earlier detection and improving patient outcomes. By integrating microbiome science with AI-driven multi-omics analysis, this research presents a transformative approach that enhances diagnostic accuracy, facilitates early intervention, and lays the foundation for more personalized treatment strategies in pancreatic cancer management.

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