A Novel Exosome-Encapsulated-miRNA-Based Machine Learning Model for Blood-Based Diagnosis, Subtype Classification, and Stage Detection of Multiple Cancer Types

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By 2040, the global cancer burden will rise to 30 million new cases annually, with the greatest increases affecting low-to-middle-income countries. Current diagnosis methods, such as physical examinations, imaging, or biopsies, cannot accordingly support the routine diagnosis of more than 200 cancer types and subtypes, as they are expensive, invasive, and test for a single cancer type. Machine learning models utilizing cell-free circulating miRNA are currently the standard for minimally invasive and inexpensive blood-based cancer diagnosis but are limited to one cancer-diagnosing function, such as cancer diagnosis or subtype classification, that applies to a couple of cancer types at most. The purpose of this project is to develop a novel multi-functional machine learning model for simultaneous diagnosis, subtype classification, and stage detection of multiple cancer types. The model utilizes a compiled dataset of exosome-encapsulated-miRNA expressions from blood samples as biomarkers, which in contrast to standard cell-free circulating miRNAs, are more sensitive to cancer activity and not influenced by the blood-stream environment. A separately trained model performs each cancer-diagnosing function; in preliminary testing, the models classified unseen patients as healthy or cancerous, including specifying cancer type, with an average accuracy of 83.3%, and classified cancer subtypes with an average accuracy exceeding 95%. This multi-functional model is fundamental for the creation of a device for inexpensive and minimally invasive real-time cancer diagnosis to enable widespread routine pan-cancer diagnosis. This can potentially save the lives of millions of patients who were diagnosed too late and reduce the significance of cancer as a threat to the modern world.

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