A Quantum Machine Learning-Based Framework for Early Cancer Detection and Biomarker Identification Through Transcriptome Profiles

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Cancer is a broad term for diseases characterized by uncontrollable and abnormal cell growth. It is the second-leading cause of death worldwide, with 9 million deaths each year. However, early cancer detection, crucial for improving survival outcomes, remains challenging in developing countries like India. In my research, I developed a novel three-step framework based on quantum machine learning that uses transcriptome data to identify key cancer biomarkers and combines them to create mathematical expressions that can predict the presence of cancer with high accuracy using the expression levels of five or fewer genes. Instead of relying on traditional black-box machine learning, my framework utilized a recently-developed technology called the quantum lattice to produce transparent and explainable models. For each dataset, after initial filtering through XGBoost and statistical significance testing to identify differentially expressed genes, the quantum lattice was trained for 10 epochs using the Akaike Information Criterion as its loss function. The framework was trained and tested on ten datasets with data on ten different cancers, sourced from CuMiDa (the Curated Microarray Database). Median accuracies, sensitivities and specificities of 91%, 92.5% and 87.5% respectively were obtained, with the highest being 100%. Overall, the models show greater accuracies than previous research while also using far fewer genes for predictions. In all, 38 biomarkers were identified, with 17 novel results, 4 of which were lncRNAs. The results obtained can be applied in practical settings for efficient early cancer detection and can provide insights into associations between certain genes and types of cancer.

Awards Won:
Fourth Award of $500
American Statistical Association: In-Kind membership to ASA for all winners, including honorable mentions
American Statistical Association: Third Award of $500