Quantum Machine Learning for Multi-Omics Integration in

Personalized Medicine and Predictive Diagnostics

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***Abstract*—Multi-omics integration has become a cornerstone of personalized medicine, enabling researchers to connect genomic, transcriptomic, proteomic, metabolomic, and epigenomic data to reveal complex biological mechanisms and individualized disease signatures. However, the extreme dimensionality, heterogeneity, and nonlinear interactions across omics layers challenge even the most advanced classical machine learning methods. Quantum Machine Learning (QML) offers a powerful alternative by exploiting quantum superposition, entanglement, and high-dimensional feature embeddings to model multi-omics interactions more efficiently. This study proposes a hybrid quantum–classical framework that combines quantum kernel estimation, variational quantum classifiers, and quantum-enhanced feature fusion networks to generate integrative biological signatures for precision diagnostics. Simulation results using benchmark multi-omics datasets demonstrate improved classification accuracy, enhanced sensitivity to weak biological signals, and reduced computational overhead compared to classical baselines. These findings highlight the potential of QML to accelerate multi-omics insights and pave the way toward truly personalized, predictive healthcare.**

Personalized medicine increasingly depends on the ability to integrate multiple layers of biological information—genomics, epigenomics, transcriptomics, proteomics, and metabolomics—to achieve high-resolution patient stratification and individualized treatment planning. While multi-omics data provide unprecedented biological insight, they also exhibit extreme complexity: high dimensionality, sparse structure, batch effects, nonlinear interdependencies, and heterogeneous measurement noise [4]. Classical machine learning techniques, though essential to current integrative pipelines, often struggle to model these complex relationships in an efficient and scalable manner.

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Quantum Machine Learning (QML) has emerged as a promising solution to these challenges. By encoding biological features into quantum states and leveraging the exponential representational capacity of quantum Hilbert spaces, QML algorithms can uncover patterns that remain obscured in classical models [6]. Quantum kernels, variational quantum classifiers (VQCs), and hybrid quantum neural architectures have shown the ability to handle high-dimensional data, capture subtle biological signatures, and accelerate computationally intensive tasks such as feature selection, clustering, and biomarker discovery [3].

In multi-omics integration, where complex cross-talk pathways define disease phenotypes, the

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