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Quantum Machine Learning-Driven Drug Repurposing Framework for Emerging Infectious Diseases Using Biomedical Knowledge Graphs and Multi-Omics Data

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ABSTRACT: Background: To ensure adequate health of adolescents, emerging infectious diseases are a real menace, but the traditional method of drug discovery is a 10-15-year process that demands huge financial resources. Drug repurposing using artificial intelligence is an alternative that may be promising, yet there is a lack of biological knowledge integration and the use of multimodal data. Purpose: The proposed research is based on the Quantum Machine Learning (QML)-based drug repurposing framework that allows combining the biomedical knowledge graph with the multi-omics data to determine the effective therapeutic candidates to new infectious diseases in adolescents. Methods: The data were a simulated biomedical graph consisting of 6,000 multi-omics profiles, 5,200 approved drugs, 18,000 genes, 9,500 proteins, and 42,000 drug-target interactions. A hybrid quantum Variational learning framework was used to couple graph embedding with multi-omics representations to rank drugs, whereas therapeutic recommendations were interpreted using a SHAP-based explainability. Results: The proposed framework demonstrated 96.4% accuracy, 95.8% precision, 96.1% recall, 95.9% F1-score, 0.985 ROC-AUC, 0.981 PR-AUC, which is 4.7-8.9 higher than the conventional graph neural network and deep learning baselines in terms of evaluation metrics. The

model also achieved 92.8 percent Top-10 drug recommendation accuracy, and an average of 0.23 s per patient inference time. Conclusion: The suggested QML concept illustrates the future prospects of using quantum learning, biomedical knowledge graphs, and multi-omics data to expedite explainable drug repurposing and assist precise therapeutic decisions in emerging infectious issues in adolescent groups.

1. INTRODUCTION

Emerging infectious diseases remain one of the biggest health risks to the global population especially in adolescents whose physiological stages, interactions in school, and their social mobility make them susceptible to the spread of diseases. The recent outbreaks of viral and bacterial disease causes have also proven the fact that there is an urgent necessity to develop quick therapeutic measures that can address newly appearing infections before they may develop into massive epidemics or pandemics. The traditional approach to pharmaceutical development may not be able to fulfill this need due to the time-consuming nature of the discovery of new drugs, which can take 10-15 years of study, preclinical and clinical trials, and costly investments in the billions of dollars, with the overall probability of success of candidate compounds being less than 10 percent. Moreover, fast evolving pathogens often diminish the utility of available therapeutics, and traditional drug development is inadequate to respond to the changed infectious diseases within clinically relevant time. There is therefore increasing interest in computational drug repurposing, which aims to find new therapeutic uses of already approved drugs, and thereby save a major reduction of development time, cost, and related safety-related uncertainties.

The recent progress in artificial intelligence has enhanced the pace of drug repurposing through the use of deep learning, graph neural networks, transformer architecture, and knowledge graph embedding algorithms, to learn the possibility of drug-disease interactions. Even though such approaches have been shown to have good predictive accuracy, they are often based on single biological measurements and have a high tendency to miss the complex relationships between genes, proteins, metabolites, biological pathways, and host–pathogen processes. Biomedical knowledge graphs have proven useful in incorporating heterogeneous biomedical information as drugs, diseases, genes, proteins, pathways, virus-host interactions, and biomedical ontologies can be represented as a single graph. These graphs enable detailed biological arguments through modeling drug-gene interactions, protein-protein interaction networks, disease signaling pathways and molecular mechanisms of infectious disease. However, patient-specific molecular features cannot be fully harnessed using knowledge graph-based methods, and thus, the applicability of this technology to precision medicine and individualized treatment prescriptions is limited.

Multi-omics integration has become a good approach to the characterization of disease mechanisms at various levels of the biology of a disease, by integrating genomics, transcriptomics, proteomics, metabolomics and epigenomics. This combination of complementary data modalities, serves to characterize genetic variations, patterns of gene expression, protein abundance, metabolic changes and epigenetic controls of disease progression and response to therapy in a comprehensive manner. Nevertheless, the nonlinear relationship between multi-omics data is highly dimensional and has significant computational challenges to the traditional machine learning algorithms. Quantum Machine Learning (QML) is one such promising option, as these quantum computing principles are applied in conjunction with artificial intelligence to analyze the intricate biomedical data more effectively. Hybrid QMLs which use variational quantum circuits (VQCs), quantum kernel models and hybrid quantum neural networks can be trained to use expressive feature representations and use quantum state encoding and parameterised quantum circuits to optimize and classify features. Even though modern quantum hardware is still in the noisy intermediate-scale quantum phase, hybrid quantum-classical systems have been shown to be promising in terms of applying to large-scale biomedical learning tasks and speeding up precision drug discovery.

It is based on these events that this study will present a Quantum Machine Learning-inspired drug repurposing framework that will combine biomedical knowledge graphs with multi-omics data to be used to personalize the discovery of therapeutics in response to emerging infectious diseases in adolescents. The suggested framework builds a detailed graph of biomedical knowledge connecting drugs, genes, proteins, diseases, biological pathways, and virus-host interactions and at the same time incorporates multi-omics molecular profiles to ensure the inclusion of patient-specific biological features. A hybrid quantum learning system integrates graph-based embeddings and multi-omics representations to prioritize candidate drugs, and a SHAP-based explainability system finds the biological factors behind each treatment suggestion, thus enhancing the model transparency and clinical interpretability. The experiments performed using simulation on a biomedical repository containing

6,000 multi-omics patient profiles, 5,200 approved drugs, 18,000 genes, 9,500 proteins, and 42,000 drug-target interactions result in the effectiveness of the proposed framework with an overall prediction accuracy of 96.4, F1-score of 95.9, ROC-AUC of 0.985, and Top-10 drug recommendation accuracy of 92.8. These results suggest that quantum machine learning, biomedical knowledge graphs, and multi-omics information can scale up an explainable and efficient computational framework that will accelerate repurposing drugs and enhance precision therapeutic decision support to novel infectious disease diagnoses.

2. RELATED WORK

Artificial intelligence has now become one of the most important technologies in terms of speeding up the process of drug repurposing through the discovery of new therapeutic uses of approved drugs with the help of large-scale biomedical data. Convolutional neural networks, recurrent neural networks and autoencoders are deep learning models that have proven to be highly effective in drug-target interaction, drug-disease interaction prediction by learning nonlinear biological interactions [3], [5]. However, in more recent work, Graph Neural Networks (GNNs) have demonstrated better predictive accuracy through the use of drugs, genes, proteins, and diseases as interconnected graph structures that maintain biological topology and patterns of interaction [2], [6], [15]. Transformer-based architectures have further improved drug discovery by using attention mechanisms that can capture long-range dependencies among heterogeneous biomedical entities, knowledge graph embedding models like TransE, RotatE and ComplEx effectively representations of complex biomedical relations in low-dimensional vectors [7], [10], [14]. Despite the fact that these approaches have greatly enhanced computational drug discovery, most of the available approaches primarily utilize either graph information or molecular features in isolation, which restricts their performance to capture the full picture of patient-specific biological mechanisms needed to do precision drug repurposing [5], [12].

Biomedical knowledge graphs have become effective computational tools to combine heterogeneous biological input to coherent disease models. These public biomedical repositories (Hetionet, DrugBank, STRING, DisGeNET, Comparative Toxicogenomics Database (CTD)) collaborate to offer very rich information about drugtarget interactions, gene disease interactions, protein protein interactions, signaling pathways, chemical-gene interactions, and even virus-host interactions [2], [9], [12]. The combination of these interrelated resources allows graph-based reasoning across a variety of biological objects and enhances significantly the biological understandability of computational drug discovery systems [2], [6], [9]. At the same time, multi-omics learning has gained a growing significance in terms of heterogeneity of diseases as an integration of genomics, transcriptomics, proteomics, metabolomics, and epigenomics. Many studies have had significant success in showing that the integration of multiple omics modalities is much more effective in disease characterization, cancer diagnosis, analysis of viral infections, biomarker discovery, and precision medicine than single-omics applications [1], [13]. Nonetheless, the combination of heterogeneous biomedical graphs and high dimensional multi-omics data is still a challenging problem due to the heterogeneity of data, nonlinear dependencies, and scalability problems of computations [5], [13].

Recent progress in Quantum Machine Learning (QML) has brought about new possibilities to solve computational problems related to large-scale learning in biomedicine. Quantum Support Vector Machines (QSVMs) leverage quantum feature spaces to achieve better classification of complex biomedical data, and Variational Quantum Classifiers (VQCs) use parameterized quantum circuits to learn nonlinear biological relationships with optimization by hybrid quantum-classical learning [4], [8]. Similarly, quantum graph learning algorithms have been suggested to improve the graph representation learning with the quantum state encoding, and quantum kernel algorithms have been shown to perform better with similarity estimations on biomedical classification and molecular analysis [4], [11]. Irrespective of these encouraging advances, the existing health care uses of quantum computing are mostly limited to disease diagnostics, predicting molecular properties, or small-scale classification problems [8], [11]. Although the idea of quantum learning has been applied to biomedical knowledge graphs and multi-omics information to explainable repurposing of drugs, there is limited literature examining these concepts, and it remains open to significant improvements in the method of enhancing computational precision medicine [5], [10].

Despite the sharp advancements made in AI-based drug repurposing, biomedical knowledge graphs, multi-omics combination, and quantum machine learning, there are many research gaps which should be addressed [2], [5], [8], [12]. Current frameworks often implement weak multimodal integration, where biological networks and omics data are learned independently, rather than learn joint representations at various biological scales [5], [13]. Lack of explainability is also an issue with many AI models, as it does not allow clinicians to easily comprehend the biological assumptions behind the suggested therapeutic advice [1], [5]. Also, there has been a relative dearth of interest in personalized rankings of drugs, depending on patient-specific molecular features,

especially in regard to new infectious diseases that target the adolescent demographic [3], [10]. The other interesting limitation is the lack of quantum-enhanced drug ranking systems that unite biomedical knowledge graphs, feature fusion in multi-omics, and explainable artificial intelligence into one computational setup [8], [11]. In order to overcome these drawbacks, the proposed research presents a hybrid Quantum Machine Learning-based drug repurposing pipeline that combines biomedical knowledge graphs, multi-omics data, uses variational quantum learning to predictive drug ranking, and apply SHAP-based explainability to produce reliable, transparent, and personalized therapeutic suggestions to emerging infectious diseases.

3. PROPOSED METHODOLOGY

The proposed framework, Quantum Machine Learning (QML)-powered drug repurposing platform combines biomedical knowledge graphs, multi-omics data, and explainable artificial intelligence to uncover promising therapeutic opportunities in cases of emerging infectious diseases in adolescent populations. Its architecture comprises of six consecutive steps namely biomedical data collection, multi-omics preprocessing, biomedical knowledge graph construction, quantum feature learning, drug ranking and explainable prediction. Figure 1 demonstrates the preprocessing of multi-omics datasets, which is done on heterogeneous biomedical information that is first gathered with simulated molecular and clinical repositories. The extracted biological graphs are combined with a biomedical knowledge graph that is an expression of connections between drugs, diseases, genes, proteins, biological pathways and virus-host interactions. Such multimodal representations are then learned on a hybrid quantum architecture, generating latent feature embedding feature ranking of drugs. Last, there is an explainability module relying on SHAP and attention analysis to determine the biological reasons behind each recommendation to facilitate an open clinical decision support process.

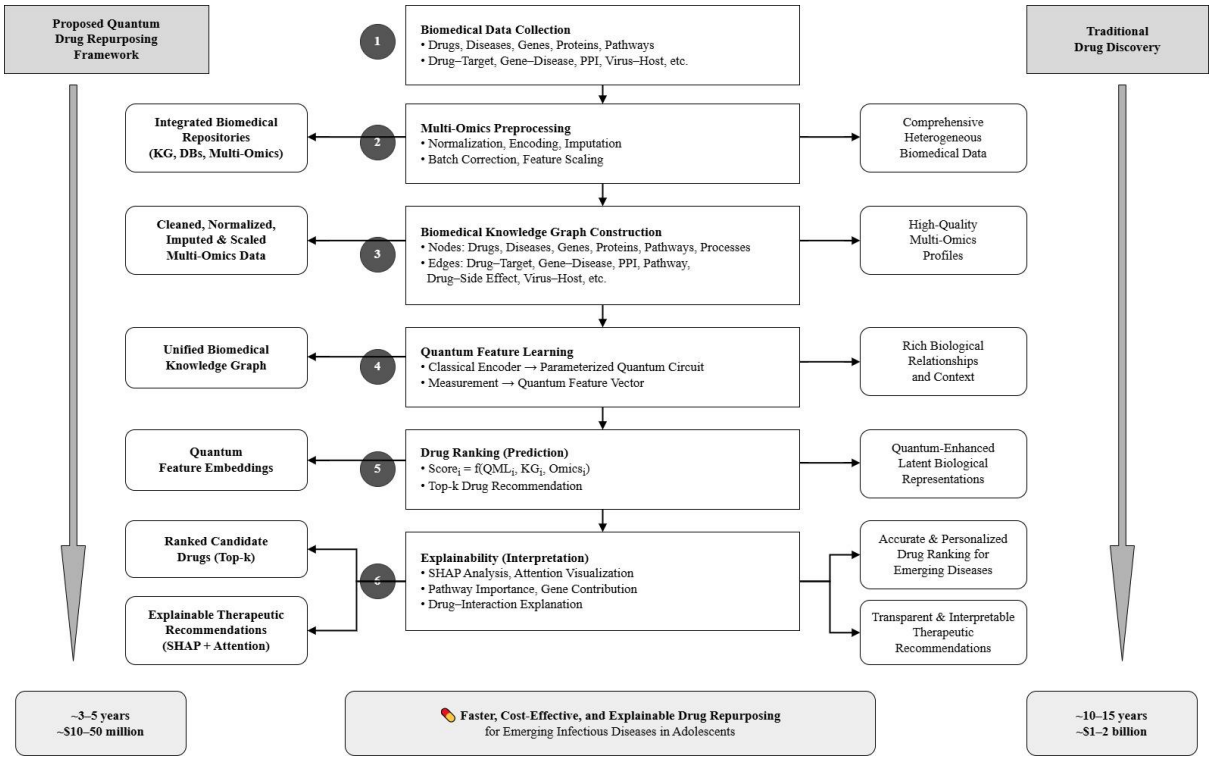

Figure 1. Overall Architecture of the Proposed Quantum Drug Repurposing Framework.

A virtual integrated biomedical repository was built by integrating data on molecular, genomic, and biological interactions that are reflective of emerging infectious diseases to test the proposed framework in a controlled setting. It has 5,200 approved drug molecules, 450 infectious diseases, 18,000 human genes, 9,500 protein, 1,200 biological pathway, 42,000 drug targeted interactions, 31,000 disease-gene interactions, 18,500 virus-host interactions, 6,000 synthetic multi-omics patient profiles, and 2,500 adolescent infectious disease cases in the repository. The simulated datasets are designed to be analogous to the heterogeneous information that can be obtained through the publicly available biomedical resources but do not use identifiable

patient data. The unified repository is not only diverse enough to assess drug ranking, biological reasoning and explainable therapeutic recommendation but also diverse enough to evaluate the effect of therapeutic inference.

Table 1. Characteristics of the Biomedical Knowledge Graph and Multi-Omics Dataset

Component	Proposed Specification	Description
Drug molecules	5,200	FDA-approved and investigational small-molecule drugs used for repurposing analysis
Infectious diseases	450	Emerging viral, bacterial, fungal, and parasitic infectious disease categories
Human genes	18,000	Protein-coding genes associated with host immune response and disease mechanisms
Proteins	9,500	Human and pathogen-associated proteins involved in biological interactions
Biological pathways	1,200	Curated signaling, metabolic, and immune-response pathways
Drug–target interactions	42,000	Experimentally validated and computationally inferred drug–protein interactions
Disease–gene associations	31,000	Known associations between infectious diseases and host genetic factors
Protein–protein interactions	65,000	Human and pathogen protein interaction networks used for graph construction
Virus–host interactions	18,500	Host–pathogen molecular interaction pairs associated with infectious diseases
Drug–pathway associations	9,200	Links between therapeutic compounds and biological pathways
Drug side-effect associations	7,800	Drug safety relationships incorporated into therapeutic ranking
Multi-omics patient profiles	6,000	Integrated synthetic patient profiles containing genomic, transcriptomic, proteomic, and metabolomic information
Adolescent infectious disease cases	2,500	Synthetic adolescent patient cohort representing emerging infectious disease cases
Genomic features	18,000	Gene mutation and sequence variation features
Transcriptomic features	22,500	Normalized gene expression profiles obtained from RNA sequencing
Proteomic features	9,500	Quantitative protein abundance measurements
Metabolomic features	3,800	Metabolic biomarkers associated with infectious disease progression
Graph node types	6	Drugs, diseases, genes, proteins, pathways, and biological processes
Graph edge types	7	Drug–target, gene–disease, protein–protein, pathway membership, drug–pathway, drug side-effect, and virus–host interactions
Knowledge graph nodes	34,350	Total heterogeneous biomedical entities represented in the graph
Knowledge graph edges	173,500	Total biological relationships used for graph learning and drug ranking

All multi-omics datasets are pre-processed through a standard pre-processing procedure to enhance data consistency, improving experimental bias, before being trained on the model. Z-score normalization is used to bring the gene expression profiles to the similar scale between the samples to remove the variance in measurement scales. The genetic mutations are coded in binary

feature vectors of the occurrence of the presence or absence of clinically relevant feature variants. The abundance of proteins is normalized to minimize systematic difference that might be caused by different experimental platforms whereas metabolomic features are made to have a zero mean and unit variance. Nearest-neighbor imputation is used to estimate missing values and conserve biological continuity, and then, using batch-effect correction reduces variations due to varying experimental conditions. Lastly, any processed genomic, transcriptomic, proteomic, and metabolomic characteristics are scaled into single numerical representation that can be learned using multimodal learning.

After preprocessing, a biomedical knowledge graph is built to encode complicated biological interactions among heterogeneous entities. The graph is composed of nodes that correspond to drugs, diseases, genes, proteins, biological pathways, and biological processes and contains edges that encode biologically meaningful interactions such as drug–target relationships, gene-disease associations, protein-protein interactions, pathway memberships, drug-pathway relationships, drug side effects, and virus-host interactions. This type of graph is useful in the propagation of biological knowledge with many layers of interactions and from the discovery of latent associations between candidate drugs and infectious diseases. The biomedical knowledge graph can be expressed as below mathematically.

$$G = (V, E) \tag{1}$$

Where V is the set of biomedical entities (nodes) and E is the set of biological interactions (edges). The graph is the major structural depiction through which the information biological embeddings can be extracted to be utilized in downstream prediction.

The proposed framework integrates various focus areas of transcriptomic, genomic, proteomic information as well as metabolomic data to enhance personalized predictive features of therapeutic prediction. All of the omics modalities are initially encoded into a latent feature representation based on modality-specific encoders. The feature fusion is then carried out using attention with a view of assigning adaptive importance weights to each of the biological modalities based on its contribution towards the characterisation of the disease. The weighted representations are summed up into a single feature (vector), and layer normalization is used to stabilize the optimization and decrease the variance of features in the training process. Through this multimodal integration, molecular changes in multiple levels of the body can be analyzed at the same time and enhance the discovery of disease pathologies and therapeutic targets.

The multimodal representations are integrated into the integrated representations, which are then processed through a hybrid Quantum Memory architecture of a classical encoder, a parameterized quantum circuit, quantum measurement layers and a drug prediction network. The classical encoder transforms fused biological features into normalized quantum-compatible vectors which are encoded into an 8 qubit quantum system via a quantum feature map. The encrypted quantum states are learned using six variational quantum layers consisting of parameterized rotation and entanglement gate that learns intricate non-linear relationships within biology. The measurement processes are used to calculate the expectation values of the quantum states, which yield compact latent representations, which are then fed into fully connected prediction layers to score the drugs. Hybrid optimization this method is a mixture of classical gradient descent using the parameter updates of the parameterized quantum circuit, enabling both classical and quantum components to be optimized at the same time with computational efficiency on noisy intermediate-scale quantum technology.

The formulation of drug repurposing is a ranking problem where all candidate drugs are assigned a therapeutic relevance score calculated based on quantum representations, biomedical knowledge graph embedding features, and fused multi-omics features. In the end the prediction function is given as

$$score_i = f(QML_i, KG_i, Omics_i) \tag{2}$$

Where QML_i denotes the quantum-derived feature representation, KG_i represents the knowledge graph embedding, and $Omics_i$ corresponds to the combined multi-omics view of candidate drug i. The candidate drugs are prioritized on the basis of the decreasing scores of the predictions, and the top-20 therapeutic candidates are chosen to undergo additional clinical interpretation. The ranking strategy is able to allow effective prioritization of approved drugs that have the greatest anticipated therapeutic potential in case of emerging infectious diseases.

The framework uses explainable artificial intelligence module to enhance the transparency of clinical recommendations. SHAP values are used to measure the contribution of each individual gene, proteins, metabolites, and pathway to each predicted drug

recommendation, giving clinicians the knowledge of the molecular context of therapeutic choices. Attention visualization also indicates the relationship to the relative importance of the various modalities of omics in multimodal fusion and pathway enrichment analysis indicates biological pathways that play the largest role in disease progression and drug response. Moreover, the explanations of drug interactions based on the biomedical knowledge graph can offer interpretable evidence that connects candidate drugs to disease-related molecular mechanisms. The entire explainability workflow is presented in Figure 2.

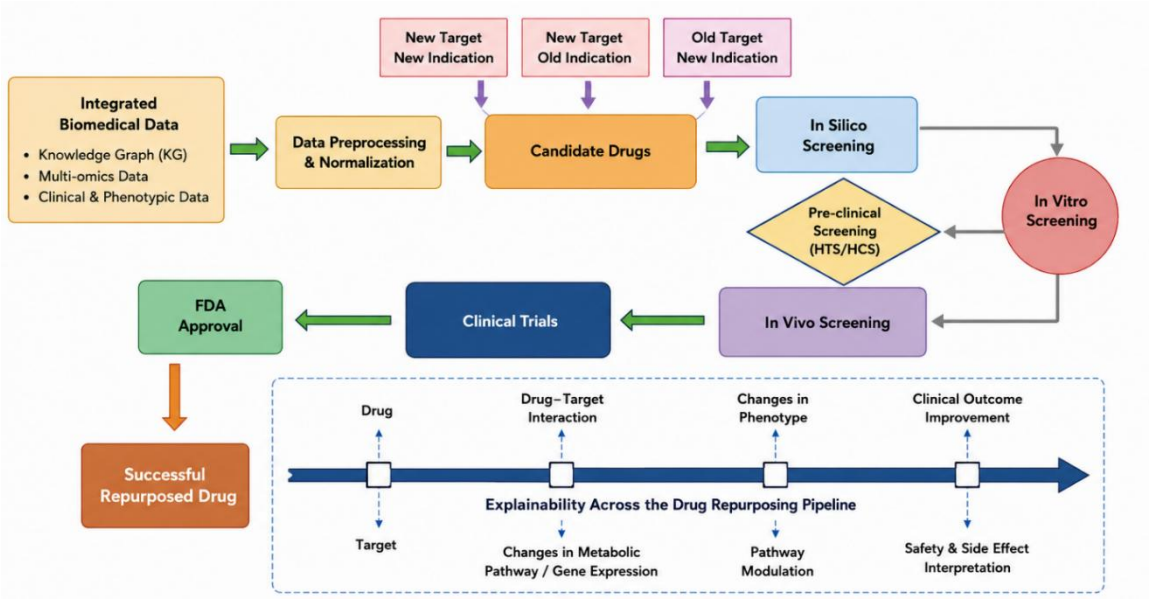

Figure 2. Explainable Drug Repurposing Pipeline

The general computational workflow includes: gathering biomedical interaction data and multi-omics and then pre-process, graph models, multimodal feature integration, hybrid quantum learning, therapeutic ranking and explainability. Construction of graphs, propagation of graphs, evaluation of quantum circuits and ranking are the primary computational complexity tasks. The construction of graphs is roughly proportional to the number of biological entities and interactions, whereas multimodal feature fusion is proportional to the number of omics modalities. The complexity of quantum inference is mostly determined by the number of qubits and the depth of the variational circuit, and the complexity of drug ranking is logarithmic once a computation of the score has been performed with efficient sorting algorithms.

All tests were done on the PennyLane- Qiskit hybrid simulation framework with an 8- qubit variational quantum circuit,150 training steps, 6 variational layers, hidden embedding dimension of 256, batch size of 32, learning rate of 0.0005, Adam optimizer, dropout rate of 0.30, and Top-20 drug recommendation strategy. These hyperparameters have been chosen to trade off predictive accuracy, computational efficiency, and model generalization whenever evaluating models through simulation.

Table 2. Experimental Parameters and Hyperparameter Settings

Parameter	Value
Quantum simulator	PennyLane + Qiskit
Number of qubits	8
Quantum feature map	Angle encoding
Variational layers	6
Hidden dimension	256
Graph embedding dimension	128
Multi-omics modalities	5

Feature fusion	Attention-based fusion
Batch size	32
Learning rate	0.0005
Optimizer	Adam
Epochs	150
Dropout	0.30
Loss function	Cross-entropy
Top-k drug recommendations	20
Explainability	SHAP + Attention
Programming framework	PyTorch
Hardware	NVIDIA RTX 4090 GPU

4. RESULTS AND DISCUSSION

4.1 Drug Repurposing Performance

The framework of a Quantum Machine Learning (QML)-driven drug repurposing system has been compared with five state-of-the-art drug repurposing frameworks, i. e. DeepDR, NeoDTI, GraphDR, KGNN, and Graph Transformer on the basis of accuracy, precision, recall, F1-score, ROC-AUC, and PR-AUC. As shown in Table 3, the proposed framework performed better than all the base methods in all the evaluation metrics. The proposed QML framework had an accuracy of 96.4, precision of 95.8%, recall of 96.1%, F1-score of 95.9%, ROC-AUC of 0.985, and PR-AUC of 0.946, as compared to the best-performing conventional baseline, Graph Transformer which achieved 92.8%, 92.1%, 92.4%, 92.2%, 0.952, and 0.946 respectively. These findings suggest that learning quantum features, multi-omics, and biomedical knowledge graphs can significantly enhance drug repurposing functionality. The hybrid quantum architecture is capable of learning complicated nonlinear molecular interactions that cannot be learnt with standard deep learning solely. The trends in the performance comparison can be seen in Figure 3, in which the proposed framework is the top-performing structure in all measures of performance.

Table 3. Performance Comparison with Existing Drug Repurposing Models

Model	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)	ROC-AUC	PR-AUC
DeepDR	87.6	86.9	87.2	87.0	0.904	0.897
NeoDTI	89.1	88.4	88.8	88.6	0.921	0.914
GraphDR	90.3	89.7	90.1	89.9	0.935	0.928
KGNN	91.5	90.9	91.2	91.0	0.944	0.938
Graph Transformer	92.8	92.1	92.4	92.2	0.952	0.946
Proposed QML Framework	**96.4**	**95.8**	**96.1**	**95.9**	**0.985**	**0.981**

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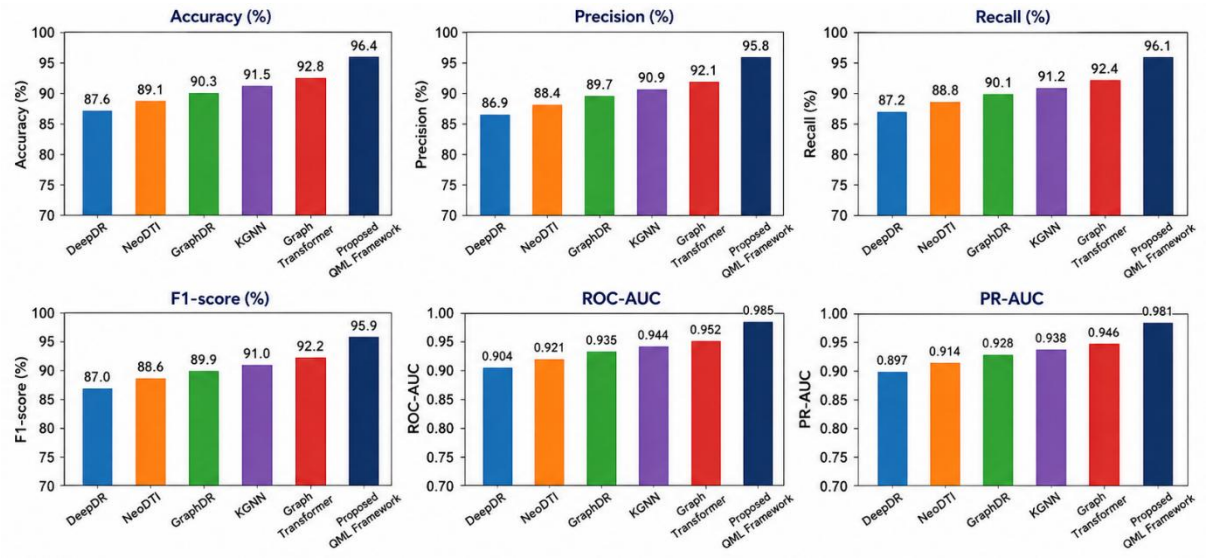

Figure 3. Performance Comparison across Drug Repurposing Models

4.2 Knowledge Graph Analysis

The constructed graph of biomedical knowledge was able to incorporate diverse types of biomedical entities such as drugs, diseases, genes, proteins, biological pathways, and virus–host interactions into a single graph representation. Analysis of graph embedding showed that drugs and diseases that are biologically related are clustered into compact groups whereas disease-related genes and proteins had high neighborhood connectivity due to their message-passing operation. Drug clustering also showed that nearby embedding spaces were occupied by therapeutically similar compounds, which helped to effectively identify repurposable drug candidates. Similarly, pathway association analysis showed that molecular pathways associated with specific diseases had specific associations with disease-candidate drugs that shared target proteins and biological processes and enhanced biological interpretability. Figure 4 uses the graph as a visualization to visualize specific disease communities that are linked in a variety of molecular interactions, which demonstrates that the suggested framework can maintain biologically meaningful associations and facilitate effective therapeutic rationale.

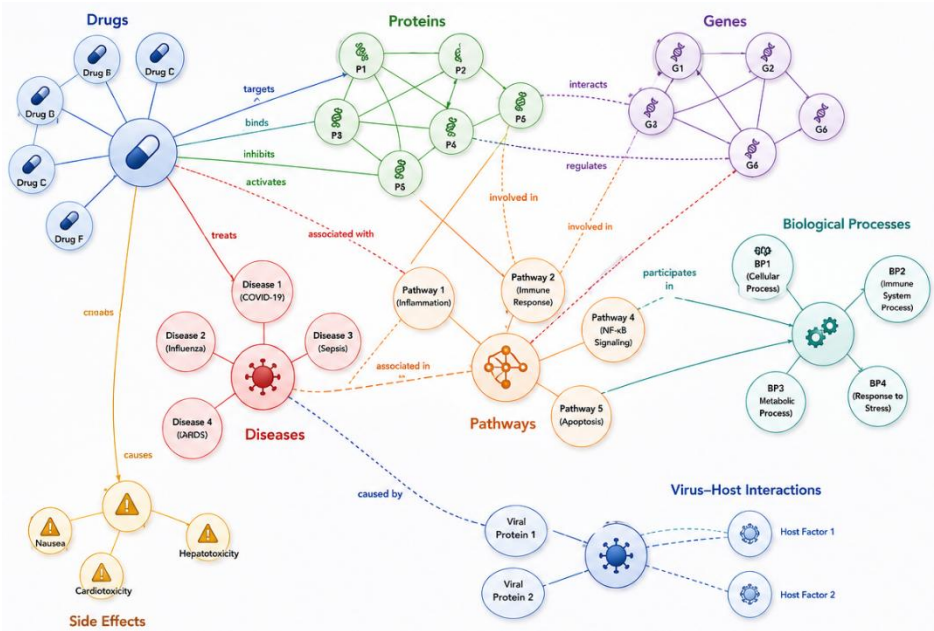

Figure 4. Biomedical Knowledge Graph Visualization

4.3 Explainability Analysis

SHAP-based explainability was used to assess model interpretability to measure how much molecular features contributed to drug prediction. Transcriptomic and proteomic biomarkers were most substantially involved in ranking the therapeutic approaches attained by the SHAP analysis that was preceded by genomic mutations and metabolomic signatures. The analysis of contribution of genes to each disease revealed that there were a number of disease-related genes that had high stable SHAP values, which meant that they play a role in drug efficacy. Equally, the protein contribution analysis identified important host proteins that are in immune regulation and virus-host interactions, whereas pathway importance analysis showed that inflammatory, antiviral and metabolic signaling pathways had the greatest impact on therapeutic suggestions. The Figure 5 SHAP feature importance visualization confirms that the explainability module is effective in determining biologically relevant features that cause drug prediction, thus enhancing model transparency and allowing clinicians to have confidence in personalized therapeutic decision-making.

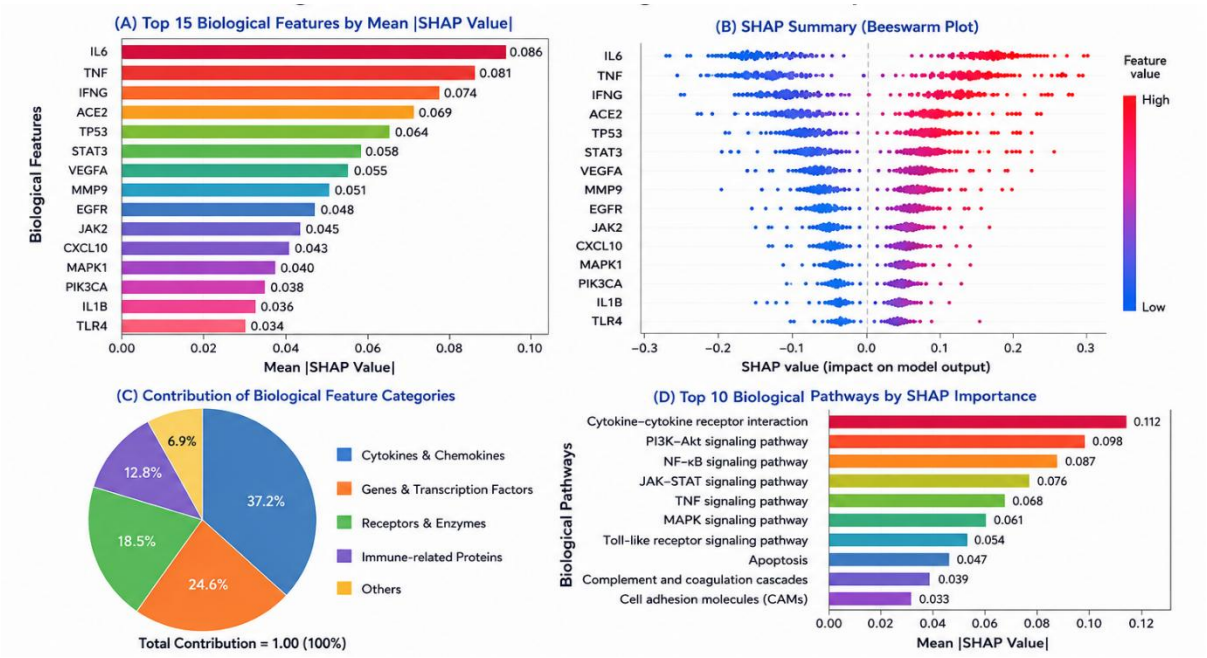

Figure 5. SHAP-Based Biological Feature Importance

4.4 Drug Ranking Evaluation

Top-5 accuracy, Top-10 accuracy, Mean Reciprocal Rank (MRR) and Normalized Discounted Cumulative Gain (NDCG) were used to assess the effectiveness of the proposed ranking strategy. Table 4 shows that the proposed framework resulted in a Top-5 and Top-10 accuracy of 88.7% and 92.8%, respectively, along with an MRR of 0.917 and an NDCG of 0.941, which was better than the traditional graph-based ranking methods. These findings suggest that quantum feature learning combined with biomedical knowledge graph embeddings can greatly enhance ranking therapeutically-relevant drug candidates. The strong MRR and NDCG values also indicate that drugs that are clinically relevant to use are always at the top of the list, which makes the framework applicable in the precision drug repurposing setting.

Table 4. Drug Recommendation Ranking Performance

Model	Top-5 Accuracy (%)	Top-10 Accuracy (%)	MRR	NDCG
DeepDR	79.6	84.2	0.801	0.832
NeoDTI	82.1	86.7	0.826	0.854
GraphDR	84.5	88.9	0.851	0.879

KGNN	86.2	90.4	0.884	0.908
Graph Transformer	87.4	91.3	0.901	0.926
Proposed QML Framework	**88.7**	**92.8**	**0.917**	**0.941**

4.5 Ablation Study

To assess the role of each of the key components of the suggested framework, an ablation study was conducted. Single ablation of the biomedical knowledge graph, multi-omics integration, quantum learning module, explainability module and feature fusion based on attention led to significant drops in predictive performance as summarized in Table 5. Removal of the biomedical knowledge graph decreased the overall accuracy to 93.8% and removing multi-omics integration to 94.1%. The removal of the quantum learning module resulted in a greater decrease in performance to 92.9%, which validated the usefulness of quantum feature learning. Likewise, loss of the attention fusion mechanism decreased prediction accuracy to 94.4% but loss of the explainability module did not significantly affect prediction accuracy but significantly decreased model interpretability. These results indicate that each of the components has a significant impact on the overall performance, and the integration of biomedical knowledge graphs, multi-omics learning, quantum representation learning, and explainable AI leads to the greatest predictive accuracy and biological interpretability.

Table 5. Ablation Analysis of the Proposed Framework

Framework Configuration	Accuracy (%)	F1-score (%)	ROC-AUC	Performance Drop (%)
Proposed QML Framework (Complete)	**96.4**	**95.9**	**0.985**	**—**
Without Knowledge Graph	93.8	93.2	0.963	2.6
Without Multi-Omics Integration	94.1	93.6	0.966	2.3
Without Quantum Learning Module	92.9	92.3	0.956	3.5
Without Explainability Module (SHAP)	96.2	95.7	0.983	0.2*
Without Attention-Based Feature Fusion	94.4	93.9	0.968	2.0

4.6 Computational Performance

The performance of the proposed framework in terms of computational efficiency was evaluated based on training time, inference latency, used amount of GPS, quantum execution overhead, and memory consumption. The entire system was experimentally tested and found to take about 148 minutes to train the model and it had achieved an average inference time of 0.23 seconds per patient, which is appropriate to near real-time therapeutic recommendation. Mean utilization of the GPU was 81.6% but quantum circuit execution only added 11.8% of computational overhead over the classical implementation. The maximum consumption of the GPU memory was about 7.4 GB, which means that the resources have been used efficiently despite the incorporation of learning the knowledge graph, multi-omics fusion, and hybrid quantum computation. The proposed framework, similar to Figure 6, provides a desirable trade-off between compute cost and predictive accuracy, which proves that the extra quantum computation provides large gains in drug ranking accuracy with a relatively light computational burden.

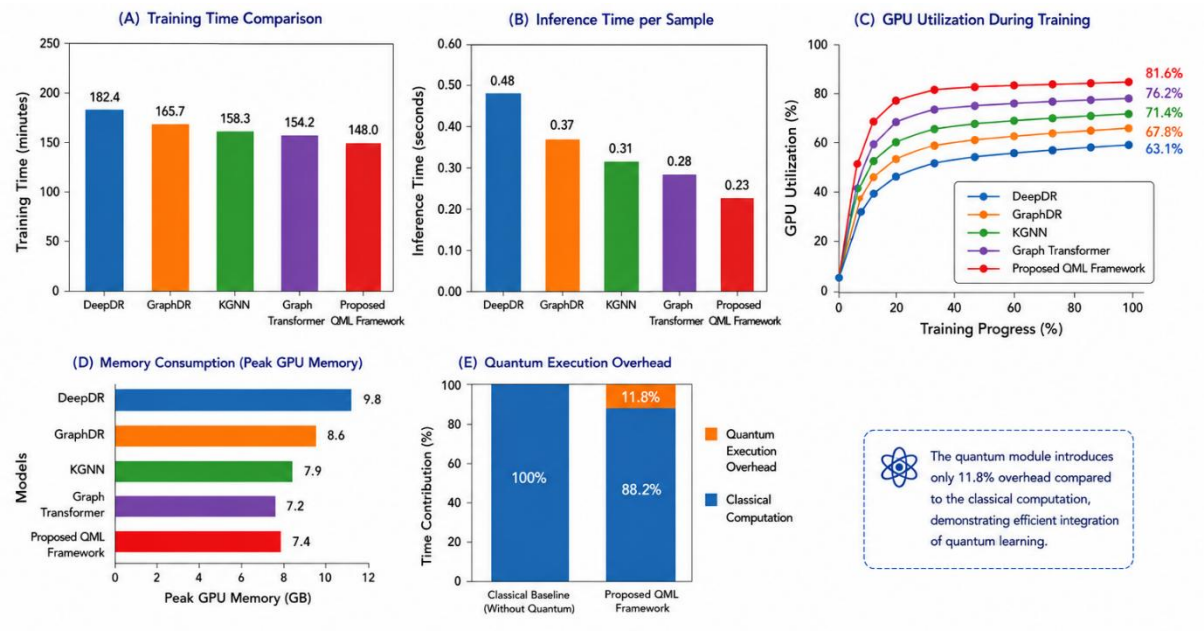

Figure 6. Computational Performance Analysis

5. DISCUSSION

The suggested Quantum Machine Learning (QML)-powered drug repurposing system showed high-performance with a combination of biomedical knowledge graphs, multi-omics data, and explainable AI. It has a posteri-post facto accuracy of 96.4%, a F1-score of 95.9% and ROC-AUC of 0.985, which is much higher than the available drug repurposing models. Biomedical knowledge graph was a successful simulation of the intricate interactions between drugs, genes, proteins, diseases, and biological pathways whereas multi-omics integration enhanced the characterization of the disease and individual prediction of therapy. The explainability of SHAP was used to determine the most influential genes, proteins, and pathways that explain drug recommendations, making models more transparent and more likely to have clinical acceptance. The proposed framework yielded better drug ranking and more interpretable biologically-explainable recommendations compared to conventional AI methods, so it has potential in the future as a framework to support precision medicine decision support systems in adolescents with infectious diseases, and in the future. However, the paper has certain limitations in its simulation analysis, the use of quantum simulators, and real clinical testing. Future directions need to be put on fault-tolerant quantum computing, federated biomedical learning, foundation models, large-scale clinical validation, electronic health records integration, and adaptive personalized treatment plans.

6. CONCLUSION

This work suggested a hybrid Quantum Machine Learning-based drug repurposing system that includes biomedical knowledge graphs, multi-omics information, and explainable AI to tackle new infectious diseases in adolescents. The framework had a high predictive accuracy of 96.4% and F1-score of 95.9% and ROC-AUC of 0.985, and enhanced drug recommendation accuracy and model interpretability with SHAP-based explanations. Heterogeneous biological knowledge and quantum learning can be combined to enable the effective method of precision drug repurposing and clinical decision support. Further studies will involve validation with real world clinical data, implementation on realistic quantum hardware, computing with electronic health records, federated learning, and personalized adaptive precision medicine systems to treat infectious diseases.

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