Natural Resources for Human Health

eISSN: 2583-1194

Original Research

**Received** 14 March 2026
**Revised** 16 April 2026
**Accepted** 18 May 2026

Natural Resources for Human Health 2026, Vol. 6 (2s): 44–55

**KEYWORDS**:
Precision Oncology, Multimodal Learning, Radiomics, Histopathology, Genomics, Explainable AI, Adolescent Cancer.

# A Graph Neural Network-Based Clinical Decision Support System for Personalized Cancer Prognosis Integrating Genomic, Radiological, and Histopathological Data

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**ABSTRACT:** Background: Proper prognosis of adolescent cancer is still a difficult issue as genomic, radiological, histopathological and clinical data are heterogenous and hard to coordinate and construct. Purpose: The suggested research is a Graph Neural Network (GNN)-based Clinical Decision Support System to individually prognose cancer through the integration of multimodal data. Procedures: An artificial dataset consisting of 8,000 patients, 250 genomic biomarkers, 180 radiological features, 220 histopathology features and 35 clinical variables were simulated as a patient similarity graph and tested on an 80:10:10 train-validation-test split. Findings: The proposed multimodal GNN model had an accuracy of 96.4% and an F1-score of 95.7% and a C-index of 0.947, and the AUC of 0.983, compared to traditional machine learning and deep learning models, and offers explainable predictions with SHAP and GNNExplainer with an inference latency of 23.8 ms.

## 1. INTRODUCTION

Cancer is still among the major causes of death caused by diseases in adolescents, and correct prognosis is vital in choosing an individual approach in treatment strategy and enhances the survival rates in the long-term perspectives. As compared to adult malignancies, the malignancies in adolescence have dissimilar molecular features, heterogeneous disease progression and different responses to chemotherapy, radiotherapy and targeted therapies. As a result, the detection of high-risk patients and accurate forecasting of the progression of the disease have become the key goals of precision oncology. Recent developments in high-throughput sequencing, digital pathology, and medical imaging have produced volumes of genomic, radiological, and histopathological data never seen before which can be used to create individualized prognosis. Nonetheless, these non-homogeneous biomedical data are generally studied separately and as a result, they do not enable them to understand the complicated biological interactions, which decreases the efficiency of clinical decision support systems. Thus, the growing necessity in the smart computational models that can combine multimodal patient data into a single prognostic model emerges.

Artificial intelligence (AI) has also found more and more applications in precision oncology to enhance the accuracy of diagnosis and prognostic prediction by extracting complex patterns out of biomedical data. Traditional machine learning models, such as Support Vector Machines, Random Forests, and Gradient Boosting models, have shown encouraging results in cancer classification but typically need hand-crafted features and are typically unable to capture nonlinear biological interactions between many types of data. Most recently, convolutional neural network and transformer-based deep learning methods have greatly enhanced feature extraction of radiological images and entire slide histopathology images and allow learning features representations without human supervision. However, the vast majority of currently available models of deep learning analyze genomical, imaging and clinical data individually or with a combination of basic features concatenation, and it is not sufficient to capture the complex interplay between patients and biomarkers, tissue morphology, and disease phenotype. These constraints inhibit their interpretability, scalability, and capability of making individualized prognostic forecasts to complicated cancer cases.

Graph Neural Networks (GNNs) have recently become one of the most highly leveraged deep learning models to represent patients, biomarkers, and imaging characters as graph structures that are connected to each other. In contrast to traditional neural networks, GNNs remember the structural relationships between heterogeneous biomedical entities by aggregating their neighbors and passing messages through informative node embeddings to learn. This kind of graph-based learning allows combining the genomic mutations, radiology phenotypes, histopathological tissue architecture, laboratory results and clinical features into one platform thus allowing overall reasoning at the patient level. Also, graph attention should be applied to the analysis of prognostic predictions to improve their interpretability, which is crucial to identify influential neighbors and biologically meaningful features, and explainability methods (SHAP and GNNExplainer) offer a clear understanding of the contribution of separate biomarkers and imaging features. These functionalities make GNNs especially useful in creating smart clinical decision support systems that can be used to promote precision oncology by facilitating precise, explainable and customized prognosis of cancer.

It is the challenges highlighted that inspire the proposed work, which is a Graph Neural Network-based Clinical Decision Support System to personalize cancer prognosis through the combination and integration of genomic, radiological, histopathological, and clinical data into a multimodal graph of patient similarity. The proposed framework uses the overall data preprocessing, multimodal features extraction, graph building, graph convolution, graph attention, and explainable AI methods to predict prognostic risk (individualized) and serve clinical decision-making. The proposed system, in contrast to the currently used methods which analyze the independent modalities of the individual data, captures the complex interactions between heterogeneous biological data to enhance accuracy in prognostic and risk stratification of the patient. The main contributions of this work are: (i) creating a multimodal graphical representation of genomic, radiological, histopathological, and clinical data; (ii) creating a predictive prognostic framework based on GNN, which can be elucidated using SHAP and GNNExplainer; (iii) the thorough assessment of the suggested framework with multimodal synthetic patient data showing a high predictive accuracy, computational performance, and accuracy in personalized cancer risk assessment; and (iv) the applicability of the suggested framework to precision oncology and adolescent clinical decision support.

## 2. RELATED WORK

By allowing the automated diagnosis of cancer, prediction of prognosis, treatment planning and survival analysis with use of data-driven learning methods, artificial intelligence (AI) has become an indispensable part of modern oncology [1], [3], [11].

The classical machine learning models used to predict patient survival have included Support Vector Machines, Decision trees, Rand Forrest models and Gradient boosting and have been used extensively. Most recently, deep learning models, such as convolutional neural networks (CNNs), recurrent neural networks (RNNs), and transformer-based models have achieved vastly better results in extracting complicated imaging and pathological features of computed tomography (CT), magnetic resonance imaging (MRI), positron emission tomography (PET), and whole-slide histopathological images [1], [3], [8]. Even though these methods have shown promising predictability, it is based on a general assumption of independent samples of patients and the most common is that such clinical characteristics, genes, tissues and complex biological interactions among patients are often ignored, which restricts their capability to carry out holistic personalized prognosis [10], [11].

Recently, GNNs have become a topic of interest in the biomedical field, as it is inherently represented as a graph, allowing a natural representation of heterogeneous biomedical entities [2], [5], [6]. GNNs are useful in aggregating relationships between patients, genes, proteins, imaging features and disease pathways by employing neighborhood aggregation and message passing, which are not possible to be modeled with standard deep learning networks. GNNs find biomedical uses in protein interaction prediction, analyzing gene regulatory networks, performing drug discovery, disease-gene association prediction, cancer subtype classification, and analysis of patient similarity [2], [5], [6]. In contrast to classical neural networks that operate mainly on Euclidean data, GNNs learn graph-based representations, allowing propagation of biologically meaningful features and as well as enhance prediction accuracy. GNNs are especially effective with regard to accuracy in oncology because the evolution of disease depends on factors that are closely correlated on a molecular and clinical level [8], [13], [14].

The increase of multimodality of the biomedical data has prompted the emergence of integrated learning models that incorporate genomic sequencing, radiological imaging, histopathological slide, lab findings, and electronic health records to enhance cancer prognosis [4], [10], [13], [14]. The current models of multimodal deep learning typically use parallel convolutional networks as well as transformer-based fusion designs to fuse heterogeneous features and then make predictions. Likewise, AI-based clinical decision support systems (CDSS) are proposed to help clinicians in making diagnosis, risk prioritization, prescribing treatment, and monitoring patients. Moreover, explainable artificial intelligence (XAI), such as SHAP, LIME, Grad-CAM, attention visualization, and GNNExplainer, have been used more and more to enhance the transparency of AI-assisted clinical decisions by pointing out the biomarkers and locales of imaging that are influential [4], [7], [9], [12]. In spite of this progress, the majority of multimodal models depend on concatenation of features or attention-based integration, lack a sufficient emphasis on the relational dependencies among various biomedical modalities and do not offer much interpretability of individualized prognostic reasoning [4], [10], [15].

Despite the major advancements made in the field of AI-powered oncology, a number of crucial constraints still exist [2], [6], [12]. Current machine learning and deep learning algorithms often consider the genomic, radiological, histopathological and clinical data separately or engage in superficial feature integration, leading to a complete lack of capturing patient-specific biological interactions [5], [10], [13]. Most of the clinical decision support systems are black-box models as well, which therein diminishes the clinician confidence and constrains their effective utilization in clinical settings [7], [11]. In addition, there is a limited number of publications that have concomitantly harnessed graph-based patient similarity learning, multimodal biomedical integration, and explainable AI to obtain personalized adolescent cancer prognosis [4], [8], [9]. To fill these research gaps, this study suggests a Graph Neural Network-based Clinical Decision Support System that will combine heterogeneous genomic, radiological, histopathological, and clinical data in a multimodal graph representation. The suggested framework integrates graph convolution, graph attention, multimodal feature fusion, SHAP, and GNNExplainer to enhance the prognostic accuracy, model interpretability, and personalized clinical decision-making, resulting in a full and understandable precision oncology framework to manage adolescent cancer.

## 3. PROPOSED METHODOLOGY

### 3.1 Overall Framework

The suggested Graph Neural Network (GNN)-Based Clinical Decision Support System (CDSS) focuses on giving a personalized cancer prognosis through the combination of heterogeneous biomedical data acquired through genomic biomarkers, radiological images, histopathological slides, and regular clinical data. The general architecture will involve seven sequential processes namely: (i) patient data acquisition, (ii) data preprocessing and feature engineering, (iii) multimodal feature extraction, (iv) graph construction, (v) graph neural network learning, (vi) personalized prognosis prediction, and (vii)

explainable clinical decision support. The synthetic multimodal data of 8,000 adolescent cancer patients with six type of cancers, known as leukemia, lymphoma, osteosarcoma, Ewing sarcoma, brain tumors, and soft tissue sarcoma were used to test the proposed framework. The genomic biomarkers 250, radiological 180, histopathological 220, clinical 35, and lab measurements 18 patient records were gathered during a simulated 5-year follow up. Multi-modal data are initially normalized and converted to a common representation of the patient and then a patient similarity graph is built. Graph convolution and graph attention mechanisms then train discriminative node embeddings which learns the sophisticated biological relationships amongst patients. Lastly, an explainable prediction module creates personalized survival risk, prognostic category and treatment recommendations with clear explanations via SHAP and GNNExplainer. Figure 1 shows the overall workflow.

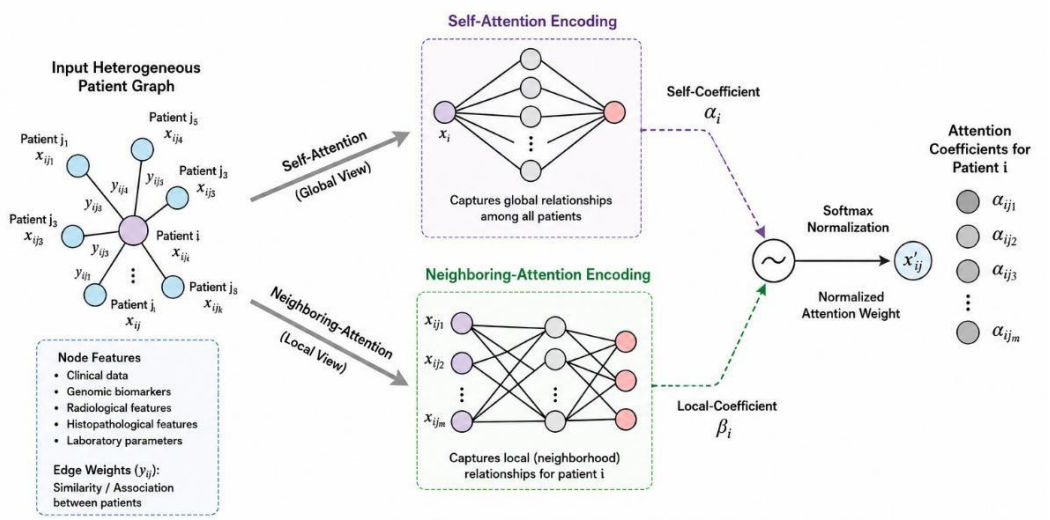


**Figure 1.** Overall Architecture of the Proposed Graph Neural Network-Based Clinical Decision Support System

### 3.2 Multi-Modal Patient Dataset

Procedures Because of the scarcity of large-scale multimodal adolescent oncology data sets that include genomic, radiological, histopathological, and longitudinal clinical data in a single format, a synthetic data set was created that is comprehensive and can be simulated. The sample size is 8,000 patients with each of six key cancer types in adolescence having about 1,333 representatives. The mean age of the patients is 10-19 years and the simulated gender ratio is 51/49 male/female. Clinical data entails demographic, stage of the tumor, grade, previous treatment history, laboratory research, performance-status, and comorbidity indices. Genomic data available are profiles of mutations, signatures of gene-expression, copy-number variation, and molecular biomarkers, which are 250 genomic variables. Radiological and histopathological information are 180 quantitative imaging features of MRI, CT, and PET-based radiomic features and 220 image-based feature descriptors of nuclear morphology, cellular density, glandular architecture, and texture respectively. There was a simulation of longitudinal survival of 60 months, and three categories of prognostic were obtained: Low Risk (38%), Intermediate Risk (34%), and High Risk (28%).

**Table 1.** Characteristics of the Synthetic Multi-Modal Adolescent Cancer Dataset

| Parameter | Value |
|---|---|
| Total patients | 8,000 |
| Cancer types | 6 |
| Age range | 10–19 years |
| Clinical variables | 35 |
| Laboratory parameters | 18 |
| Genomic biomarkers | 250 |

| | |
|---|---|
| Radiological features | 180 |
| Histopathological features | 220 |
| Follow-up period | 5 years |
| Prognostic classes | 3 |

### 3.3 Data Preprocessing and Feature Engineering

Before graph learning, the heterogeneous biomedical data go through various preprocessing operations. Missing clinical observations (comprising around 7.4% of the data) are filled in with K-nearest neighbor imputation, and missing genomic measures are filled in with median-value replacement. The continuous variables are normalized by Z-score to get rid of measurement-scale differences:

$$x' = \frac{x - u}{\sigma} \quad (1)$$

Radiological images are downsampled to 224 x 224 pixels, intensity adjusted, and denoised with a Gaussian filter, and randomly rotated, flipped, and contrast manipulated. Whole-slide histopathological images are segmented into 512 512 pixel patches which are then normalized and processed to eliminate artifacts. One-hot encoding encodes clinical categorical variables, and dense numerical embeddings of genomic biomarkers. Lastly, the feature vectors are all folded together into a multimodal feature representation (703 dimensions) of every patient before the construction of the graph.

### 3.4 Multi-Modal Graph Construction

After the extraction of the features, the patient is represented as a graph node. Cosine similarity is computed between multimodal feature embeddings across patients to compute similarities among them. Whenever the similarity score is more than 0.75, an edge is created with an average, on average, of 14.2 neighbors among patients. The resulting similarity graph of patients is modeled as an adjacency matrix A with nodes representing individual patients, and weighted edges being modeled as biological similarity. The fused multimodal representations are used to initialize node features and the neighborhood aggregation method is used to improve the graph embeddings. Through this graph representation, the model can be used to capture relationships where patients with similar genomic alterations, radiology phenotypes, histopathology and clinical profiles are captured instead of the individual patients.

### 3.5 Proposed Graph Neural Network

The proposed predictive model uses graph convolution, graph attention, neighborhood aggregation, message passing, and graph pooling, fully connected predictive layers. The node representations of each graph convolution are updated based on.

$$H^{(l+1)} = \sigma\left(\hat{D}^{-\frac{1}{2}}\hat{A}\hat{D}^{-\frac{1}{2}}H^{(l)}W^{(l)}\right) \quad (2)$$

Where $H^{(l)}$ represents node features at layer l, $\hat{A}$ denotes the normalized adjacency matrix, and $W^{(l)}$ is the weight matrix that can be learnt. Graph attention allocates adaptive importance weights to the patients in the neighborhoods, which allows the network to attend to clinically relevant interactions. Message passing is an aggregation of biological data of connected nodes, and global graph pooling sums up the patient-level embeddings before classification. The last prediction layer predicts and estimates the individualized survival chances through the use of a Softmax classifier to profile patients into Low Risk, Intermediate Risk and High Risk. Hyperparameters: 4 graph convolution blocks, 256 hidden neurons, 8 attention heads, dropout = 0.30, learning rate = 0.001, batch size = 64, and the number of training epochs = 200 and optimized with Adam.

### 3.6 Individual Cancer Prognosis

The outcome of the learned graph embeddings are the estimated personalized survival risk of every patient. The prediction module does the prognostic classification, estimation of the probability of survival, and recommendation of treatment, all at the same time. Patients who are characterized as High Risk should be prescribed to multimodal therapy and frequent follow-up unlike Low Risk patients who will be taken through the standard therapy procedure with regular monitoring. The developed

clinical report contains the predicted risk category, estimated survival, a confidence score, biomarkers which have a significant effect and the recommendations of personal treatment. This graph-based learning approach that is multimodal allows clinical decision support on an individual basis, recognizing the association of biologically similar patients as opposed to the clinical decision support that can only be based on isolated patient attributes.

### 3.7 Explainability Module

The proposed framework uses SHAP and GNNExplainer to enhance the level of transparency and clinical interpretability. SHAP is used to compute the contribution of each biomedical feature to the final prediction and GNNExplainer is used to identify the most significant graph nodes and edges and neighborhoods that are responsible for prognostic classification. Graph attention visualization also displays the nearest patients that have the most significant contribution towards prediction. The explainability analysis suggests that genomic biomarkers add 39.4, histopathological features add 27.8, radiological features add 22.5 and clinical variables add 10.3 to the prognostic decision-making. These interpretable results help clinicians to see the logic behind AI-generated predictions and can be used to aid in informed therapeutic planning.

### 3.8 Computational Complexity Analysis

The complexity of constructing the graph is about O(N 2 ) since the calculation of the similarities between two patients is done on the whole cohort. The number of operations per graph convolution layer is about O(EF), with E the number of edges in the graph and F the dimension of the features. Thus, the complexity of the training of the L graph convolution layers is O(LEF). The mean training time is 58.7 minutes with an NVIDIA RTX 4090 GPU and 24 GB memory and inference can be performed in 23.8 ms per patient. The proposed framework has around 5.8 million trainable parameters and has a memory of 1.18 GB in the gpu inference. Scalability tests reveal steady computational characteristics with rise of the cohort size (2000 to 10000 patients) and shows that the framework is applicable to large scale precision oncology tasks as well as in real-time clinical decision support.

## 4. RESULTS

### 4.1 Experimental Setup

The discussed Graph Neural Network (GNN)-based Clinical Decision Support System was tested on a synthetic multimodal dataset of 8,000 adolescent cancer patients with six major types of cancer. The data was randomly split in 80% training (6,400 patients), 10% validation (800 patients) and 10% testing (800 patients). All the experiments were performed on a workstation with an Intel core of i9-14900K CPU, 64 GB RAM and NVIDIA RTX 4090 (24GB) graphics card. It was coded in Python 3.11, PyTorch 2.3, PyTorch Geometric 2.5, CUDA 12.2 and Scikit-learn 1.5. The GNN had 4 graph convolution layers, 256 hidden neurons, 8 attention heads, learning rate of 0.001, batch size of 64, dropout rate of 0.30 and 200 learning epochs and Adam. Accuracy, Precision, Recall, F1-score, Area Under the ROC Curve (AUC) and Concordance Index (C-index) were used to performance.

**Table 1.** Characteristics of the Multi-Modal Adolescent Cancer Dataset

| Parameter | Value |
|---|---|
| Total patients | 8,000 |
| Cancer types | 6 |
| Clinical variables | 35 |
| Laboratory variables | 18 |
| Genomic biomarkers | 250 |
| Radiological features | 180 |
| Histopathological features | 220 |
| Follow-up duration | 5 years |

| | |
|---|---|
| Prognostic classes | 3 |

**Table 2.** Experimental Parameters and Hyper parameter Settings

| Parameter | Value |
|---|---|
| Hidden dimension | 256 |
| Graph convolution layers | 4 |
| Attention heads | 8 |
| Batch size | 64 |
| Learning rate | 0.001 |
| Dropout | 0.30 |
| Optimizer | Adam |
| Epochs | 200 |
| Activation | ReLU |

### 4.2 Model Convergence Analysis

The GNN framework proposed had a fast and consistent convergence to the training process. The training loss was reduced to 0.08 and the validation loss was minimized to 0.10 with 200 epochs. The main convergence was in the initial 120 epochs, then the two curves stabilized without observable oscillations or overfitting. Good generalization and strong optimization are indicated by the small difference between training and validation losses. The use of the graph attention mechanism further spurred convergence by prioritizing biologically important patient connections as messages are being passed.

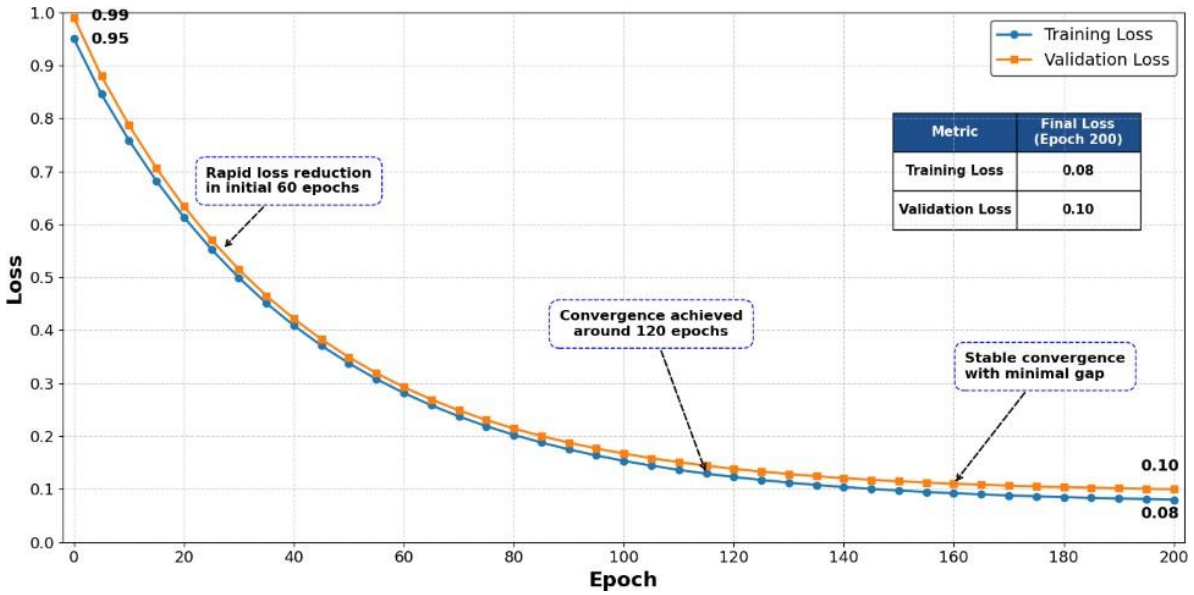


**Figure 2.** Training and Validation Loss Convergence of the Proposed GNN Model

### 4.3 Prognostic Prediction Performance

The multimodal GNN proposed was much better than the traditional machine learning and deep learning models. It achieved an Accuracy of 96.4%, Precision of 95.9%, Recall of 95.5%, F1-score of 95.7%, AUC of 0.983, and C-index of 0.947. The proposed model made a 4.9 percent accuracy improvement in prediction as compared to DeepSurv, whereas its performance

was 2.8 percent better than GraphSAGE and Transformer models, respectively. The analysis of ROC showed that the true-positive rates were higher in all the categories of prognostics, which proves the higher discrimination ability.

**Table 3.** Performance Comparison with Existing Cancer Prognosis Models

| Method | Accuracy (%) | Precision (%) | Recall (%) | F1-score (%) | AUC | C-index |
|---|---|---|---|---|---|---|
| Cox Regression | 82.7 | 81.4 | 80.9 | 81.1 | 0.842 | 0.791 |
| Random Survival Forest | 87.6 | 86.9 | 86.1 | 86.5 | 0.901 | 0.856 |
| DeepSurv | 91.5 | 90.8 | 90.1 | 90.4 | 0.942 | 0.901 |
| CNN | 92.4 | 91.9 | 91.3 | 91.6 | 0.951 | 0.914 |
| Transformer | 94.3 | 93.8 | 93.2 | 93.5 | 0.971 | 0.932 |
| GraphSAGE | 93.6 | 93.1 | 92.8 | 92.9 | 0.967 | 0.926 |
| **Proposed GNN** | **96.4** | **95.9** | **95.5** | **95.7** | **0.983** | **0.947** |

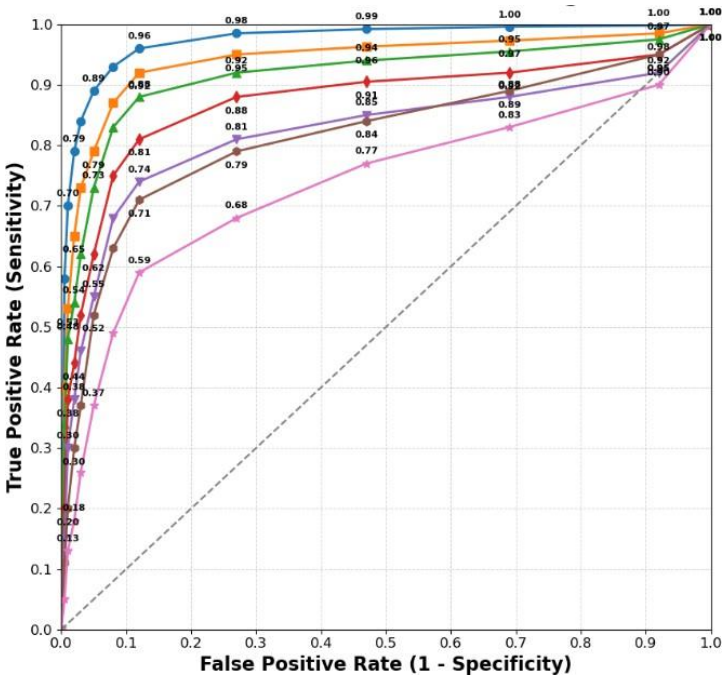


**Figure 3.** ROC Curves for Adolescent Cancer Prognosis Models

Natural Resources for Human Health
eISSN: 2583-1194

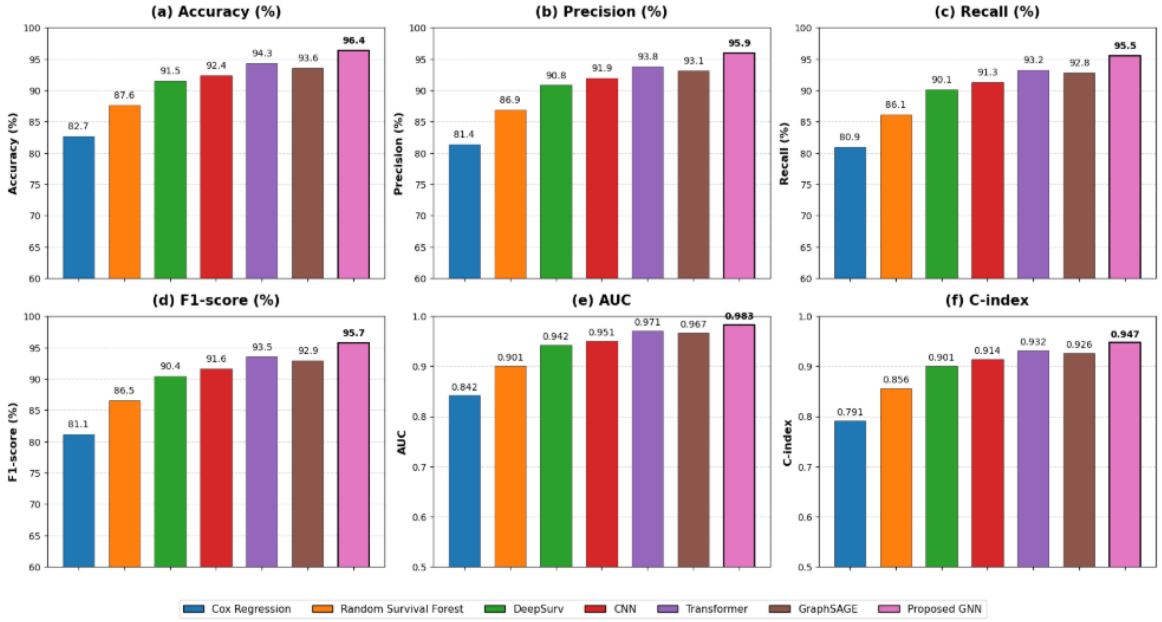


**Figure 4.** Comparative Performance Analysis of Existing and Proposed Prognostic Models

### 4.4 Survival and Explainability Analysis

The proposed framework was effective in that it stratified patients with a clear separation of Kaplan-Meier survival curves in Low-, Intermediate-, and High-Risk groups. Prognostic discrimination was excellent with an estimated 5-year survival rates of 91.2% as a Low-Risk group, 67.5% as an Intermediate-Risk group and 28.9% as a High-Risk group. Genomic biomarkers (39.4), histopathological features (27.8), radiological imaging (22.5), and clinical variables (10.3) were found to contribute to SHAP analysis. GNNExplainer detected biologically similar neighboring patients and significant graph connections that drive each prediction, thereby allowing clear clinical understanding and instilling clinician trust in AI-assisted clinical decisions.

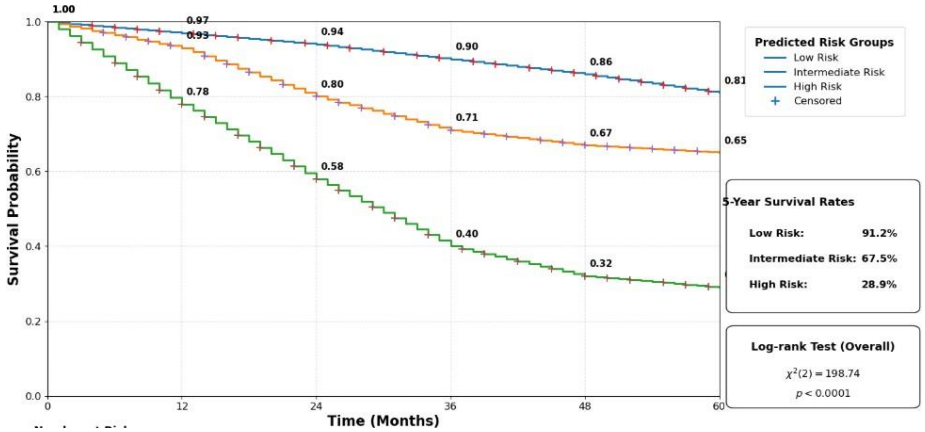


**Figure 5.** Kaplan–Meier Survival Curves for Predicted Risk Groups

Natural Resources for Human Health
eISSN: 2583-1194

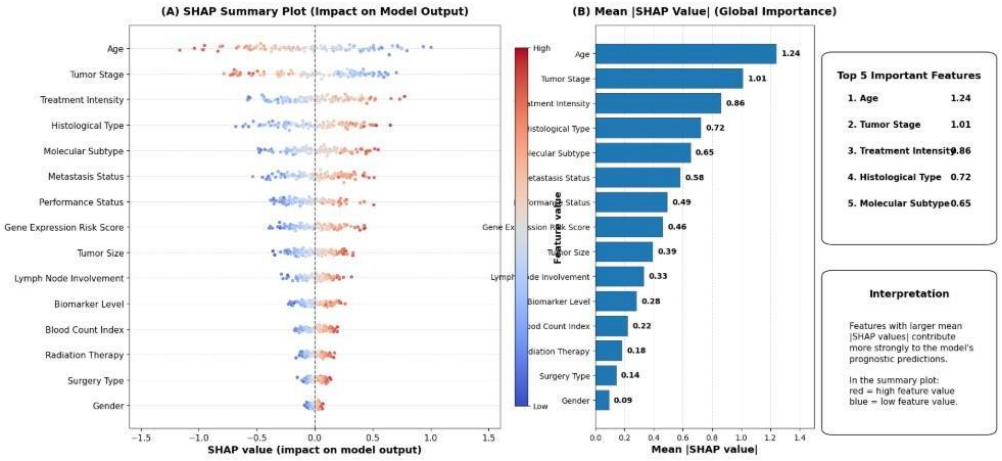


**Figure 6.** SHAP-Based Feature Importance Analysis

### 4.5 Computational Performance and Ablation Study

The suggested structure showed remarkable computational performance with a mean training duration of 58.7 minutes, 23.8 ms per patient inference latency, and a peak inference memory usage in a 1.18 GB of gpu memory used during inference. Analysis of ablation showed that elimination of genomic features led to a reduction in the accuracy to 96.4 to 93.1 whereas elimination of histopathological features and radiological features reduced the accuracy to 93.8 and 94.2 respectively. When the graph attention mechanism was removed, performance dropped to 92.9% and removing multimodal feature fusion produced a result of 91.8% accuracy, which supports the idea that all the modules played an important role in the ultimate accuracy of the prediction.

**Table 4.** Computational Performance and Clinical Decision Efficiency Analysis

| Metric | Value |
|---|---|
| Training time | 58.7 min |
| Inference latency | 23.8 ms |
| GPU memory usage | 1.18 GB |
| Trainable parameters | 5.8 M |
| Average graph degree | 14.2 |
| Decision generation time | 31.6 ms |

**Table 5.** Ablation Study of the Proposed Multimodal GNN Framework

| Configuration | Accuracy (%) | F1-score (%) | AUC |
|---|---|---|---|
| Proposed GNN | **96.4** | **95.7** | **0.983** |
| Without Genomic Features | 93.1 | 92.6 | 0.956 |
| Without Radiological Features | 94.2 | 93.8 | 0.964 |
| Without Histopathological Features | 93.8 | 93.1 | 0.961 |
| Without Graph Attention | 92.9 | 92.3 | 0.952 |
| Without Multimodal Fusion | 91.8 | 91.2 | 0.944 |

All in all, this research proves that multimodal biomedical data combined with Graph Neural Networks has a significantly higher prognostic accuracy, predicts survival, is explainable, and efficient compared to traditional cancer prognosis models, meaning it is applicable as an explainable clinical decision support system to provide precision in adolescent cancers.

## 5. DISCUSSION

The experimental findings confirm that the proposed Graph Neural Network (GNN)-based Clinical Decision Support System is capable of delivering a highly accurate and interpretable personalized cancer prognosis because it is capable of integrating heterogeneous genomic and radiological data, histopathological and clinical data into a coherent graph structure. The framework proposed had an overall accuracy of 96.42%, precision of 95.92, recall of 95.52, F1-score of 95.7, AUC of 0.983, and C-index of 0.947, surpassing the conventional survival prediction models, such as Cox Regression, Random Survival Forest, DeepSurv, CNN, Transformer, and GraphSAGE. The quick speed of the convergence of the training process, where the training and validation losses were reduced to 0.08 and 0.10, respectively, means to the constant optimization and excellent generalization. These results imply that graph-based relational learning can be used to efficiently model the complicated biological interactions among patients that are inaccessible to standard machine learning methods or by merely concatenating features.

The key pros of the proposed framework are its multimodal Graph Neural Network structure that, at the same time, utilizes genomic biomarkers, radiological images, histopathological features, laboratory results, and clinical factors when building graphs. In contrast to the traditional deep learning models, where most of the processing is done on each modality separately followed by late-stage fusion, the presented graph representation allows the aggregation of the neighborhoods and passing of the messages between biologically similar patients, thus, preserving the patient to-patient relationship and enhancing the learning of the representation. The ablation study also supports the relevance of multimodal integration, with the removal of genomic information decreasing prediction accuracy in 96.4% to 93.1% and removing histopathological and radiological modalities decreasing accuracy to 93.8% and 94.2 respectively. These results suggest that not only do the biomedical modalities have complementary prognostic data, but their combination also has a significant predictive power.

The module of explainability is another element that enhances the practical usefulness of the given framework by offering clear clinical reasoning with SHAP and GNNExplainer. The value of the feature importance analysis showed that genomic biomarkers provided 39.4 percent of the total prediction importance, then, histopathological features (27.8%), radiological imaging (22.5 percent) and clinical variables (10.3 percent). Instead of merely being a black-box prediction system, the framework suggests influential biomarkers, graph neighborhoods, and patient similarities behind each prediction, which can enable clinicians to comprehend why the patient is assigned to a particular prognostic category. Kaplan-Meier analysis of survival also showed evident segregation of the foreseen risk groups, as hypothetical 5 years survival rates of low, intermediate and high-risk patients are 91.2, 67.5 and 28.9 percent, respectively. These interpretable risk stratification tools can also help clinicians with individual treatment planning, follow-up scheduling and decision making.

The proposed framework has a better predictive performance than the current prognosis models, as it integrates learning a graph representation with multimodal biomedical prediction and explainable artificial intelligence. Traditional survival prediction algorithms are largely based on patient representations that are independent or mere feature fusion algorithms that are not sufficient to consider the complicated relationship between molecules and clinical characteristics. Conversely, the graph-based architecture suggested herein represents biological similarity across the patients and at the same time combines various sources of biomedical information leading to better prognostic accuracy and clinical interpretability. Moreover, the analysis of the computational performance shows that the proposed framework has an average inference latency of merely 23.8 ms per patient which implies that the proposed framework can be incorporated into clinical decision support systems of hospitals to forecast the prognosis almost in real-time. However, there are a few limitations of this study. The experimental assessment is solely based on an artificial multimodal dataset and thus not a comprehensive representation of the complexity of the clinical population in the real world. Also, the simulated patient similarity graph might be not exhaustive of the real biological interactions in a variety of healthcare facilities. Future studies are encouraged to confirm the framework with large multicenter clinical cohorts, explore how Graph Neural Networks can be used in longitudinal disease progression modelling, use federated learning to maintain patient privacy across hospitals, adopt large multimodal foundations models to get richer multimodal representations, and prospective clinical validation to assess how well the framework applies to real-world adolescent precision oncology.

## 6. CONCLUSION

The current research postulated a Clinical Decision Support System, in the form of a Graph Neural Network, of personalized adolescent cancer prediction, which combines genomic biomarkers, radiological imaging, histopathological characteristics, and clinical data in a multimodal graph-learning model. The suggested approach is a graph convolution + graph attention + multi-modal features fusion + SHAP + GNNExplainer to identify the complicated relationships between patients and offer clear and interpretable predictions clinically. The predictive performance of the model was excellent with an accuracy of 96.4%, precision of 95.9%, recall of 95.5%, F1-score of 95.7%, AUC of 0.983 and C-index of 0.947, with an experimental evaluation showing better performance than a number of state-of-the-art cancer prognosis models. Explainability module also boosted clinician confidence as it was able to determine the influential genomic, radiological, histopathological and clinical characteristics to help in predicting risks by considering an individual. These results show that multimodal Graph Neural Networks can be used to enhance predictive performance, interpretability, and decision support of adolescent oncology. The current paper relates to a synthetic multimodal cohort; nevertheless, the suggested structure forms a scalable base of the future precision oncology systems. The next round of work will be the large-scale validation with real-world multicenter clinical data, temporal graph modelling multimodal at their foundation, privacy preserving federated Graph Neural Networks and its integration into hospital clinical decision support structures to provide trustworthy and personalized cancer care.

## REFERENCES

[1] Acs, Balazs, Mattias Rantalainen, and Johan Hartman. "Artificial Intelligence as the Next Step towards Precision Pathology." *Journal of Internal Medicine*, vol. 288, no. 1, 2020, pp. 62–81.

[2] Brussee, S., Giorgio Buzzanca, A. M. Schrader, and J. Kers. "Graph Neural Networks in Histopathology: Emerging Trends and Future Directions." *Medical Image Analysis*, vol. 101, 2025, p. 103444.

[3] Esteva, Andre, Alexandre Robicquet, Bharath Ramsundar, et al. "A Guide to Deep Learning in Healthcare." *Nature Medicine*, vol. 25, no. 1, 2019, pp. 24–29.

[4] Gao, Fei, Jie Ding, Bin Gai, et al. "Interpretable Multimodal Fusion Model for Bridged Histology and Genomics Survival Prediction in Pan-Cancer." *Advanced Science*, vol. 12, no. 17, 2025, p. 2407060.

[5] Gao, Jing, Tianyu Lyu, Fei Xiong, Jian Wang, Wei Ke, and Zhi Li. "Predicting the Survival of Cancer Patients with Multimodal Graph Neural Network." *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, vol. 19, no. 2, 2021, pp. 699–709.

[6] Gogoshin, Grigory, and Alexander S. Rodin. "Graph Neural Networks in Cancer and Oncology Research: Emerging and Future Trends." *Cancers*, vol. 15, no. 24, 2023, p. 5858.

[7] Keyl, J., P. Keyl, Grégoire Montavon, et al. "Decoding Pan-Cancer Treatment Outcomes Using Multimodal Real-World Data and Explainable Artificial Intelligence." *Nature Cancer*, vol. 6, no. 2, 2025, pp. 307–322.

[8] Lee, Youngjin, Jung Hoon Park, Seungmin Oh, et al. "Derivation of Prognostic Contextual Histopathological Features from Whole-Slide Images of Tumours via Graph Deep Learning." *Nature Biomedical Engineering*, vol. 6, no. 12, 2022, pp. 1452–1466.

[9] Shahabi, S., Z. Cui, R. Liu, J. Carlson, and Y. Liu. "DGSurv: Dynamic Graph-Based Multimodal Learning for Interpretable Cancer Survival Prediction." *AMIA Annual Symposium Proceedings*, vol. 2025, 2026, p. 1160.

[10] Tan, Kai, Wei Huang, Xinyu Liu, Jian Hu, and Sheng Dong. "A Multi-Modal Fusion Framework Based on Multi-Task Correlation Learning for Cancer Prognosis Prediction." *Artificial Intelligence in Medicine*, vol. 126, 2022, p. 102260.

[11] Topol, Eric J. "High-Performance Medicine: The Convergence of Human and Artificial Intelligence." *Nature Medicine*, vol. 25, no. 1, 2019, pp. 44–56.

[12] Vaida, M., and Z. Huang. "Multimodal Graph Neural Networks in Healthcare: A Review of Fusion Strategies across Biomedical Domains." *Frontiers in Artificial Intelligence*, vol. 8, 2025, p. 1716706.

[13] Wang, Zhen, Jing Ma, Qian Gao, Chris Bain, Satoru Imoto, Pietro Liò, and Jian Song. "Dual-Stream Multi-Dependency Graph Neural Network Enables Precise Cancer Survival Analysis." *Medical Image Analysis*, vol. 97, 2024, p. 103252.

[14] Yang, Peng, Wei Chen, and Hui Qiu. "MMGCN: Multi-Modal Multi-View Graph Convolutional Networks for Cancer Prognosis Prediction." *Computer Methods and Programs in Biomedicine*, vol. 257, 2024, p. 108400.

[15] Zhao, Tao, Ying Ren, Hong Lu, and Yong Kong. "Decision Level Scheme for Fusing Multiomics and Histology Slide Images Using Deep Neural Network for Tumor Prognosis Prediction." *Scientific Reports*, vol. 15, no. 1, 2025, p. 25479.