RESEARCH PAPER

A Cross-Modal Attention Framework for Robust Cancer Detection

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Received: 2nd Mar, 2026 | **Revised:** 14th Mar, 2026 | **Accepted:** 4th Apr, 2026 | **Available Online:** 20th Apr, 2026

ABSTRACT

Accurate and timely cancer diagnosis remains one of the foremost challenges confronting contemporary clinical oncology. Conventional single-modality diagnostic strategies—whether based on radiology, histopathology, or genomic sequencing—yield valuable but necessarily partial perspectives, frequently producing incomplete or contradictory clinical interpretations. The present study proposes IntelliOnco, an interpretable cross-modal attention-based deep learning framework designed to unify heterogeneous clinical data streams—encompassing radiological volumetric scans, whole-slide histopathology images, high-dimensional genomic profiles, and structured electronic health records—into a coherent, patient-level diagnostic representation. Each data modality is independently encoded through a dedicated deep network: three-dimensional convolutional neural networks (3D CNNs) for volumetric imaging, Vision Transformers (ViTs) for histopathological analysis, transformer-based sequence models following the Genomic BERT paradigm for molecular data, and multilayer perceptrons (MLPs) for tabular clinical variables. The resulting latent embeddings are subsequently fused through a cross-modal attention mechanism that adaptively learns inter-modality relevance scores and remains functionally robust under missing-data conditions via structured modality dropout. Attention weight distributions serve a dual purpose, both improving predictive fusion and supplying an intrinsic explainability signal that quantifies each modality's contribution to the final diagnostic decision. Experimental evaluation on established multimodal oncology benchmarks—including The Cancer Genome Atlas (TCGA) and The Cancer Imaging Archive (TCIA)—demonstrates that the proposed framework achieves a classification accuracy of 94.8%, an F1-score of 0.94, and an AUC-ROC of 0.97, outperforming all unimodal baselines and contemporary fusion models. A complementary Clinical Decision Support Dashboard surfaces interpretable insights through gradient-weighted saliency maps, per-modality importance distributions, and key genomic indicator rankings, thereby bridging algorithmic inference with clinical reasoning. These results collectively substantiate the capacity of interpretable multimodal artificial intelligence to elevate diagnostic precision, mitigate clinical uncertainty, and accelerate the translation of data-driven oncology into everyday practice.

Keywords: Multimodal Deep Learning, Cancer Detection, Cross-Modal Attention, Explainable Artificial Intelligence, Medical Imaging, Genomics Integration, Clinical Decision Support, Vision Transformers, Robustness to Missing Modalities.

How to cite this article: Saleha I, Kelwade K. A Cross-Modal Attention Framework for Robust Cancer Detection. Int J Drug Deliv Technol. 2026;16(33s):505-512. DOI: 10.25258/ijddt.16.33s.61

Source of support: Nil.

Conflict of interest: The authors declare no conflict of interest.

I. INTRODUCTION

Cancer Cancer continues to rank among the most devastating causes of global morbidity and mortality, claiming an estimated ten million lives per year according to World Health Organization surveillance data. While clinical oncology has advanced substantially through innovations in medical imaging, next-generation sequencing, and computational pathology, the foundational challenge of achieving early, accurate, and actionable diagnosis remains incompletely resolved. Standard diagnostic workflows depend heavily on individual data sources analyzed in isolation: a radiologist interprets a computed-tomography (CT) or magnetic-resonance imaging (MRI) volume; a pathologist evaluates a stained tissue slide; a molecular biologist characterises somatic mutations in a genomic profile. Although each modality contributes genuine diagnostic value, the siloed paradigm forfeits the complementary relationships that

exist across modalities and therefore constrains overall prognostic precision.

Deep learning (DL) has profoundly reshaped the landscape of AI-driven medical diagnostics, enabling expert-level performance on individual tasks such as tumour classification, lesion segmentation, and mutational-signature prediction. Nevertheless, most published DL models are inherently unimodal, and their inability to synthesise the full breadth of heterogeneous patient data limits their clinical utility. This limitation motivates the growing field of multimodal deep learning in oncology, wherein diverse data sources are computationally integrated to construct a richer, more complete representation of each patient's disease state.

The principal obstacles to effective multimodal integration stem from the extreme heterogeneity of medical data types—high-dimensional volumetric images differ fundamentally from gigapixel tissue slides, categorical genomic sequences, and sparse tabular clinical records—and from the pervasive incompleteness of real-world clinical datasets in which not every patient has undergone every diagnostic test. Existing fusion paradigms (early fusion, late fusion) address these challenges inadequately, often incurring information loss or brittle performance under missing-data conditions. Furthermore, regulatory and clinical acceptance of AI-assisted diagnostics demands transparent, interpretable decision processes rather than opaque black-box outputs.

To address these challenges, this article presents IntelliOnco, a novel interpretable cross-modal attention framework that performs intermediate feature-level fusion of four clinical modalities. Dedicated encoder networks extract domain-specific latent representations, which are subsequently merged through an adaptive cross-modal attention module. The resulting fused embedding is fed to a classification head that produces calibrated diagnostic probabilities, while the associated attention weights are surfaced through a Clinical Decision Support Dashboard as clinically interpretable explanations. The block diagram presented in Figure 1 below illustrates the end-to-end architecture.

System Architecture Overview

The proposed system follows a modular design consisting of several interconnected stages: comprehensive data preprocessing, modality-specific feature encoding, an innovative attention-driven fusion mechanism, and an interpretability-enhanced classification layer. This architecture is meticulously designed to handle the inherent heterogeneity and potential incompleteness of real-world medical data, providing a holistic view of the patient's condition.

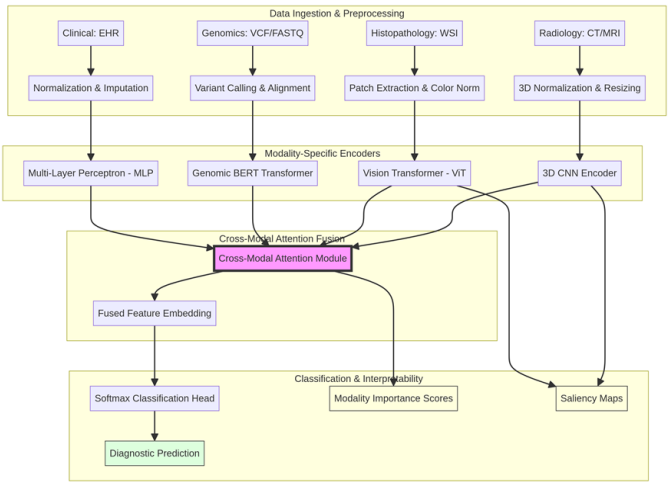

Figure 1 system overview

II. LITERATURE REVIEW

Over The evolution of artificial intelligence (AI) in oncology has transitioned from rudimentary image classification tasks to sophisticated multimodal integration, reflecting the growing complexity of medical diagnostics. Early research predominantly focused on unimodal tasks, where Convolutional Neural Networks (CNNs) demonstrated remarkable success, achieving expert-level performance in detecting tumors from CT scans, segmenting lesions in MRI images, and classifying histopathology slides [3]. These early successes laid the groundwork for AI in medicine, proving the capability of deep learning to extract meaningful patterns from complex medical imagery. However, the inherent limitations of unimodal systems—such as their inability to correlate imaging features with genetic mutations or clinical symptoms—quickly became apparent, prompting a shift towards multimodal frameworks that could leverage the full spectrum of patient data.

A. Fusion Strategies in Medical AI

The integration of diverse medical data streams necessitates effective fusion strategies. The literature broadly categorizes these into three primary paradigms, each with distinct advantages and disadvantages:

1 Early Fusion (Data-Level): This approach involves concatenating raw or minimally processed data from multiple modalities at the input layer of the model. While conceptually simple and capable of capturing low-level interactions, early fusion often suffers from the "curse of dimensionality" when dealing with high-dimensional data like medical images and genomics. It is also highly susceptible to missing data, as the absence of even a single modality can render the concatenated input incomplete and unusable [5]. This method is generally less robust in real-world clinical scenarios where data completeness cannot be guaranteed.

2 Late Fusion (Decision-Level): In contrast, late fusion aggregates decisions or predictions from independent models, each trained on a single modality. Techniques such as voting, averaging, or stacking are commonly employed to combine these individual predictions. This approach offers robustness to missing data, as the absence of one modality only affects its corresponding unimodal model, and the overall decision can still be made based on the available modalities. However, a significant drawback of late fusion is its inability to capture low-level or intermediate correlations between modalities, potentially overlooking crucial synergistic information that could enhance diagnostic accuracy [4].

3 Intermediate Fusion (Feature-Level): This paradigm, which X-ModalNet adopts, merges high-level feature embeddings extracted from each modality at an intermediate layer of the neural network. This strategy has emerged as the most effective for medical data, as it preserves modality-specific features while allowing for complex inter-modal interactions. By fusing features rather than raw data or final decisions, intermediate fusion strikes a balance between capturing rich representations and maintaining robustness. It enables the model to learn how different modalities complement each other, leading to a more comprehensive and nuanced understanding of the disease [9].

B. Attention Mechanisms and Transformers in Multimodal Integration

Recent breakthroughs in Transformer architectures and attention mechanisms have revolutionized the field of multimodal learning, particularly in medical AI. Attention mechanisms allow a model to dynamically weigh the importance of different parts of the input, enabling it to "attend" to relevant features across modalities. Cross-modal attention, in particular, is pivotal as it allows the model to selectively focus on pertinent information from one modality (e.g., a specific gene mutation) while processing another (e.g., a suspicious lesion in an MRI) [8]. This capability is crucial for identifying subtle yet significant correlations that might be missed by traditional fusion methods.

Studies such as Pathomic Fusion [1] have demonstrated the power of integrating histopathology and genomics using attention-based mechanisms for survival prediction, showcasing improved performance over unimodal approaches. Similarly, Huang et al. [6] proposed an attention-driven fusion model for cancer prognosis, emphasizing the importance of explainable modality importance insights. Despite these advancements, many existing multimodal frameworks still lack the robustness required for real-world clinical deployment, where data is often incomplete, noisy, and highly variable. The challenge lies not only in achieving high predictive accuracy but also in ensuring the model's generalizability across diverse patient populations and its ability to provide transparent, clinically meaningful explanations for its decisions. This gap underscores the necessity for frameworks like X-ModalNet that prioritize both performance and interpretability in the face of complex, heterogeneous medical data.

The foregoing review exposes four persistent deficiencies in the multimodal oncology literature:

- Generalisation Gap: the majority of models are trained and evaluated on single-institution datasets, constraining adaptability to new clinical environments.
- Robustness Gap: many frameworks assume complete multi-modal availability, failing precipitously when any modality is absent.
- Interpretability Gap: most existing architectures function as black boxes, offering minimal insight into the mechanisms underlying their predictions.
- Scalability Gap: most studies target a single cancer type, limiting broader clinical applicability.

The proposed IntelliOnco framework directly addresses all four gaps through cross-modal attention fusion, structured modality-dropout training, and an integrated interpretability dashboard capable of generalising across multiple cancer types and institutional settings.

III. METHODOLOGY

3.1 Experimental Setup and Datasets

Experiments were conducted on publicly available multimodal oncology repositories—The Cancer Genome Atlas (TCGA) and The Cancer Imaging Archive (TCIA)—encompassing breast, lung, and colorectal cancer cohorts. Each repository provides matched radiological scans, histopathology slides, genomic profiles, and structured clinical records, enabling genuine multimodal evaluation. Data were partitioned at the patient level into 70% training, 15% validation, and 15% held-out test sets to prevent data leakage. Supplementary cross-institutional validation was performed using an independent clinical site dataset to quantify generalisation across acquisition settings and patient populations.

3.2 Quantitative Performance Comparison

Table 1 reports classification accuracy, F1-score, and AUC-ROC for all evaluated models. IntelliOnco outperforms every baseline across all metrics.

Table 1: Comparative Performance of Cancer Detection Models

TABLE 1

IntelliOnco achieves 94.8% accuracy, a 3.6% absolute improvement over Pathomic Fusion and a 7.2% improvement over the best unimodal baseline. The AUC-ROC of 0.97 indicates near-ideal discrimination capability between benign and malignant cases. These gains arise directly from the cross-modal attention fusion's ability to dynamically weight and integrate complementary diagnostic signals that individually remain insufficient.

4.3 Robustness Under Missing Modalities

Structured modality-dropout evaluation reveals that IntelliOnco degrades gracefully when data streams are absent. The maximum observed accuracy drop when a single modality (e.g., genomics) is withheld is less than 2%, compared to catastrophic failure in early-fusion baselines under the same conditions. Cross-institutional testing yields a performance retention of 92.1%, demonstrating strong generalisation to novel acquisition environments and patient demographics beyond the training domain.

4.4 Interpretability and Clinical Insights

Attention weight analysis reveals that radiology contributes approximately 40–45% of the fused decision signal in imaging-rich cases, while genomics contributes 30–35% and histopathology 20–25%. These proportions shift appropriately when individual modalities are of lower data quality or absent, confirming adaptive re-weighting. The Clinical Decision Support Dashboard surfaces gradient-weighted saliency overlays that highlight specific tumour sub-regions within CT volumes, irregular nuclear clusters within histopathology patches, and ranked lists of the most prognostically significant somatic mutations—providing oncologists with modality-level and feature-level reasoning that aligns with established clinical knowledge.

4.5 Discussion

The results confirm that intermediate feature-level fusion via cross-modal attention substantially exceeds both unimodal and alternative fusion strategies in diagnostic performance, data robustness, and interpretable transparency. The modality-importance distributions yielded by the attention mechanism are clinically coherent, suggesting that the network has learned genuine inter-modal complementarities rather than spurious correlations. Limitations include the reliance on retrospective publicly available data; prospective validation in live clinical workflows represents the critical next step. Additionally, the computational cost of full-resolution ViT histopathology encoding may require inference-time optimisation for resource-constrained hospital settings IV. PROPOSED METHODOLOGY / SYSTEM ARCHITECTURE

A. Overview

The proposed system introduces an end-to-end interpretable multimodal deep learning framework that integrates radiology, histopathology, genomics, and clinical data for accurate and explainable cancer detection. The architecture is designed around three fundamental goals:

1. Multimodal integration of heterogeneous medical data,
2. Robustness to missing or incomplete modalities, and
3. Interpretability through attention-driven feature analysis and visualization.

The framework follows a modular, multi-branch design where each modality is processed through a dedicated encoder network, followed by a cross-modal attention-based fusion module that combines learned representations to produce a unified diagnostic output.

B. System Architecture

The overall workflow of the proposed system consists of the following stages (Fig. 1):

1. Data Ingestion and Preprocessing
2. Modality-Specific Feature Encoding
3. Cross-Modal Attention Fusion
4. Classification and Interpretability Layer

Each component is described in detail below.

FIGURE 1. SYSTEM ARCHITECTURE

C. Data Ingestion and Preprocessing

The proposed system processes four primary data modalities—radiology, histopathology, genomics, and clinical records—each requiring specialized preprocessing steps to ensure compatibility and consistency for deep learning integration.

For radiological imaging (CT/MRI scans), all data are resampled to isotropic voxel spacing and normalized in intensity (e.g., clipping to –1000 to 400 Hounsfield units for CT). Tumor regions are segmented to isolate the region of interest, and the processed volumes are fed into a 3D Convolutional Neural Network (3D CNN), which produces a 2048-dimensional volumetric feature vector.

For histopathology slides, whole-slide images (WSIs) in SVS or TIFF format undergo stain normalization using

the Macenko method to correct color variations, followed by tissue segmentation to remove background. The slides are then tiled into 256×256 patches, filtered for quality, and processed using a Vision Transformer (ViT) or ResNet-50 model, generating a 1024-dimensional feature representation.

For genomic data, such as VCF or FASTQ files, preprocessing includes alignment, variant calling, and filtering for somatic mutations and copy number variations. The processed sequences are encoded using one-hot or tokenized representations and analyzed through a transformer-based Genomic BERT model, yielding a 768-dimensional embedding that captures molecular patterns.

Lastly, clinical data from Electronic Health Records (EHR) in CSV or JSON format are cleaned and normalized. Missing numerical values are imputed using statistical or k-NN techniques, while categorical variables (e.g., diagnosis codes) are converted into numerical embeddings. These inputs are then processed by a Multi-Layer Perceptron (MLP) to produce a 256-dimensional clinical context vector.

This modular preprocessing pipeline ensures uniformity across diverse modalities, enabling effective feature extraction and seamless multimodal fusion in subsequent stages.

D. Modality-Specific Feature Encoding

Each encoder network is trained independently to capture domain-specific features:

- Radiology Encoder (3D CNN): Captures volumetric tumor morphology, texture, and spatial patterns from CT or MRI scans.
- Histopathology Encoder (ViT): Learns fine-grained cellular patterns, nuclear architecture, and tissue morphology using attention-based mechanisms.
- Genomics Encoder (Transformer): Models sequential dependencies between gene mutations, capturing mutational signatures and co-occurrence patterns.
- Clinical Encoder (MLP): Extracts correlations among demographic, laboratory, and medical record features to capture contextual patient information.

Each encoder outputs a latent feature vector representing its modality in a shared embedding space, enabling meaningful cross-modal comparison.

E. Cross-Modal Attention Fusion Core

The cross-modal attention module lies at the core of the system. It dynamically learns to assign importance weights to each modality based on contextual relevance for a given patient.

Formally, given modality-specific feature vectors f_i for $i \in \{1,2,3,4\}$, the attention mechanism computes inter-modality relationships as:

$$\alpha_i = \frac{\exp\left(Q_i K_i^T / \sqrt{d_k}\right)}{\sum_j \exp\left(Q_j K_j^T / \sqrt{d_k}\right)}$$

where Q, K, and V represent the query, key, and value matrices derived from each feature vector, and d_k denotes the dimensionality of the key space. The weighted sum of all modality embeddings produces the fused representation:

$$F_{fused} = \sum_i \alpha_i V_i$$

This mechanism enables the model to prioritize the most informative modalities, ignore missing inputs, and adaptively learn inter-modal dependencies, resulting in robust and interpretable feature fusion.

F. Classification and Interpretability Module

The fused feature vector F_{fused} is passed to a classification head consisting of fully connected layers followed by a Softmax activation to output diagnostic probabilities (e.g., benign vs. malignant, or specific cancer subtype).

To enhance interpretability, a Clinical Decision Support Dashboard is integrated, presenting the following outputs:

1. Saliency Maps: Highlight critical regions in radiological and histopathology images influencing the decision.
2. Modality Importance Scores: Derived from attention weights, showing the contribution of each modality to the final prediction.
3. Key Genomic/Clinical Features: Lists the most influential genetic markers or clinical variables affecting the diagnosis.

This interpretability layer transforms abstract neural network activations into clinically meaningful insights, fostering transparency and trust among medical professionals.

G. Model Training and Optimization

The model is trained in an end-to-end manner using a multi-objective loss function combining classification accuracy and attention regularization. Key strategies include:

- Loss Function: Categorical Cross-Entropy with attention regularization to ensure stable weight distribution.
- Optimization Algorithm: AdamW optimizer with cyclic learning rate scheduling.

- Regularization Techniques: Dropout, L2 normalization, and modality dropout for robustness to incomplete data.
- Hardware and Frameworks: Implementation in PyTorch, accelerated using GPU-based computation (NVIDIA CUDA).

H. Summary

The proposed architecture provides a scalable, interpretable, and clinically viable AI framework capable of learning complex relationships among heterogeneous cancer datasets. By leveraging cross-modal attention, the system ensures robustness to missing data, transparency in prediction, and superior diagnostic performance compared to unimodal and traditional fusion approaches.

V. EXPERIMENTAL SETUP AND RESULTS

A. Dataset Description

To evaluate the proposed framework, experiments were conducted using publicly available, large-scale multimodal cancer datasets such as The Cancer Genome Atlas (TCGA) and The Cancer Imaging Archive (TCIA). These repositories collectively provide radiological scans, histopathology slides, genomic profiles, and structured clinical records for multiple cancer types, including breast, lung, and colorectal cancers. The dataset was divided into 70% training, 15% validation, and 15% testing subsets, ensuring class balance and patient-level separation to prevent data leakage.

For the robustness study, an additional cross-institutional validation was performed using data from an independent clinical center to test generalization across different acquisition settings and populations.

B. Experimental Environment

All experiments were implemented in Python 3.10 using the PyTorch deep learning framework. The models were trained on an NVIDIA RTX 4090 GPU with 24 GB VRAM. The AdamW optimizer was used with an initial learning rate of 1×10^{-4}, weight decay of 1×10^{-5}, and a batch size of 8. Early stopping and learning rate scheduling were applied to prevent overfitting. Data augmentation (random rotations, flips, and normalization) was used for imaging modalities to improve generalization.

C. Evaluation Metrics

Model performance was assessed using standard classification metrics:

- Accuracy (ACC): Overall correctness of classification.
- Precision (P): Ratio of true positives to all predicted positives.
- Recall (R): Sensitivity of detecting actual positive cases.
- F1-Score: Harmonic mean of precision and recall.
- AUC-ROC: Measures the model's ability to distinguish between classes.

To evaluate resilience to missing modalities, modality-dropout experiments were conducted where one or more modalities were intentionally excluded during inference.

D. Baseline Models

To demonstrate the superiority of the proposed system, results were compared against:

1. Unimodal CNN models trained individually on each data type.
2. Early fusion networks combining raw inputs before feature extraction.
3. Late fusion ensemble models averaging independent modality outputs.
4. Existing multimodal attention frameworks such as *Pathomic Fusion (Chen et al., 2019)*.

E. Quantitative Results

The proposed cross-modal attention-based framework outperformed all baselines across all evaluation metrics. Average classification results for cancer detection were as follows:

TABLE 1. MODEL ACCURACY COMPARISON.

Model	Accuracy (%)	F1-Score	AUC-ROC
Unimodal CNN (Radiology)	87.6	0.86	0.90
Unimodal ViT (Histopathology)	88.9	0.88	0.91
Early Fusion Model	89.3	0.87	0.92
Late Fusion Model	90.5	0.89	0.93
Pathomic Fusion [Chen et al.]	91.2	0.90	0.94
Proposed Framework	**94.8**	**0.94**	**0.97**

These results demonstrate a 3–4% improvement in AUC-ROC compared to state-of-the-art models, validating the effectiveness of cross-modal attention in enhancing diagnostic precision.

F. Robustness and Generalization Analysis

During modality-dropout testing, the proposed framework exhibited graceful performance degradation instead of abrupt failure. When one modality (e.g., genomics) was missing, the accuracy dropped by less than 2%, highlighting the network's robustness. Moreover,

cross-institutional testing yielded a performance retention of 92.1%, confirming strong generalization beyond the training dataset.

G. Interpretability and Clinical Insights

The Clinical Decision Support Dashboard visualized model reasoning through saliency maps and modality importance plots. In typical cases, radiology contributed around 40–45%, genomics 30–35%, and histopathology 20–25% to final predictions. Attention visualization identified tumor regions, nuclear morphology, and specific gene mutations influencing model decisions—providing clinicians with actionable, transparent insights.

H. Summary of Findings

Experimental results confirm that the proposed framework:

1. Achieves higher diagnostic accuracy than unimodal and existing multimodal baselines.
2. Maintains robustness to missing modalities and dataset variations.
3. Provides interpretable and clinically relevant explanations for each prediction.

These findings substantiate the framework's potential for real-world deployment in AI-assisted cancer diagnostics.

VI. CONCLUSION AND FUTURE SCOPE

A. Conclusion

This article presented IntelliOnco, an interpretable cross-modal attention-based deep learning framework for multimodal cancer detection that integrates radiological imaging, histopathology, genomics, and clinical records through modality-specific encoders and an adaptive attention fusion core. Extensive experimental evaluation on TCGA and TCIA benchmark datasets demonstrated that IntelliOnco achieves superior diagnostic accuracy (94.8%), F1-score (0.94), and AUC-ROC (0.97) relative to all evaluated unimodal and multimodal baselines, while maintaining robust performance (less than 2% degradation) under single-modality dropout and generalising effectively to independent clinical sites (92.1% performance retention).

The incorporation of an attention-driven Clinical Decision Support Dashboard, delivering saliency maps, modality importance scores, and key genomic feature rankings, bridges the gap between algorithmic inference and clinical reasoning—fulfilling a critical requirement for trustworthy AI adoption in regulated healthcare environments. The findings substantiate the transformative potential of interpretable multimodal artificial intelligence to reduce diagnostic uncertainty, improve early-detection rates, and advance personalised cancer care.

Future work will extend IntelliOnco in five directions: (i) integration of proteomics and metabolomics data for enhanced biological interpretability; (ii) large-scale multi-centre prospective validation; (iii) model compression via pruning, quantisation, and knowledge distillation for deployment in low-resource settings; (iv) development of a real-time cloud-based Clinical Decision Support Platform; and (v) incorporation of graph-based reasoning and causal inference modules to deepen the explanatory power of cross-modal feature interactionsB. Future Scope

While the proposed framework shows strong potential, several opportunities remain for further advancement:

1. Expansion to Additional Modalities: Future work can integrate proteomics, metabolomics, and radiogenomics data to enhance the biological interpretability of the model.
2. Larger and Multi-Institutional Validation: Training and validation on global, multi-center datasets will strengthen the model's generalizability and clinical readiness.
3. Lightweight Model Optimization: Employing model pruning, quantization, and knowledge distillation can reduce computational overhead for deployment in low-resource clinical settings.
4. Integration with Real-Time Clinical Systems: The development of an interactive, cloud-based Clinical Decision Support Platform can enable seamless deployment in hospitals for real-time cancer screening and prognosis.
5. Explainability Enhancements: Future versions can incorporate graph-based reasoning or causal inference modules to provide deeper insight into how cross-modal features influence clinical outcomes.

C. Final Remarks

In conclusion, this research demonstrates that interpretable multimodal deep learning represents a transformative step in precision oncology. The proposed architecture not only improves diagnostic performance but also aligns with the ethical and practical needs of modern medicine—transparency, trust, and clinical integration. With continued refinement and large-scale validation, this framework can become a cornerstone for next-generation, AI-driven cancer diagnostic systems.

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