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Adaptive Deep Fusion Network For Multi-Modal Cancer Progression Prediction: A Scalable and Real-Time Approach

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Abstract

It is important to have an accurate prognosis of the course of cancer to facilitate early intervention and personalized treatment. It leads to improved patient outcomes. However, existing methods frequently encountered with scalability, class imbalance, multi method data integration and computation efficiency which limits their applicability in real time medical situations. Generally, these existing methods are not effective. The objective is to present a novel framework known as the Adaptive Deep Fusion Network (ADFN) to overcome the existing methods. It utilizes the adaptive learning strategies and deep fusion method for predicting the progression of cancer. A hierarchical multi method fusion mechanism is employed into the ADFN method. This mechanism combines the data from different sources such as clinical records, histopathological data and genomic data. The utilization of attention-based layers to prioritize key features allows this integration and enhancing the prediction accuracy when balancing the computing complexity. To overcome the issues of class imbalance, the ADFN makes use of cost sensitive loss function and targeted loss layers. This method ensures accurate prediction of cancer stages which are essential. Furthermore, an adaptive learning method is based on learning continuously updates method parameters which enable the ADFN to handle large scale dataset efficiently without the human intervention. The method is able to provide the real time prediction because it reduces the amount of computational load by replacing lightweight transformer for typical recurrent neural network (RNN). The ADFN method exceeds existing methods in terms of accuracy, precision, recall and f1-score in experimental evaluations using cancer datasets. As a result, it is reliable for the real time clinical settings and monitors the evolution of cancer, provide proactive treatment methods and efficient method in cancer management.

Keywords: *Cancer Progression, Adaptive Learning, Multi-modal Data Fusion, Real-time Prediction, Transformer Layers, Class Imbalance, Personalized Medicine.*

1. INTRODUCTION

Despite the fact that millions of new cases are diagnosed every year, cancer evolves to be biggest cause of death around the globe. To achieve early detection and personalized treatment, it is essential to have ability to properly predict the evolution of cancer. The conventional method of diagnosis requires significant amount of manual labor and frequently results in errors caused by human intervention. Moreover, it is possible that these existing methods do not represent the multifaceted and complicate nature of cancer, specifically in early stages.

The recent developments in machine learning (ML) and deep learning (DL) have made it possible to automate and improve the accuracy of cancer detection and prognosis which leads

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to potential alternatives. Existing deep learning methods has some limitations which limit their clinical usefulness in the real world. One of the most significant problem is scalability in which the large detests are not able to manage due to complexity and computations and the memory needs. Moreover, the integration of multi modal data which includes histopathological images, clinical records and genetic sequences which leads to substantial problem.

Many methods are unable to employ different types of sources into cohesive framework. Class imbalance is another significant issue that has to be addressed. This happens when specific stage of cancer is under represented in databases, which results in large prediction for uncommon but significant instances.

The dependence of complicated designs such as Long Short-Term Memory (LSTM) networks and Recurrent Neural Network (RNN) which increase in amount of computing burden, which limits the possibility of making real time predictions in clinical settings. This research proposed an Adaptive Deep Fusion Network (ADFN) is developed with addressing this issue.

This proposed ADFN method was developed to integrate numerous data modalities in an efficient manner, handle large scale datasets and deliver real time prediction with high degree of accuracy during its development. Moreover, it makes use of an adaptive learning method which dynamically adjusts method parameters based on the complexity and scale of the data. This ensures that system is both scalable and efficient in terms of computing. To integrate genomic, histopathological and clinical data, a hierarchical multi modal method is presented.

This method makes use of attention-based layers to prioritize the most significant aspect from each modality. The ADFN integrates a cost sensitive loss function and focal loss layers to address the issue of class imbalance. It results in an enhancement in the predicted accuracy for rare cancer types and stages during the process.

Moreover, the lightweight transformer layers have replaced typical RNN which has resulted in significant reduction in computing requirements when maintaining high level reliability in temporal prediction.

The objective of the proposed ADFN method is to provide the scalable solution for cancer progression prediction. This will allow it to be suited for real time medical situations and will enhance the efficiency of cancer management in personalized medicines.

The remainder of this paper is organized as follows: Section II reviews the limitations of current cancer progression prediction methods and related work in the field. Section III presents the proposed methodology, including data preprocessing, model architecture, and adaptive learning strategies.

Section IV discusses the experimental setup, datasets used, and performance evaluation. Finally, Section V concludes the study and outlines potential future research directions.

2. RELATED WORKS

This Related Work section compares various cancer progression prediction methods using different machine learning and deep learning techniques.

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Table 1: Existing methods on cancer progression

Refence Number	Technique used	Merits	Demerits
[1]	Artificial neural network	Growth rate of nodule must be detected earlier	Less efficient method
[2]	Machine learning models	High accuracy is obtained	
[3]	XGBoost+ Denoising auto encoder	The multi-omics data analysis could bring more information about the cancer survival.	Many censored samples in the data limited the accuracy of predicting cancer outcomes.
[4]	LSTM	. It is more appropriate for real-world endoscopic situations.	High computational process
[5]	VGG-19+U-NET	This method is faster, more accurate, and more efficient than the current technique	Less scalable process
[6]	1D-CNN, 2D-Vanilla-CNN, and 2D-Hybrid-CNN	This CNN model had the benefit of capturing high-order interactions among these genes to make accurate predictions.	The cancer is not predicted earlier.
[7]	Ensemblelearning + Neural network	The model suggested has proved to be more efficient and beneficial for breast cancer classification,.	No integration from different data modalities
[8]	CNN+DNN	It is heterogeneous deep learning-based ensemble model for effective breast cancer prediction using multi-modal data.	This method has less data modalities
[9]	DRNN	One of the efficient methods	Less scalable method
[10]	TL+CNN	It is best network for cancer detection	Less accuracy is obtained

The table 1 serves to summarize and critically compare existing methodologies in the field of cancer progression prediction. It highlights where current techniques excel and where they fall short.

By pointing out these limitations, the table sets the stage for the introduction of your proposed Adaptive Deep Fusion Network (ADFN), which aims to overcome these challenges (e.g., improving scalability, integrating multi-modal data, and achieving higher accuracy).

This comparison allows readers to understand the context and relevance of your approach relative to previous research, establishing the novelty and value of the ADFN framework.

3. PROPOSED METHODOLOGY

The proposed Adaptive Deep Fusion Network (ADFN) is a comprehensive framework for predicting cancer progression by integrating multiple data modalities and addressing key challenges in scalability, real-time applicability, and class imbalance.

The ADFN utilizes an adaptive learning mechanism, hierarchical fusion of multi-modal data, and efficient prediction strategies, making it suitable for dynamic and large-scale clinical datasets. Below, the detailed components of the proposed method are provided, including necessary equations and formulations.

The ADFN model requires comprehensive multi-modal data for accurate cancer progression prediction. The main data types used are:

- Genomic Data: Includes gene and protein expression levels, mutations, and other biological information relevant to cancer progression.

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- Histopathological Images: Provide spatial information regarding the structure and cellular organization of tumors.
- Clinical Data: Patient demographics, cancer stage, previous treatment records, and other medical history details.

The Preprocessing Steps are as follows:

- Noise Reduction: Noise in histopathological images is removed using advanced filters, such as Wiener filter, to enhance image quality.
- Data Augmentation: Techniques like random rotations, flips, and color normalization are applied to address class imbalance and ensure a well-distributed dataset.
- Feature Extraction: Deep learning models like EfficientNetV3 and Transformer Encoders are used to extract high-level features from each data modality.

The ADFN integrates multi-modal data through a two-stage fusion mechanism: Feature-Level Fusion and Decision-Level Fusion.

a. Feature-Level Fusion

- Genomic Data: Encoded using a Transformer-based embedding layer, capturing relationships between genes and proteins. Let Type equation here.represent the genomic feature vector at time t.
- Histopathological Image: Feature extraction from images is performed using EfficientNetV3, producing a feature vector
- Clinical Data: Encoded using a transformer layer that captures temporal changes in clinical records, resulting in a feature vector Type equation here.

The Feature-Level Fusion combines these feature vectors using an attention mechanism:

$$f_{fused}^{t} = Attention(f_{fgen}^{t}, f_{hist}^{t}, f_{fclin}^{t}) \quad (1)$$

Where:

- $-f_{fused}^{t}$ is the fused feature vector at time t.
- The attention function assigns weights to each modality's feature vector based on its relevance.

b. Stage 2 - Decision-Level Fusion

The fused features are passed through multiple classification heads to make preliminary predictions. The results are then combined using a decision-level fusion layer that applies a weighted average to optimize final predictions:

$$\mathcal{Y}final = \sum_i w_i .\ y_i \quad (2)$$

Where:

- $\mathcal{Y}final$ is the final prediction output.
- y_i represents individual predictions from different classification heads.
- w_i are the learnable weights assigned to each prediction, optimized during training.

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The adaptive learning strategy employs a reinforcement learning-based optimizer to adjust model parameters dynamically. This allows the model to handle variations in data complexity and scale effectively.

The adaptive learning rate nt at time t is updated based on the complexity of the data batch using a reward signal:

$$nt + 1 = nt + \alpha.\mathcal{R}_t \quad (3)$$

Where:

α is the step size (hyperparameter).

$\mathcal{R}_t$ is the reward signal based on model performance for the current batch.

To address class imbalance, the ADFN model incorporates a cost-sensitive loss function and focal loss.

These strategies emphasize the correct classification of underrepresented classes, such as rare cancer stages.

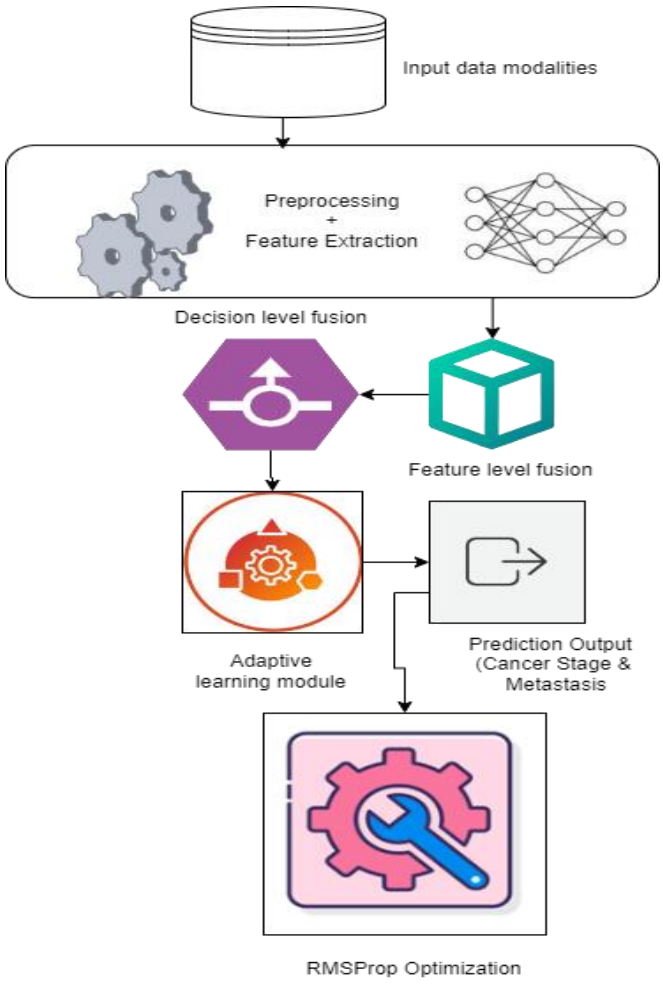

Figure 1: Proposed framework

A penalty is applied to the loss function for misclassifying rare classes. The loss for each class c is weighted inversely to its frequency:

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$$L_{weighted} = \sum_c w_c.\ y_c.\log(p_c) \quad (4)$$

Where:

- $w_c$is the weight for class c (inversely proportional to class frequency).
- p_c is the predicted probability for class c.
- $y_c$is the true label for class c.

Focal loss focuses on difficult-to-classify samples, allowing the model to prioritize challenging cases:

$$L_{focal} = \alpha_t(1-p_t)^{\gamma}.\log(p_t) \quad (5)$$

Where:

- p_t is the predicted probability for the true class.
- α_t is the weighting factor.
- $\alpha_t$focusing parameter that adjusts the importance of hard-to-classify examples.

The ADFN predicts cancer progression by processing temporal and spatial data through light weight Transformer Layers, replacing traditional RNNs for computational efficiency:

$$h_i^{(T)} = Transformer(h_i^{(t)}, \dots, h_i^{(T-1)}) \quad (6)$$

Where:

- $h_i^{(T)}$ is the final embedding for node i at the final time step T.
- The transformer layer captures the temporal dependencies between the data points.

The final predictions include:

- Cancer Stage Prediction: Predicting the stage (early, intermediate, advanced) using a SoftMax function:

$$P(stage) = Softmax\ (W_S.h + b_s) \quad (7)$$

- Metastasis Prediction: Predicting the likelihood of cancer spreading to other regions using a sigmoid function:

$$P(Metastasis) = Sigmoid\ (W_m.h + b_m) \quad (8)$$

Where:

- $W_S$and W_m. are learnable weight matrices.
- b_s and $b_m$are bias terms.

The ADFN model is trained using a combined loss function that includes cross-entropy for classification tasks and cost-sensitive loss for class imbalance:

$$L_{total} = \lambda_1.L_{CE} + \lambda_2.L_{Weighted} \quad (9)$$

Where:

λ_1) and$\lambda_1$are hyperparameters controlling the contribution of each loss component.

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The model is optimized using the RMSProp optimizer for fast convergence and efficient handling of the complex optimization landscape associated with multi-modal data fusion. The ADFN's lightweight architecture, featuring transformer layers and adaptive learning, is designed for real-time clinical application. The model efficiently integrates spatial, temporal, and multi-modal data, enabling dynamic and accurate predictions that are crucial for timely clinical interventions. This detailed methodology provides a robust solution to existing challenges in cancer progression prediction, ensuring high accuracy, computational efficiency, and scalability for real-world applications.

4. EVALUATION METRICS

4.1 Dataset

The Cancer Genome Atlas (TCGA) is a highly regarded and extensive repository that offers a comprehensive collection of genomic, histopathological, and clinical data across a wide range of cancer types. It is known for its high-quality, well-annotated datasets that facilitate integrative analyses, making it an ideal choice for complex research that requires multi-modal data integration. The strengths of TCGA lie in its thorough curation and the diverse types of data it encompasses, which include gene expression profiles, mutation data, histological images, and detailed clinical records. This richness in data supports robust analysis, enabling researchers to build sophisticated models that leverage varied sources of information. For your Adaptive Deep Fusion Network (ADFN) framework, which requires genomic, histopathological, and clinical inputs to predict cancer progression, TCGA provides the perfect data foundation. The multi-modal nature of TCGA's resources aligns seamlessly with your model's design and objectives, allowing for comprehensive training, validation, and testing of the framework to ensure high predictive accuracy and clinical applicability.

4.2 Accuracy

Accuracy measures the proportion of correctly classified instances (both positive and negative) out of the total number of instances. It is a general metric to assess the overall performance of the model.

$$\text{Accuracy} = \frac{\text{Total Instances (TP + TN + FP + FN)}}{\text{True Positives (TP)+True Negatives (TN)}} \quad (10)$$

Where,

- TP indicates true positive rate
- FP indicates false positive rate
- TN indicate true negative rate
- FN indicate false negative rate

Table 2: Comparison of Accuracy Values

Methods	Accuracy
Ensemble learning + Neural network [7]	84%
CNN+DNN [8]	85%
Multimodal Deep Neural Network [9]	86%
CNN+ Ensemble method [10]	87%
Proposed	92%

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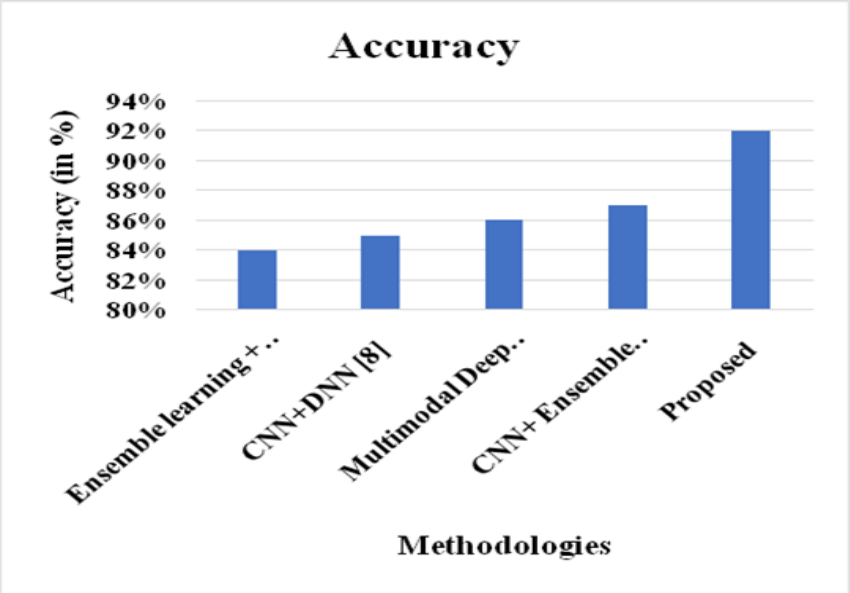

Figure 2: Accuracy analysis

Figure 2 shows the accuracy of various cancer progression with proposed method is presented. Despite the fact that existing methods provide competitive levels of accuracy, the graph demonstrates that the proposed ADFN outperforms these methods with a significant improvement obtaining the highest degree of accuracy. This superiority can be due to the hierarchical multi modal fusion method and adaptive learning method which are employed into ADFN. These components enhance the capacity of method to efficiently interpret complicate large-scale datasets.

4.3 Precision

Precision measures the proportion of correctly predicted positive instances (e.g., cases where cancer metastasis is predicted) out of the total predicted positives. It is crucial in cancer prediction as it reflects how many of the predicted positive instances (e.g., advanced stages or metastasis) are actually positive.

$$Precision = \frac{\text{True Positives (TP)}}{\text{True Positives (TP)+False positivites}} \quad (11)$$

Table 3: Comparison of Precision Values

Methods	Precision
Ensemble learning + Neural network [7]	82.5%
CNN+DNN [8]	84.6%
Multimodal Deep Neural Network [9]	85.8%
CNN+ Ensemble method [10]	86.9%
Proposed	91.1%

A high precision indicates that the model has fewer false positives, which is essential in medical applications to avoid over-diagnosis.

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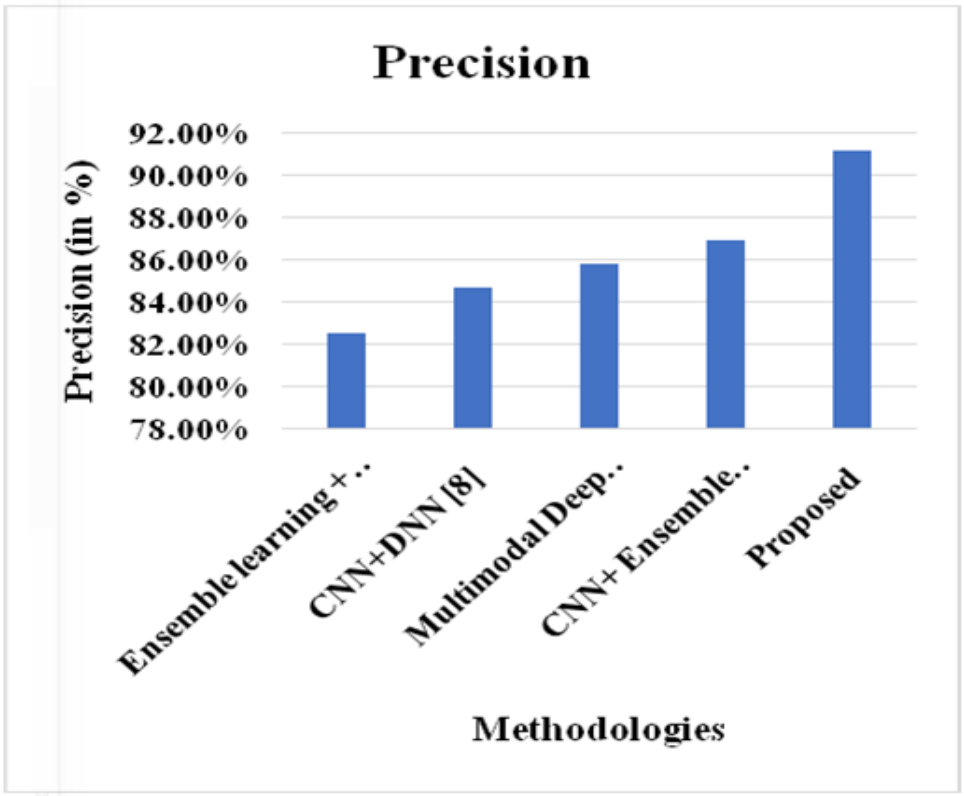

Figure 3: Precision analysis

The precision values for number of different cancer progression with proposed method are depicted in figure 3. According to figure 3, the ADFN is capable of achieving a significantly greater level of precision in comparison to other methods. This improvement indicates the capacity of method to prioritize relevant feature through attention based fusion layers. This helps to reduce the number of false positive predictions and ensures that method is more dependable when it comes to clinical decision making.

4.4 Recall

Recall (or Sensitivity) measures the proportion of actual positive instances (e.g., true advanced cancer cases) that are correctly predicted by the model. In cancer prediction, high recall is essential to ensure that no critical cases are missed.

$$\text{Recall} = \frac{\text{True Positives (TP)}}{\text{TruePositives (TP)+False Negativites}} \quad (12)$$

Table 4: Comparison of Recall Values

Methods	Recall
Ensemble learning + Neural network [7]	78.1%
CNN+DNN [8]	81.2%
Multimodal Deep Neural Network [9]	83.5%
CNN+ Ensemble method [10]	84.7%
Proposed	90.4%

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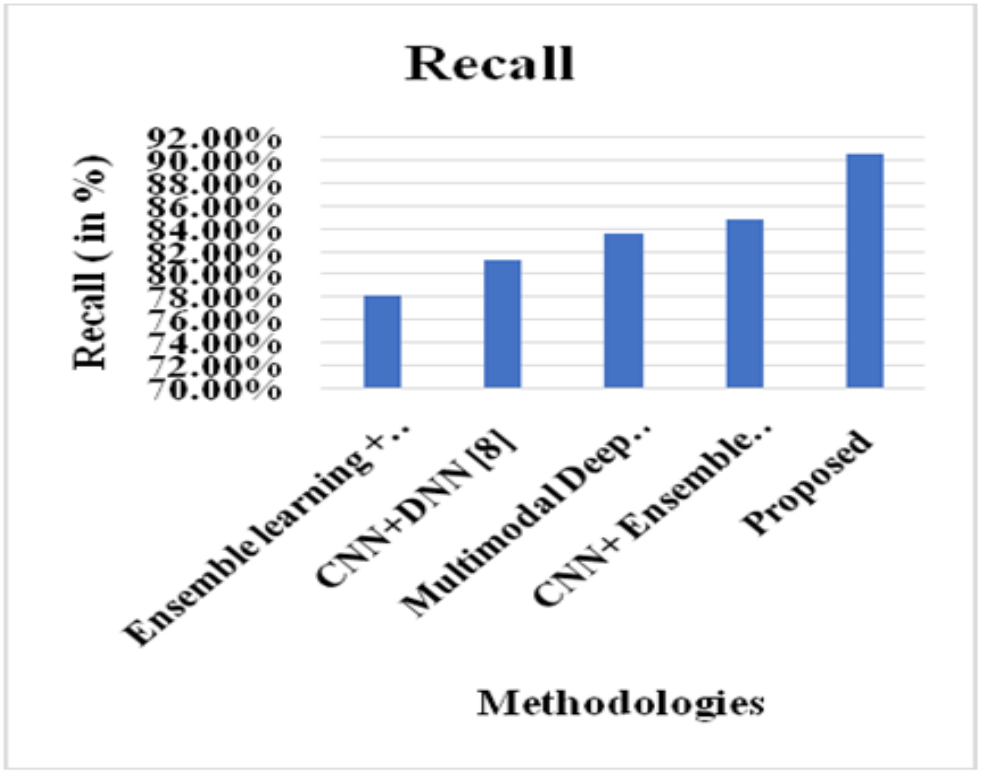

Figure 4: Recall analysis

Figure 4 illustrates the recall of different cancer prediction methods with proposed method. The graph illustrates that the ADFN achieves the highest recall among the methods that were evaluated, which indicates that it has greater ability to find true positives cases in an efficient manner. It is due to the utilization of cost sensitive loss function and focal loss layers, which enables the ADFN to focus on and accurately classify clasess in dataset, hence addressing the issue of class imbalance.

4.5 F1-Score

The F1-Score is the harmonic mean of Precision and Recall. It provides a balanced evaluation by considering both false positives and false negatives, making it a useful metric when the class distribution is imbalanced (e.g., more mild cases than severe cases).

$$\mathrm{F1-Score} = 2 \times \frac{\mathrm{Precision+Recall}}{\mathrm{Precision \times Recall}} \quad (13)$$

Table 5: Comparison of F1-score values

Methods	F1-Score
Ensemble learning + Neural network [7]	80.9%
CNN+DNN [8]	82.5%
Multimodal Deep Neural Network [9]	84.6%
CNN+ Ensemble method [10]	85.3%
Proposed	90.9%

A high F1-Score indicates that the model strikes a good balance between precision and recall, ensuring that it performs well in both identifying positive cases and minimizing false positives.

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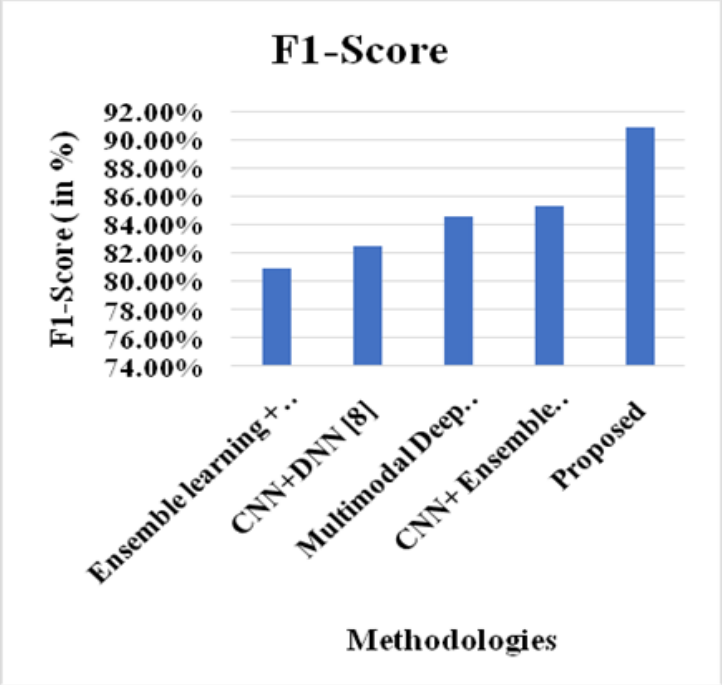

Figure 5: F1-Score analysis

A comparison of the F1-Score for the different cancer prediction method with proposed method is presented in Figure 5. The evaluation of performance on imbalanced datasets in which certain classes many be more prevalent than others, is particularly effective application of this technique.

Due to the fact that it achieved the greatest F1-Score, the figure 5 illustrates the ADFN performs better than other methods. This suggest that the ADFN achieves a successful equilibrium between precision and recall which makes it efficient and privacy option for precise prediction of the cancer evolution. This balanced performance is important for ensuring that the method detects positive cases and minimizes the false alarms.

This study shows the potential of the proposed ADFN solve the cancer progression prediction problems. Existing methods generally struggle to integrate multi modal input, address class imbalances or retain computational efficiently in real time applications. A hierarchical fusion method employs genomic, clinical data and histopathological data and attention-based layer which prioritize relevant data improves accuracy in the ADFN method.

ADFN method excels in its adaptive learning method, which adapts model parameters based on data complexity and scale. The reinforcement learning based method enhances scalability and generalization by allowing the method handle big datasets without human intervention.

The lightweight transformer layers are used to reduce the computing effort while gaining the temporal prediction accuracy. For managing different and complex data, adaptive learning and attention methods must be integrated. Cost sensitive loss functions and targeted loss layers also correct class imbalance, precisely predicting rare but important cancer stages. The proposed ADFN has findings but it needs more clinical data to prove its efficiency in real time applications.

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Integrating radiological imaging and patient reported data may enhance prediction performance. The multi modal ADFN and adaptive design support personalized, timley and successful cancer therapy.

5. CONCLUSION

The proposed Adaptive Deep Fusion Network (ADFN) is developed to overcome the significant issues that are connected with prediction of cancer progression. These challenges include scalability, class imbalance, multi modal data integration and computational efficiency. In comparison to existing method, the proposed ADFN method displays substantial developments through the employment of hierarchical multi modal fusion method, lightweight transform layers and adaptive learning methodologies.

The findings of the experiments demonstrate that the ADFN method performs better than other approaches in terms of accuracy, fi1-score, prediction and recall. This demonstrates the reliability of ADFN and its capacity to be applied in clinical environments in real time.

The capability of the method to balance a wide variety of data sources, including clinical records, genetic data, histopathological data and ensures accurate and complete monitoring of evolution of cancer. It leads to personalized medication and early intervention. In future, this framework must focus on different data types such as radiological imaging, patient's lifestyle and utilization in more extensive clinical applications.

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