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A Self Explainable Graph EfficientNet Framework and Deep Survival Modeling for Brain Tumor classification and Prognosis

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Abstract
Clinical neuro-oncology faces difficulties classifying and predicting prognosis of brain tumors. These difficulties stem from heterogeneous tumor morphology, like image data noise and limited deep learning model interpretability. The study proposes a novel framework for accurately classifying brain tumors as well as predicting prognosis named the Self-Explainable Graph EfficientNet model (SEGE-Net) that incorporates a deep survival model into its architecture. First adaptive Kalman filtering (AKF) is applied to multivariate Magnetic Resonance Imaging (MRI) scans to reduce noise and stabilize image intensity enhancing the quality of MRI scans. Second a modified version of the context-aware feature pyramid network (CFPNet-M) is used to segment the tumors sub regions in order to extract the most discriminative features and improve generalization through geometric augmentation. Next a Global Binary Pattern (GBP) and Completed Local Binary Pattern (CLBP) method is used for texture feature extraction. SEGE-Net combines the EfficientNet model with self-explainable graph-based neural networks (GNN) to model the relationships between extracted textures using discriminative radiomic features. Finally DeepSurv was used to generate patient specific survival probabilities and risk scores. The proposed method achieved segmentation score for precision is 0.93, recall is 0.90 and classification for accuracy is 98.2% and F1-score is 99%.Through experimentation on the BRATS 2020 dataset and Brain Tumor MRI dataset the SEGE-Net provided improved classification accuracy, reliable survival estimates and enhanced explainability of the models prediction processes.

Keywords: Self-Explainable Graph EfficientNet, adaptive Kalman filtering, Magnetic Resonance Imaging, Global Binary Pattern, Completed Local Binary Pattern

1. Introduction

Abnormal cell growths in the brain (brain tumors) are defined as having a benign or malignant origin and can be identified using Magnetic Resonance Images (MRI) scans as well as other medical records [1]. Traditional classification and prognosis of brain tumors has improved with the advent of deep learning technology and the analysis of MRI scans along with its clinical histories [2] using Self-Explainable Graph EfficientNet (SEGE-Net) for patient-specific treatment recommendations and predictions of treatment outcomes. SEGE-Net utilizes the EfficientNet model and incorporates Graph Learning to model the spatial relationships between the different regions of the tumor [3] while providing on the fly interpretability for the user [4]. By combining Neural Networks with Survival Analysis, deep survival Modeling allows for the modeling of the complex non-linear

relationships that exist between imaging and clinical data for that same patient. Previous techniques like Grad-CAM, XAI-CNN, GRU-Surv and LSTM-Surv increased classification accuracy [5] but these earlier methods did not provide much or any explainability as to why, nor did it account for how heterogeneous a tumor might be or how well they could integrate multiple modes of data when modeling the patient's brain tumors [6]. By combining the strengths of SEGE-Net and Deep Survival Modeling are able to provide more accurate [7] and better explainable predictions for brain tumor patients on an individual basis [8].

Contribution

This study provides numerous advances in approaches for performing analysis of brain tumors which include the creation of SEGE-Net a framework for tumor classification that combines both traditional deep learning models (EfficientNet) and graph based methods. The multitude of advancements that was made in improving the image quality of multi modal MRI with the use of AKF and the potential to accurately segment tumors and tumor sub regions using modified CFPNet linked with the 3D MRI pipeline. The hybrid fusion of radiomics and deep features through GBP and CLBP radiomic measures provides more accurate and consistent representation of tumors. Lastly the delivery of patient specific survival risk scores and survival curves using DeepSurv

based survival modeling assists with both diagnosis and prognosis of patients being treated for brain tumors.

Organization

Section 2 elaborates the existing studies based on existing brain tumor classification and Prognosis models and Section 3 designs the proposed methodology. Section 4 deliberates the experimental results and the paper ended up in Section 5.

2. Literature survey

Bogacsovics et al. (2025) [9] investigated how to develop different types of automatic methods for classifying brain tumors using various deep learning ensemble methods. Created different complementary models of Convolutional Neural Networks (CNN) combined its output using fusing and voting methods resulting in improved tumor classification accuracy and greater robustness in terms of the models performance.

Noorani and Di Ieva (2024) [10] discussed the progress made in classifying brain tumors using advanced technologies such as imaging, radiomics, and artificial intelligence (AI). It highlight that new approaches like deep learning and machine learning have improved the ability to identify brain tumors accurately and have enabled the development of improved methods for making decisions about neuro-oncological care.

Steyaert et al. (2023) [11] have used multimodal deep learning methods that combine imaging, molecular and clinical data to predict prognosis for brain tumors in both adults and children. This study has taken a unified deep learning approach that utilizes many sources of data to enhance the accuracy of prediction of survival and outcomes for patients with brain tumors.

Wu et al. (2025) [12] investigated results of possible causal and prognostic associations between human gut micro biota and brain tumors. It combined genetic analysis of patient samples and machine learning techniques to create genetic models of brain tumor progression and to make predictions about the likely outcome of patients based on the gut micro biota of individuals with the same range of types of brain tumors.

Sandhya and Raja (2024) [13] studied deep learning techniques such as CNN were combined with optimized machine learning models to enhance the classification ability of brain tumors by combining automated deep feature extraction and an optimized classification algorithm that yielded superior performance and efficiency in the detection of brain tumors in MRS images.

2.1 Problem statement

Currently there are many problems with studies into the analysis of brain tumors. These problems include high computational complexity, limited interpretability and reliance on manually tuned or dataset specific models. Most deep learning methods do not generalize well due to the lack of large well curated multimodal datasets in real clinical environments. Some work uses computational inferences rather than experimental validation others use pre-trained networks that were not designed specifically for medical imaging which leads to poor feature learning. All of these restrictions demonstrate the need for improved efficient adaptable and clinically reliable frameworks for accurate brain tumor classification and prognosis predictions.

Figure 1 represents the overall systematic representation of proposed methodology. A method for processing the MRI scans consists of initially processing the scans of the MRI scan data through the AKF after collecting the MRI scans of the BRATS 2020 dataset and Brain Tumor MRI dataset. Afterward the MRI scans are segmented using CFPNet-M and then used in conjunction with data augmentation methods using geometric transformations to create more robust models for the segmentation of the brain tumors. Next the radiomic features are obtained from GBP and CLBP and fed through the new SEGE-Net (combination of Efficient-Net and SE-GNN) that allows for a more accurate tumor classification. Finally the features from DeepSurv are used to create personalized survival predictions for each patient.

3. Proposed methodology

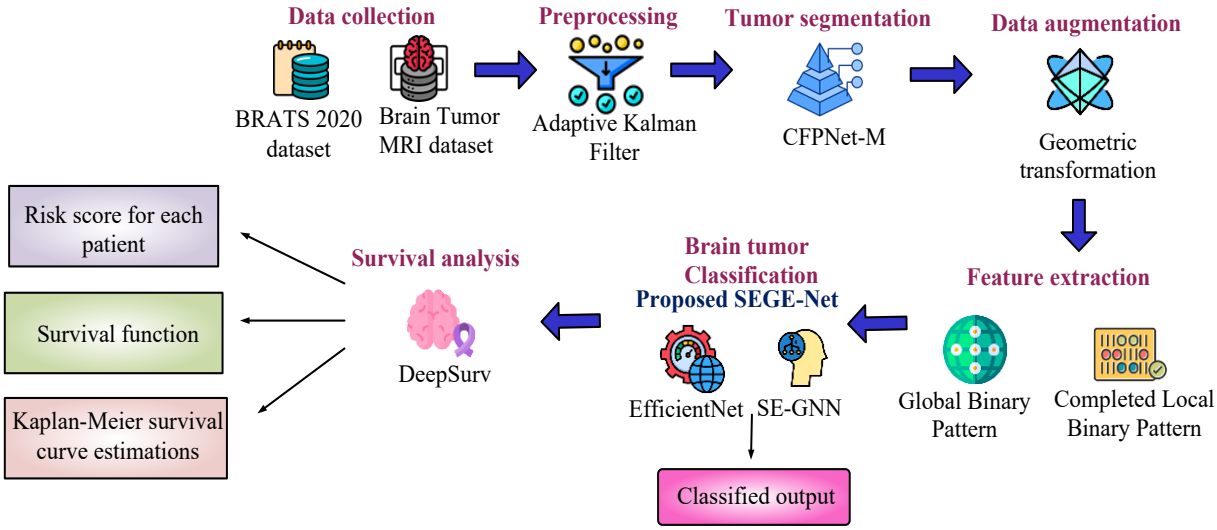


Figure 1 Overall systematic representation of proposed methodology

3.1 Data collection

Data are collected from the BRATS 2020 dataset and the Brain Tumor MRI dataset. These publicly available and clinically validated sources provide various types of MRI sequences (classes T1, T2, FLAIR, and T1CE) and expert annotated corresponding labels. The Brain Tumor MRI dataset contains 3 primary tumor types; glioma, meningioma and pituitary tumor. Together both datasets provide various forms of high quality MRI data that enable the framework to account for the differences in tumor type and MRI acquisition. Assume L as the dataset $L = \{L_1, L_2, ..., L_d, ..., L_k\}$, where k denotes the total number of patient records. Thus using these datasets also allow for increased accuracy during the preprocessing, segmentation, classification and survival prediction stages of the workflow.

3.2 Preprocessing

Once data has been collected, a preprocess step prepare the MRI images for proper analysis. Here, L is the input for preprocessing using AKF. The AKF [16] multimodal images first reduced noises smooth out the intensity variations and thereby enhance the quality of the entire MRI image. The result after applying the AKF process was clean and stable MR image inputs that are easy to identify by the following segmentation and extract features process to accurately find the tumor forms in the MRI data. Preprocessing bridges the gap between the collection of data and the downstream processing of that data through the proposed framework by providing the user with standardized and enhanced MRI data input. Figure 2 represents the Adaptive kalman filter.

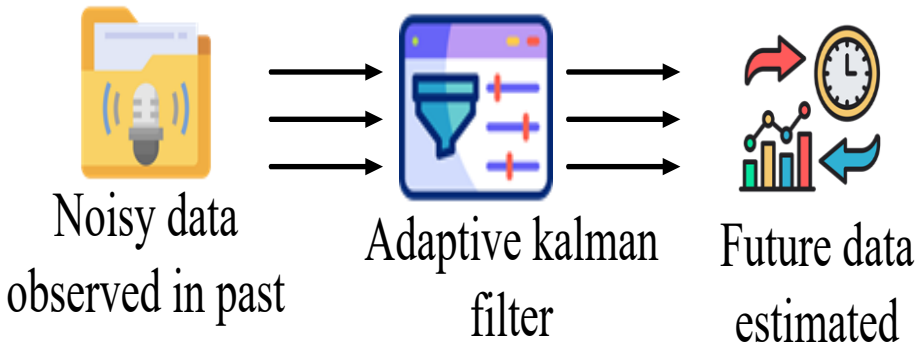


Figure 2 Adaptive kalman filter

3.3 Tumor segmentation

After the MRI images preprocessed for improved clarity next comes tumor segmentation in which clean scans are inputted into our updated CFPNet-M model to isolate and locate tumor region accurately. O_{akf} is taken as a input for tumor segmentation. The use of a neural network trained with both Local and Contextual characteristics make precise discrimination of tumor Sub-regions possible. The output of this process provides accurately defined areas around tumor regions which enable accurate Feature Extraction, classification and conducting Survival Studies in the future stages of the framework.

CFPNet-M

As a lightweight yet comprehensive solution for Multiscale Feature Extraction, CFPNet-M is a key component in integrating the SE-GNN framework [17]. It first performs three sequential image processing operations (convolution with a window of 3 X 3 pooling through an average) then its CFP module clusters feature representations using dilation factor combinations of [2,2], [4,4,8,8,16,16] to create the final feature map F_2 from which enriched feature representations allow for improved classification of brain tumors and prognostic performance via deep survival modeling.

3.4 Data augmentation

The isolated tumor regions are augmented following its segmentation which increases the data diversity and allows for improved robustness of the segmentation model. U_{CF} is taken as a input for data augmentation. Data augmentation consists of applying geometric transformations (rotation, scaling and flipping) to the segmented images to obtain an additional variation which increases the number of images and diversity of the dataset allowing for better model performance and greater generalization to various tumor shapes and orientations.

3.5 Feature extraction

Once training samples are augmented the next step is to extract features from the augmented tumor regions which provide useful information for creating informative texture patterns from the augmented samples. The input is p_f for feature extraction of brain tumor detection. These texture patterns are extracted using two different methods GBP and CLBP. GBP captures both global texture features and Local texture features that can be used to create detailed radiomic features describing the shape and intensity and micro texture of the tumors. The features extracted from the tumors are used to accurately classify the tumor and predict the survival of cancer patients at a later stage in the model.

Global binary pattern

The GBP descriptor is a reliable means of obtaining texture information from an image. The GBP [17] descriptor assigns a binary label to each pixel of the image thus allowing for the image to be divided into uniform cells. Due to its straightforward nature GBP creates a very high dimensional feature space which is useful in many different types of applications. Because it is based on the concept of texture GPB is an essential tool in many computer vision applications including the classification of textured images and the removal of backgrounds from images.

$$g_3 = \sum \varepsilon\left(\left\| J_b(m,n,o) - J_C(m,n,o) \right\| + \sum_{e=1}^{p} \varepsilon(m_e,n,o) 2^{-e} \right) \quad (1)$$

In the above equation (1), g_3 is the GBP feature, $J_b(m,n,o), J_C(m,n,o)$ are the intensity values of selected pixel pairs, ε represents the binary threshold function, m_e denotes the pixel index, q is the total number of pixel and 2^{-e} denotes the weighting factor.

Completed Local Binary Pattern

The CLBP [18] is a value added modification of Local Binary Pattern (LBP) which captures richer texture details than LBP because it uses 3 components the center pixel value the sign difference and the magnitude difference. When these 3 elements are combined together get a more complete representation of texture and improved discrimination between textures therefore allowing it to be used more effectively for tasks such as texture analysis and image classification.

$$CLBP\_Z(h_z) = t(h_z - s) \quad (2)$$

In equation (2) h_z is the intensity of center pixel, s is the threshold value, t is the threshold function and $CLBP\_Z(h_z)$ the center pixel component.

$$CLBP\_Y(h_z)=\sum_{a=0}^{q-1} t(h_a-h_z)2^a \quad (3)$$

In equation (3), h_a is the intensity of neighboring pixel a, q denotes the total number of neighbors, 2^a denotes the sign difference between center and neighbor and $CLBP\_Y(h_z)$ represents the sign component.

$$CLBP\_X(h_z)=\sum_{a=0}^{q-1} t(n_a-z)2^a \quad (4)$$

In equation (4) $CLBP\_X(h_z)$ represents the magnitude difference, n_a denotes the magnitude difference between center and neighbor and z is the average of magnitudes.

3.6 Classification

After extracting the radiomic features the methodology moved to classification using a proposed model structurally and functionally based on SEGE-Net. $CLBP\_X(h_z)$ is taken as the input for classification of brain tumor. Specifically it utilized the EfficientNet architecture for learning high level deep features and the SE-GNN architecture for capturing the relationship between radiomic and deep representations. The combination of these two strengths of the SEGE-Net model allows for classification of tumors into glioma, meningioma or pituitary tumor and produces an understandable rationale through various methods such as important nodes or the dependency of features to assist clinicians with interpreting the basis of the model's predictions.

EfficientNet

The EfficientNet [19] is a series of CNN models that utilize a unique method called compound scaling to create high performing networks with less overall parameter use than previous methods. Compound scaling involved achieving a balance between a networks depth, width and resolution using a single scaling factor. EfficientNet is able to provide a powerful yet lightweight solution to image analysis tasks.

$$a=\alpha^{\phi}, b=\beta^{\phi}, c=\gamma^{\phi} \quad (5)$$

$$\alpha.\beta^2.\gamma^2 \approx 2 \quad (6)$$

In the above equation (5) a denotes the depth of the network, b denotes the width of the network, c denotes the input image and ϕ represents the scaling coefficient.

SE-GNN

SE-GNN uses the predictive power of GNN with intrinsic interpretability. The model uses an explanation extractor to map the input graph to a relevant sub graph that can be classified for prediction [20].

$$x(G)=z(y(G)) \quad (7)$$

In the above equation (7) $y(G)$ denotes the extractor, G is the input graph, output sub graph $S \subseteq G$ contain the most relevant edges and nodes for prediction and $z(S)$ denotes the final classifier. Using a thresholding or top-K approach the extractor assigns one edge or one node relevance scores to ultimately yield a sub graph. SE-GNN is trained either under sparsity or the Information Bottleneck objective so that the resulting extracted sub graph provides adequate information for making accurate predictions. SE-GNN therefore provide greater transparency into their predictions along with a constrained set of parameters resulting in improved performance as compared to traditional methods of graph based decision making, making it an attractive candidate for clinical applications such as classifying brain tumors. The proposed framework comprises two main components EfficientNet as the extraction method of deep features and SE-GNN a self-explainable GNN to build relationships between features and give predicted classifications and prognoses with explanations. Together create SEGE-Net a model that can accurately classify and perform prognosis on brain tumors in an explainable manner. The Self-Explainable Graph EfficientNet Framework architecture is displayed in Figure 3.

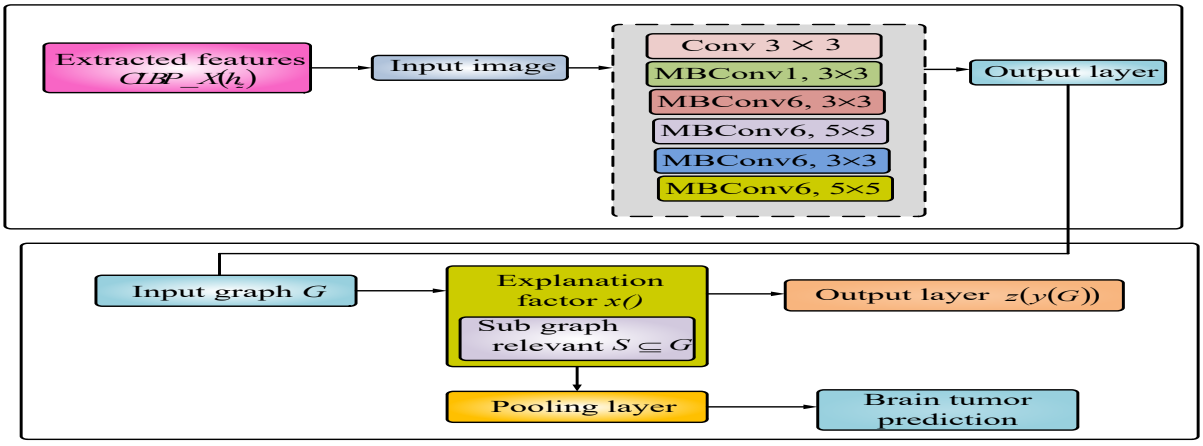


Figure 3 Proposed SEGE-Net model

3.7 Survival analysis

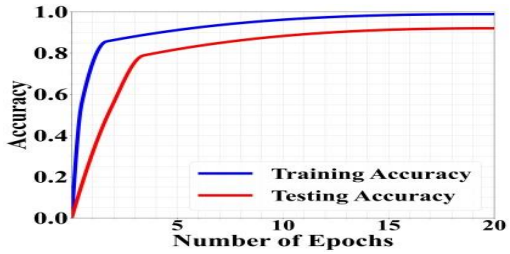
After determining the categories the framework can now classify patients based on its imaging results through DeepSurv survival prediction. The input of survival analysis is $x(G)$. From the imaging features associated with each category as well as the results of the classification DeepSurv is able to determine a risk score for each patient and the likelihood of their survival. This models how certain characteristics of a tumor affect the outcomes of patients providing a vital piece of information for clinical decision making and long term treatment strategies.

DeepSurv

DeepSurv is an advanced deep learning technique for analyzing how well patients are doing and provides a way to understand the outcome of events. It uses each of the patient's own covariates and inputs them into the model to predict how at risk the patient is. The strength of DeepSurv is that it can model nonlinear relationships between variables and outcomes and develop an individualized Survival Probability Curve for each patient giving the ability for DeepSurv to estimate risk on an individual basis. Finally the output obtained in survival analysis is $F(s)$.

4. Results and discussion

Using the BRATS 2020 dataset and Brain Tumor MRI dataset, SEGE-Net outperforms current techniques in segmentation, classification and survival prediction with greater accuracy, AUC and concordance index. The performance of this framework also confirms its applicability in a clinical context through the improvements achieved when tested on the BRATS 2020. The setup includes an Intel Core-i7 with 32GB of RAM, 1TB SSD and high speed internet running Windows 11, Python 3.12 and TensorFlow, PyTorch and Scikit-Learn. The federated and computed services using Google support communication and orchestration of federated models and patient dataset management using PostgreSQL.



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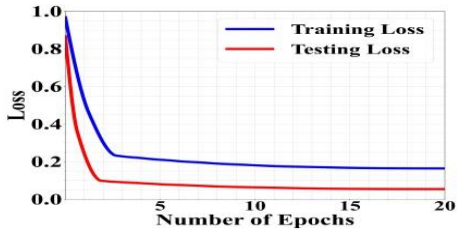
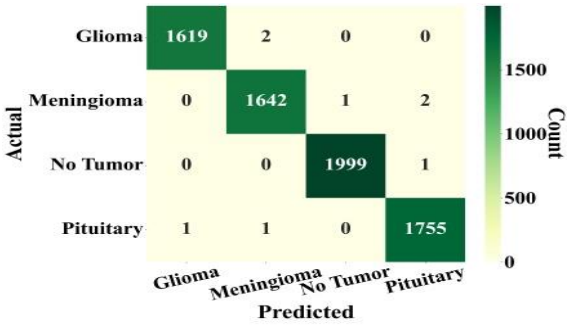


(b)

Figure 4 shows the accuracy and loss of training and testing. Both Training and Testing Accuracy continues to rise with Epochs until plateauing which indicates that the Model is learning effectively and Generalizing well. While Training Accuracy remains slightly above testing accuracy it doesn't have much over fitting. Training and Testing Loss drop quickly and converge as well. This confirms that the Model has been optimized in a Stable manner.



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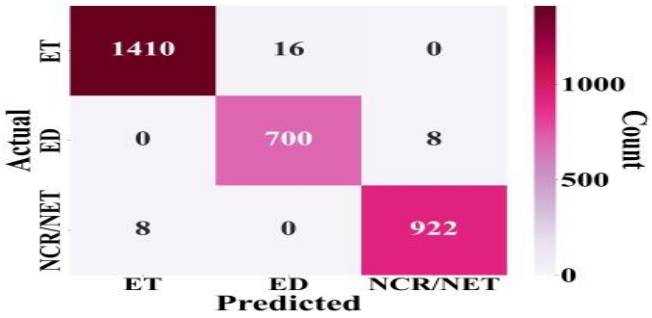
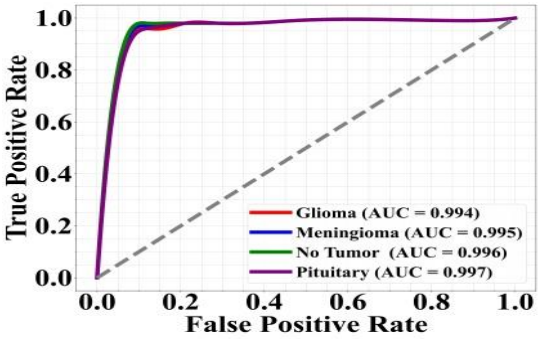


(b)

Figure 5 Confusion matrix

Figure 5 shows the confusion matrices which demonstrate high classification accuracy since most of the samples were correctly classified. There were only minimal instances where samples were misclassified into other classes, indicating very high separation between classes. These results suggest that both the accuracy of the classification is high and that the model produces reliable classifications.



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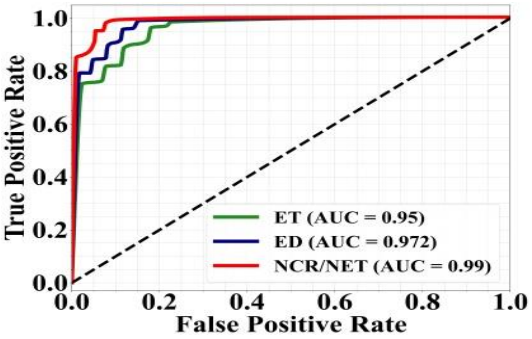
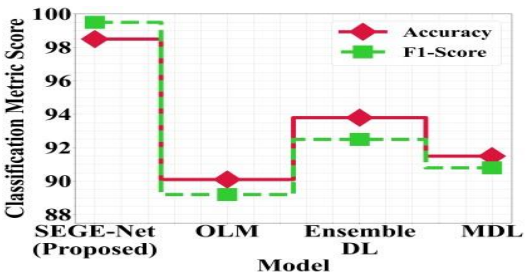


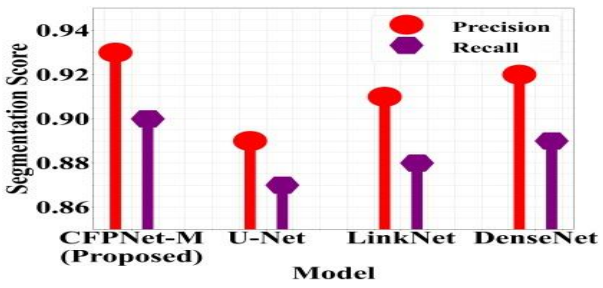
(b)

Figure 6 ROC curve

Figure 6 shows the ROC curves, the model performs well at achieving high true positives and low false positives for each of the four classes. The ROC curves are all situated near the top left corner of the graph which indicates a good classification ability based on both the high area under the curves (AUC) value and a strong ability to discriminate between categories as shown by its strong predictive ability.



(a)



(b)

Figure 7 Classification and segmentation

Classification and segmentation performance results from several different models are compared in this figure 7. The classification results show that SEGE-Net achieves the highest accuracy and F1-score while CFPNet-M has excellent precision and recall in segmentation analysis. The data presented also show how well the new models perform compared to current technologies.

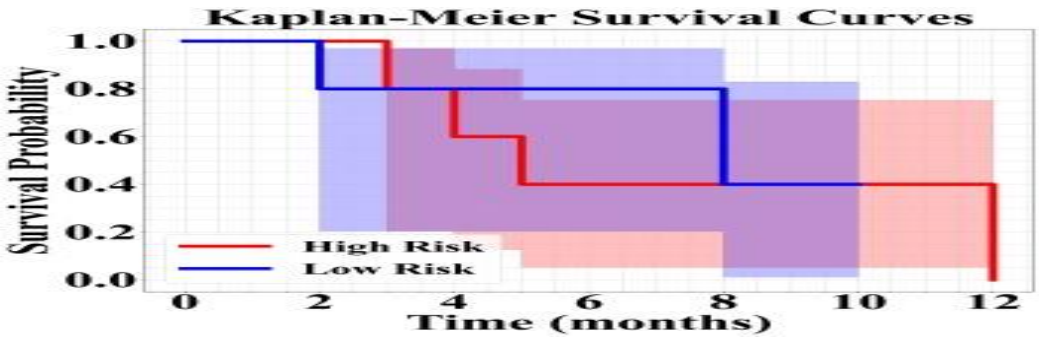


Figure 8 Kaplan-Meier survival curves

Figure 8 shows the Kaplan-Meier survival curves demonstrate that there is a marked difference in survival probabilities of patients grouped into two categories; High-Risk and Low-Risk. The high-risk patient group reaches their lowest survival probability at a faster rate than the low-risk patient group the model provides an accurate way to identify and separate the two categories of patients based on their survival probabilities.

4.1 Ablation study

Table 1 shows the classification of existing and proposed method. The proposed SEGE-Net produces the highest results in terms of classification accuracy and F1 score when compared to any other methods such as Optimized Learning Machine (OLM) [13], Ensemble DL [9] and Multimodal Deep Learning (MDL) [11]. Additionally, using an efficient network such as EfficientNet with the SE-GNN helps to provide better results overall and class balance than previous methods.

Table 1 Ablation study

Methods	**Classification**	
	Accuracy (%)	**F1-score (%)**
OLM	86.3	72
MDL	81.2	86
OLM+MDL	87.5	75
SE-GNN	85.1	78
EfficientNet	83.6	86
SEGE-Net (Proposed EfficientNet + SE-GNN)	93.5	93

5. Conclusions

The combination of segmentation, interpretable classification and survival modeling in SEGE-Net produces a more precise diagnosis of brain tumors and a more accurate prediction of brain tumor patient outcome. The results of SEGE-Net demonstrated its robustness and important clinical significance across four public benchmark datasets. Future work will extend validation to larger multi-center datasets and will include the development of an integrated system that uses clinical and genomic data to improve predictive performance and real-world application.

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