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3D Deep Learning-Based Brain Tumor Segmentation, Glioma Classification, and Survival Prediction

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***Abstract*—This paper proposes an integrated 3D deep learning framework for brain tumor analysis using the BraTS 2020 dataset. This begins with preprocessing of multimodal MRI scans (T1, T1CE, T2, and FLAIR), including skull stripping, Z-score normalization, and image resizing. Tumor segmentation was performed using a custom 3D U-Net model trained to predict whole-tumor (WT), tumor core (TC), and enhancing tumor (ET) regions. For tumor-type classification (HGG vs. LGG), a pretrained 3D DenseNet121 model was employed with stratified K-fold cross-validation. Segmentation masks were used to extract the volumetric features of WT, TC, and ET. These tumor features, combined with age and MRI inputs, were used for survival prediction using 3D DenseNet regression analysis. The evaluation included the Dice score for segmentation, accuracy and AUC for classification, and MAE, RMSE, and R^2 for survival analysis. Results showed improved performance when the tumor features were integrated. This paper demonstrates a robust multitask pipeline capable of capturing tumor heterogeneity and enhancing predictive accuracy. The framework offers an automated and reproducible approach that can reduce inter-observer variability and assist clinical decision-making. Its modular design allows for future integration of additional clinical or genomic data, paving the way for personalized neuro-oncology applications.**

***Index Terms*—3D U-Net, BraTS 2020, Brain Tumor, Classification, DenseNet121, HGG, LGG, Segmentation, Stratified K-fold Cross Validation, Survival Prediction.**

I. INTRODUCTION

Brain tumors, especially gliomas, are among the most critical and fatal forms of cancer, requiring timely and accurate diagnoses for effective treatment strategies. Manual interpretation of brain MRI scans is labor-intensive, prone to human error, and lacks consistency among radiologists. To address these limitations, automated deep learning techniques have emerged as promising solutions in neuro-oncology. This study introduces a unified 3D deep learning framework for brain-tumor analysis using the BraTS 2020 dataset. The approach begins with preprocessing multimodal MRI sequences (T1, T1CE, T2, and FLAIR) through skull stripping, Z-score normalization, and resizing to achieve a uniform shape.

Tumor segmentation was performed using a custom 3D U-Net model that predicts three tumor subregions: the whole tumor (WT), tumor core (TC), and enhancing tumor (ET). For tumor type classification, a pretrained 3D DenseNet121 model was used to distinguish between High-Grade Glioma (HGG) and Low-Grade Glioma (LGG) using stratified K-fold validation. The segmentation outputs were then used to extract the volumetric features of the WT, TC, and ET. These features, along with patient age and MRI data, were used to predict overall survival using a 3D regression model.

The evaluation metrics included the Dice score for segmentation, accuracy, and AUC for classification, as well as the MAE, RMSE, and R^2 for survival prediction. The proposed pipeline demonstrated that integrating tumor features significantly improved prediction performance. This study presents a deep learning-based 3D pipeline for brain tumor analysis using the BraTS 2020 dataset.

The system performs three major tasks:

Task 1: Tumor Segmentation

- A custom 3D U-Net model was used to segment the three tumor subregions

- Whole Tumor (WT)
- Tumor Core (TC)
- Enhancing Tumor (ET)

Task 2: Tumor Type Classification
- A pretrained 3D DenseNet121 was used to classify gliomas as
- High-Grade Glioma (HGG)
- Low-Grade Glioma (LGG)
- Stratified K-Fold cross-validation ensures balanced and robust training.

Task 3: Survival Prediction
- Tumor region volumes (WT, TC, and ET), patient age, and MRI features were used.
- A 3D regression model was used to predict the survival days of patients with HGG.

II. LITERATURE REVIEW

Brain tumor detection using MRI is an essential task in neuro-oncology because early recognition and accurate localization strongly influence treatment success. Early methods such as Support Vector Machines (SVM), Random Forests, and k-Nearest Neighbors (k-NN) depended on handcrafted features and could not analyze volumetric data effectively, which limited accuracy.
Deep learning methods, especially Convolutional Neural Networks (CNNs), improved this field by learning directly from volumetric scans. Saradha S. et al. [1] compared ResNet50, VGG19, and MobileNet, reporting that ResNet50 achieved the highest accuracy, while MobileNet was faster and more efficient. For segmentation, the U-Net architecture became widely used due to its encoder–decoder design and skip connections. Bhargav Mallampati et al. [2] improved performance by combining 3D U-Net features with hybrid classifiers (KNN + GBC), reaching 71% accuracy, which surpassed 2D U-Net–based models. Sunita Agarwala et al. [3] developed an Attention U-Net that used gating mechanisms to improve boundary detection, achieving Dice scores of 0.92 for Whole Tumor (WT), 0.87 for Tumor Core (TC), and 0.78 for Enhancing Tumor (ET) on the BraTS 2020 dataset. To improve both segmentation and classification, hybrid approaches have been studied. Anshul Ghanshala et al. [4] presented a transposed 3D CNN with skip connections, which could also support survival prediction. Because labeled datasets are limited, transfer learning has become a key solution. Noby Mathew et al. [5] applied ResGANet with transfer learning and showed deployment on cloud platforms with MLOps. Similarly, Rekha Sharmily et al. [6] found that pretrained models combined with domain-specific training improved detection and classification accuracy.

Recent work has focused on newer architectures. K. Srujan Raju et al. [7] tested ConvLSTM-based models, which capture spatio-temporal patterns in MRI scans for segmentation and classification. R. Nidya et al. [8] proposed multi-channel CNN (MCNN) models that used multiple MRI modalities to strengthen diagnostic precision. Tanvir Kaur et al. [9] applied YOLO-NAS–based techniques for fast brain tumor screening, showing the potential of advanced object detection frameworks for real-time applications.
Overall, deep learning models have transformed brain tumor detection by supporting full pipelines of segmentation, classification, and survival prediction.

3D U-Net and DenseNet3D remain strong performers on BraTS datasets. Hybrid models, ensemble classifiers, and transfer learning continue to expand accuracy and clinical relevance. Future improvements are likely to come from combining multimodal MRI data with clinical information to improve survival prediction. Automated pipelines such as transposed 3D CNN with U-Net skip connections [4], hybrid classifiers like KNN + GBC [2], and ensemble methods such as ConvLSTM [7] highlight the growing value of integrated approaches for intelligent tumor analysis.

Recent trends also emphasize the integration of radiomic features with deep learning outputs to improve prognostic assessment. Combining AI predictions with patient clinical history can further personalize treatment strategies. Furthermore, real-time inference models are being developed for intraoperative assistance, reducing decision-making time. These advancements underline the potential of AI-driven systems to enhance both diagnostic accuracy and clinical workflow efficiency.

III. PROBLEM STATEMENT

Accurate detection and analysis of brain tumors are vital in improving treatment outcomes for patients diagnosed with gliomas. However, traditional methods that rely on manual interpretation of MRI scans are often time-consuming and subject to human variability. Moreover, differentiating between high-grade and low-grade gliomas and estimating patient survival remain complex due to heterogeneous tumor characteristics and limited availability of structured clinical data. These challenges highlight the need for an automated multitasking system that can not only perform precise tumor segmentation but also classify tumor grades and predict survival outcomes. This study proposes a unified deep learning framework that leverages volumetric MRI data and employs 3D convolutional neural networks for end-to-end tumor analysis, aiming to support clinical decision making in neuro-oncology.

IV. PROPOSED METHOD

In this paper, we propose a multistage deep learning-based approach for the automated detection, segmentation, classification, and survival prediction of brain tumors using enhanced 3D MRI scans from the BraTS 2020 dataset. The method begins with the application of a 3D U-Net architecture for accurate segmentation of brain tumors. This model takes advantage of full volumetric MRI data across four modalities (T1, T1CE, T2, and FLAIR) to segment tumor subregions, including the Whole Tumor (WT), Tumor Core (TC), and Enhancing Tumor (ET). Once the tumor is localized, a 3D DenseNet121 convolutional neural network is used to classify the tumor as High-Grade Glioma (HGG) or Low-Grade Glioma (LGG).This classification model was trained using stratified K-fold cross-validation to ensure robustness and reduce bias due to data imbalance. In the final stage, a regression model based on 3D DenseNet121 was employed to predict the survival days of patients, focusing on high-grade glioma cases. All models leverage the spatial information contained in the 3D volumes, enabling more context-aware decision-making. The entire pipeline was trained and evaluated using powerful A100 GPUs on Google Colab, ensuring high computational efficiency.

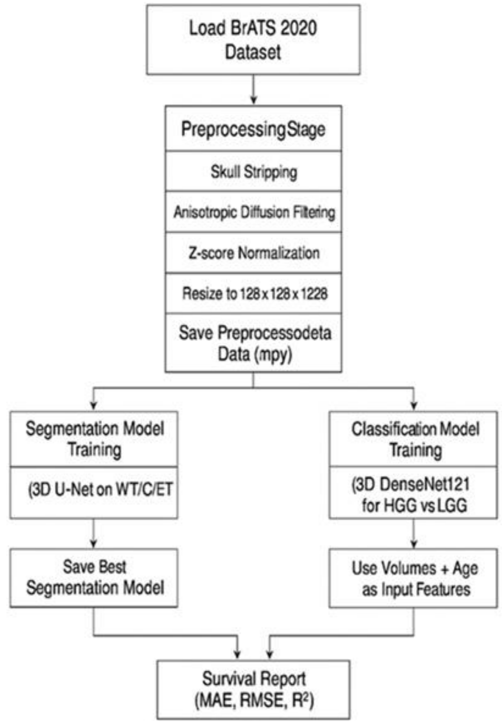


Fig. Flowchart of Proposed Method

V. METHODOLOGY

1. DATA COLLECTION: BraTS(2020)
This study utilizes the BraTS 2020 (Brain Tumor Segmentation) dataset, which provides multimodal MRI scans along with tumor type and survival information. The training set consists of 369 patients, each with four MRI modalities: FLAIR, T1, T1CE, and T2. For these cases, ground truth segmentation masks are available, and tumors are labeled as either High-Grade Glioma (HGG) or Low-Grade Glioma (LGG). The validation set comprises 125 patients, which do not include segmentation masks and are used solely for blind evaluation. For HGG patients in the dataset, additional clinical information such as age, resection status, and survival duration is provided, although this information is only available for a subset of cases.
2. DATA FORMATE: All MRI scans in the BraTS 2020 dataset are provided in NIfTI (.nii.gz) format, with each volume originally having a spatial resolution of 240 × 240 × 155 voxels. For every patient, a dedicated folder contains the four MRI modalities, a segmentation mask (available for

training cases), the tumor type label indicating HGG or LGG, and, for HGG patients, clinical information such as age, resection status, and survival duration when available.

3. DATA PREPROCESSING:

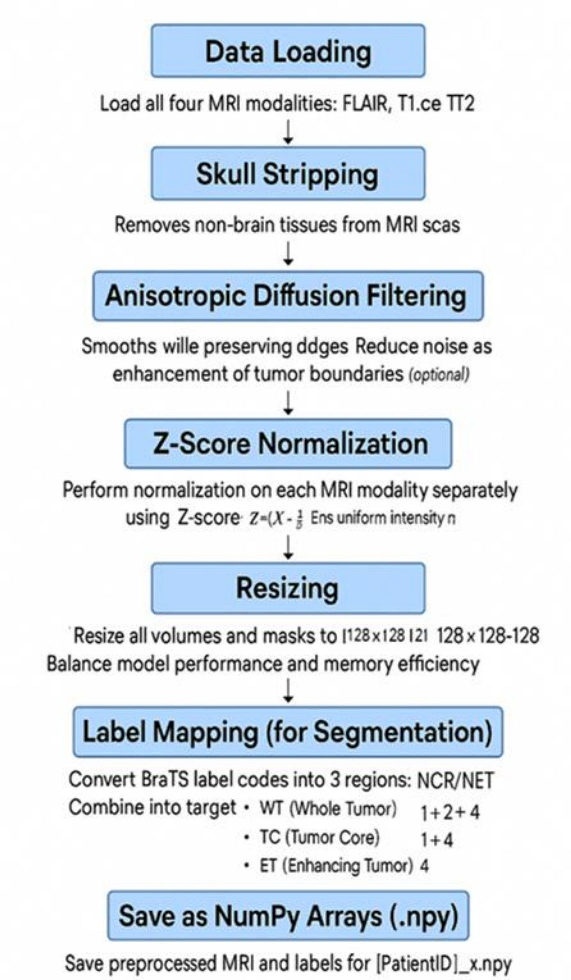


Fig. Data Preprocessing

The input to the models consists of four MRI modalities: FLAIR, T1, T1CE, and T2. Each volume undergoes a series of preprocessing steps, including skull stripping to remove non-brain tissues, anisotropic diffusion filtering to reduce noise while preserving edges, and Z-score normalization applied separately to each modality to standardize intensity values. All images are then resized to 128 × 128 × 128 voxels and stored as NumPy arrays to enable faster and more efficient training. Additionally, the segmentation masks are reformatted into three distinct tumor subregions: Whole Tumor (WT), Tumor Core (TC), and Enhancing Tumor (ET) for more detailed analysis.

4. TUMOR SEGMENTATION USING 3D U-NET:

A custom 3D U-Net model was developed to automatically segment brain tumor subregions, including Whole Tumor (WT), Tumor Core (TC), and Enhancing Tumor (ET). The network was trained using the Dice Loss function and evaluated with the Dice Similarity Coefficient (DSC) to quantify segmentation accuracy. Skip connections between corresponding layers of the encoder and decoder preserve spatial details throughout the network. The model takes a 3D MRI volume with four input channels (FLAIR, T1, T1CE, and T2) of size 4 × 128 × 128 × 128. The encoder (contracting path) consists of repeated blocks of 3D convolution → batch normalization → ReLU → 3D max pooling, which progressively extract hierarchical features while reducing spatial dimensions and doubling the number of feature channels at each level.

The bottleneck captures high-level volumetric representations through consecutive 3D convolutions. In the decoder (expanding path), 3D transposed convolutions perform upsampling, and features from the encoder are concatenated via skip connections, followed by convolutional operations to reconstruct spatial details. The output layer uses a 1×1×1 3D convolution to produce a three-channel segmentation map corresponding to WT, TC, and ET. This architecture captures spatial context across all three dimensions, enables voxel-level segmentation with high precision, and is well-suited for small medical datasets with appropriate data augmentation.

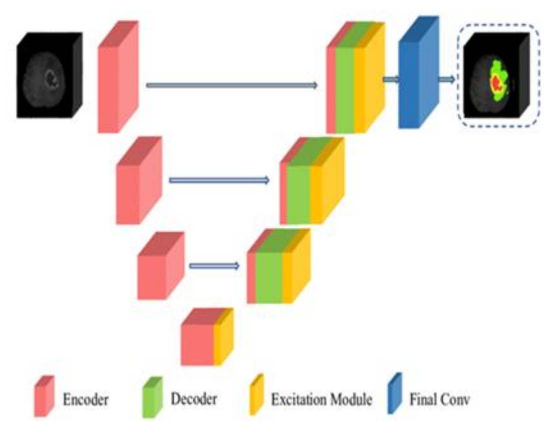


Fig. Architecture of 3D U-Net

5.TUMOR CLASSIFICATION (HGG/LGG) USING 3D DENSENET121:

To classify tumors as High-Grade Glioma (HGG) or Low-Grade Glioma (LGG), a 3D DenseNet121 network was adapted and fine-tuned for this binary task. The model processes preprocessed 3D MRI scans with four channels—FLAIR, T1, T1CE, and T2—each of size 4 × 128 × 128 × 128, and produces a predicted tumor grade. Training was performed using cross-entropy loss, and the model's performance was assessed using accuracy, precision, recall, F1-score, and ROC-AUC metrics. The network architecture starts with a 3D max-pooling layer for initial downsampling, followed by four dense blocks containing 6, 12, 24, and 16 layers respectively. Within each dense layer, batch normalization, ReLU activation, and 1×1×1 and 3×3×3 convolutions are applied, with dense connections facilitating feature reuse and smoother gradient propagation. Transition layers, consisting of 1×1×1 convolutions and 3D average pooling, reduce the feature map dimensions between dense blocks. Finally, global average pooling converts the 3D feature maps into a 1D vector, which is input to a fully connected layer with two outputs representing HGG and LGG, followed by softmax activation. This design efficiently extracts both textural and structural features from volumetric MRI data, providing robust performance for glioma grading

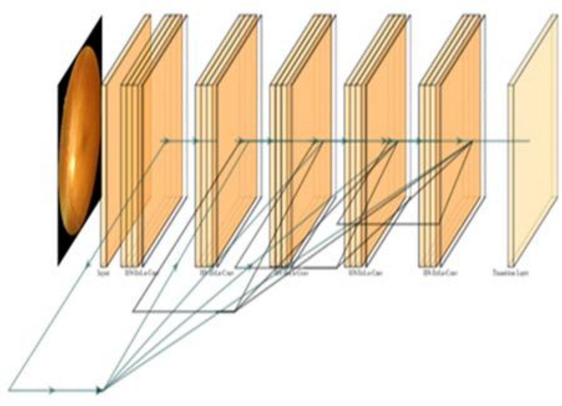


Fig. DenseNet121

6. SURVIVAL DAYS PREDICTION (FOR HGG PATIENTS):

For patients with High-Grade Glioma (HGG), survival prediction was formulated as a regression problem. The model leveraged a combination of features, including MRI-based embeddings extracted from the DenseNet network, volumetric measurements of tumor subregions—Whole Tumor (WT), Tumor Core (TC), and Enhancing Tumor (ET)—and relevant clinical information such as patient age. These features were input into a regression model to estimate the survival duration in

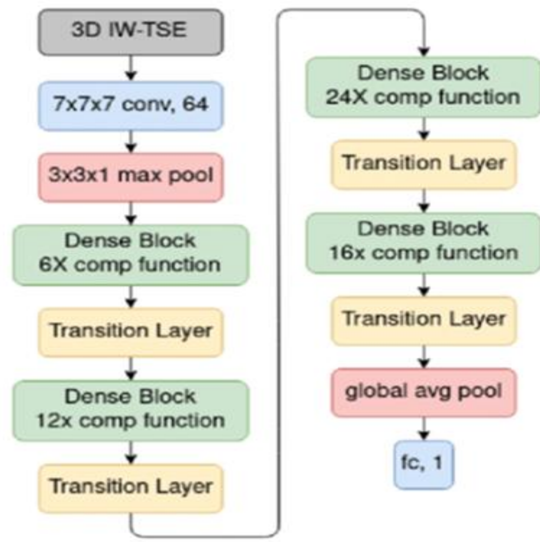


Fig. Architecture DenseNet121

days for each patient. Model performance was assessed using standard regression metrics, including Mean Absolute Error (MAE), Root Mean Square Error (RMSE), and the coefficient of determination (R^2), providing a comprehensive evaluation of predictive accuracy.

7. STRATIFIED K-FOLD CROSS VALIDATION:

All models in this study were trained and assessed using stratified K-fold cross-validation with k = 5 to ensure that each fold maintained a balanced proportion of HGG and LGG samples. This approach helps to prevent bias and provides a more reliable estimate of model performance. The final model for each task was selected based on the average validation performance across all five folds, ensuring optimal generalization and robustness.

VI. RESULTS

1. SEGMENTATION RESULTS:

The proposed model achieved the best Dice score of 79.38% at epoch 19, with consistently high accuracy (>99%) and sensitivity (>99%), demonstrating robust tumor detection. IoU and Dice values improved steadily across epochs, confirming effective learning of tumor boundaries. Specificity, which was initially low, improved to around 80–90%, indicating better discrimination of non-tumor regions as training progressed.

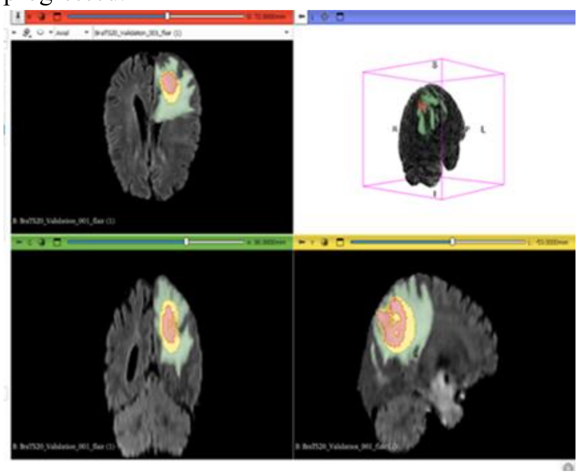
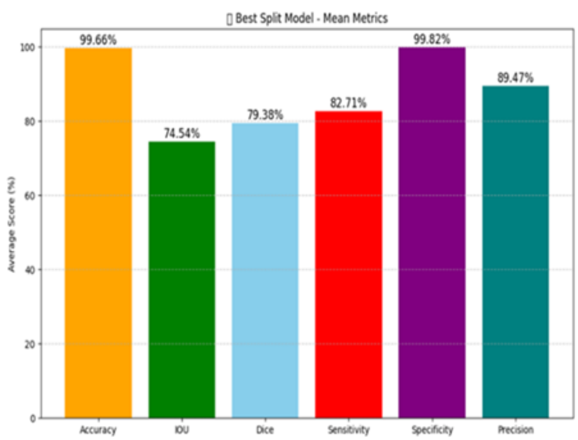


Fig. 3D Visualization of Tumor



Precision also increased over time, reducing false positives. Overall, the framework proved reliable for brain tumor segmentation, though further optimization is needed to enhance specificity.

2. CLASSIFICATION RESULTS:

proposed framework achieved a mean accuracy of 78.60% ± 2.43%, demonstrating consistent performance across all folds. A high mean precision of 0.8875 indicates the model effectively reduces false positives, while the mean recall of 0.8465 shows reliable tumor detection. The mean F1-score of 0.8619 confirms a well-balanced performance between precision and recall. Performance variations across folds reflect inherent heterogeneity in the dataset, with some splits favoring precision and others recall. across all folds. A high mean precision of 0.8875 indicates the model effectively reduces false positives, while the mean recall of 0.8465 shows reliable tumor detection. The mean F1-score of 0.8619 confirms a well-balanced performance between precision and recall. Performance variations across folds reflect inherent heterogeneity in the dataset, with some splits favoring precision and others recall. Overall, the system proves effective for 3D MRI-based tumor classification tasks. The model maintained stable learning patterns across different patient subsets, indicating robustness. Early stopping and careful training helped prevent overfitting, ensuring generalizable results. Integration of additional imaging features could further enhance The predictive accuracy. Future work may also explore advanced architectures to improve recall in challenging case

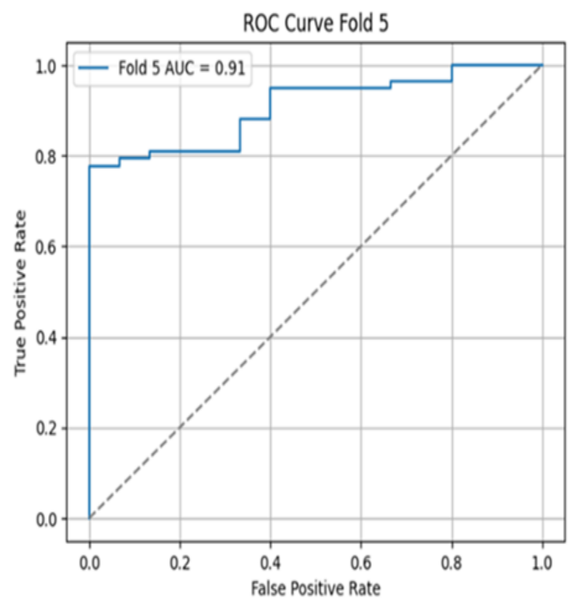
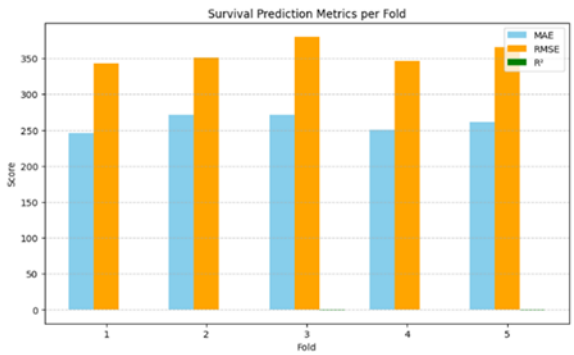


Fig. ROC Curve

3. SURVIVAL DAYS PREDICTION RESULTS:

The multi-fold survival prediction using all resections achieved moderate performance, with a mean MAE of 260.23 days and an RMSE of 357.34 days. R^2 scores were low, averaging around -0.02, indicating limited variance explanation by the model. Training losses generally decreased, but some folds showed fluctuations in validation loss, suggesting variability across data splits. Early stopping helped prevent overfitting, with the best models saved for each fold. Overall, while the model captures general survival trends, further feature refinement or advanced architectures may improve predictive accuracy.



VII. CONCLUSION

This paper introduces a robust multitask deep learning framework for brain tumor analysis, encompassing segmentation, classification, and survival prediction using the BraTS 2020 dataset. A 3D U-Net demonstrated precise tumor segmentation, while a 3D DenseNet121 effectively distinguished high-grade gliomas (HGG) from low-grade gliomas (LGG), highlighting the advantages of volumetric learning in neuroimaging. Although survival prediction remains challenging due to limited and heterogeneous clinical data, integrating tumor volumes, MRI-derived features, and patient age provides a solid foundation for prognostic modelling. The framework enhances diagnostic accuracy, streamlines clinical workflows, and supports informed decision-making in neuro-oncology. By combining imaging biomarkers with clinical parameters, the system offers a more comprehensive assessment of patient status and disease progression. Its modular design allows seamless integration with additional data modalities, such as genomic, molecular, or treatment response information, potentially improving predictive power.
The model's automated and reproducible outputs reduce inter-observer variability, fostering more consistent evaluations. With further refinement and validation across diverse datasets, this framework could pave the way for personalized treatment planning and optimized therapeutic strategies. Ultimately, such advancements bring the integration of artificial intelligence closer to real-world applications in precision medicine, contributing to better patient outcomes and more effective management of gliomas.

VIII. FUTURE WORK

future work should aim to enhance the clinical relevance and performance of the framework by incorporating additional patient-specific features, including genetic markers, treatment history, and comorbidities, to improve survival prediction accuracy. Model optimization for deployment on low-resource hardware, reducing reliance on high-end GPUs like the A100, will make the system more accessible in diverse clinical settings. Integrating explainable AI (XAI) techniques can provide insights into model decisions, increasing transparency and clinician trust. Expanding the pipeline to include other brain tumor types or multi-organ imaging datasets can improve generalization and robustness. Adapting the framework for real-time inference and seamless integration into hospital infrastructure will facilitate practical clinical use. Leveraging longitudinal patient imaging and clinical records can support dynamic monitoring of tumor progression and treatment response. Automated quality control procedures should be developed to ensure consistent and reliable predictions across varying imaging protocols and modalities. Additionally, future research could explore multimodal fusion of MRI, PET, and CT data to enhance diagnostic and prognostic performance. Incorporating federated learning approaches could enable collaborative training across institutions while preserving patient privacy. Finally, continuous validation on large, multi-center datasets will be essential to ensure clinical safety, reliability, and scalability of the system for precision neuro-oncology applications.

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