NeuroScan AI: Deep Learning for Brain Tumor Analysis

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Abstract—**The diagnosis of brain tumors is required for treatment decisions, therapy planning and survival prognosis of patients and it relies heavily on magnetic resonance imaging. Manual identification, segmentation and classification of tumors is difficult, time-consuming, and often not consistent among clinicians. The proposed NeuroScan AI system leverages patient information and multi-modal MRI scans for automatically segmentation and classification of tumors, calculation of tumor volume and survival prediction. A 3D UNet CNN is used for segmentation of the tumors while classification between HGG and LGG is performed using a Random Forest classifier. The segmentation network is provided with a number of multi-modal MRI scans (FLAIR, T1CE, T2), after they have been pre-processed (e.g. 3D cropping and normalization). Different tumor regions like tumor core, edema and enhancing tumor are quantified in cubic centimeters (using voxel spacing). Based on tumor features and age, the prediction of survival is calculated. The developed system is coded in Python with TensorFlow, Keras and scikit-learn and it has a Node.js+Express back-end and React interface, allowing real time interactions from patients and doctors.**

Index Terms— Brain Tumor Segmentation, 3D U-Net, MRI, Glioma Classification, Random Forest, Tumor Volume Estimation, Survival Prediction, Deep Learning.

I.INTRODUCTION

One of the most critical neurological disorders is brain tumor and an early diagnosis is required for an efficient and effective treatment planning and survival prediction. Since MRI provides a superior soft-tissue contrast and is able to scan the human body non-invasively, it becomes a very popular imaging technique in the detection of brain tumors. The manual segmentation of the brain tumor in the MR images takes a lot of time and causes inconsistency due to observer dependency which makes the computer- aided diagnosis system an essential need. [1]

Initial brain tumor diagnosis strategies made use of traditional image processing techniques like thresholding, clustering, region growing and feature extraction using handcrafted features [2]. Later with the development of machine learning, classification approaches like Support Vector Machines, k Nearest Neighbors, and Random Forest were developed to provide different levels of tumor grading [3]. Though these approaches offered higher classification rates, their performance was greatly dependent on human extracted features and were not generalizable across different MR datasets [4].

With the recent advent of deep learning in the medical imaging analysis, it has become an outstanding method to learn features automatically directly from imaging data. Convolutional Neural Networks have shown impressive performance in the task of medical image classification and segmentation [5] and the Fully Convolutional Networks are the ones that allow end-to-end pixel-level predictions for the biomedical segmentation task [6]. A new structure named U- Net [7] was developed which uses an encoder-decoder network architecture that retains spatial information using skip connection.

The development of volumetrically focused deep learning introduced 3D CNN which is an approach to learn contextual spatial features across different MR slices [8]. 3D U-Net showed significant and efficient performance in segmentation of different tumor subregions (tumor core, edema, enhancing tumor regions) [9]. Various well-known MR images segmentation datasets were introduced like Multimodal Brain Tumor Image Segmentation Benchmark (BRATS) for evaluating the segmentation methods in glioma [10].

Many works are now focused on integrating the segmented output of tumor with tumor grading and survival prediction systems. Volumetric features are successfully extracted from segmented regions and then classified into High-Grade Glioma (HGG) and Low-Grade Glioma (LGG) using ensemble classifiers like Random Forest [11]. Some works showed promising results in survival prediction models where tumor morphology and clinical information were used [12].

The limitations of previous studies have been addressed by research work, but most of the work done till now focused only on one specific task either segmentation or classification alone and no comprehensive pipeline exists which can take MRI scans as input and provide a tumor classification, volume and survival prediction as output which can be used directly in the clinic. Moreover, many of the work proposed are only research based [13]. Many of the current systems for the analysis of brain tumor data utilize a 3D encoder-decoder architecture as they employ the deep learning technique which can achieve higher accuracy in the system [14].

II. METHODOLOGY

The proposed NeuroScan AI framework performs automated brain tumor analysis through an end-to-end pipeline that processes multi-modal MRI scans and generates clinically meaningful outputs. The methodology consists of five major stages: data acquisition, preprocessing and normalization, deep learning–based segmentation, tumor feature extraction and classification and deployment pipeline.

The overall architecture of NeuroScan AI. The system is built to perform a series of operations on multimodal MRI scans with a focus to diagnose tumors, calculate the volume, grade it as High-Grade or Low-Grade Glioma and predict the survival estimate. It comprises of four broad steps which are described in detail below; image acquisition, preprocessing, tumor segmentation and analysis, and result delivery.

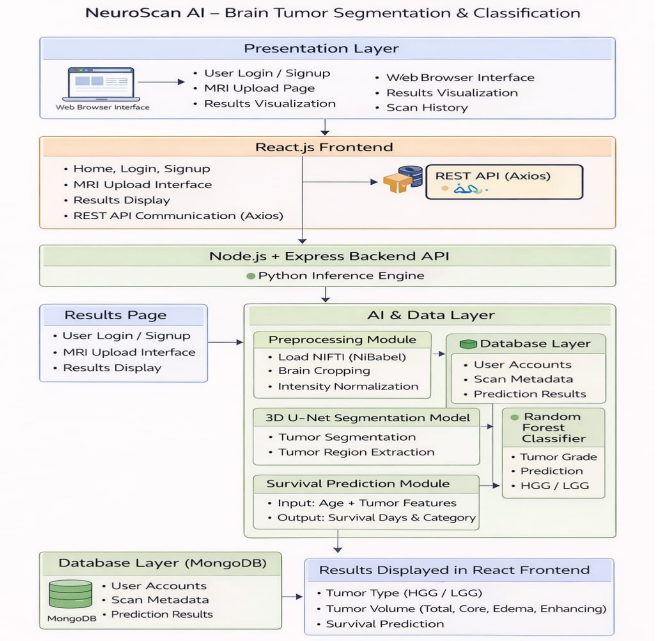


Fig.1. Architecture Diagram

A. Image Acquisition

Multimodal brain MRI volumes in NIfTI format are provided as input to the NeuroScan AI system. The model is capable of handling FLAIR, T1-weighted contrast enhanced (T1CE) and T2-weighted modalities that provide a complementary image to properly detect and segment tumors in the MRI scan. The system loads the volumes from the data and preprocesses them into volumetric format that can be fed to the neural network to perform segmented the tumor regions, three modalities are converted to multi-channel 3D tensor suitable for the CNN segmentation framework.

B. Preprocessing and Normalization

Preprocessing of MRI volumes is essential to maintain model stability of analysis in varied cases of data from different sources. The MRI images are cropped from all sides to include only the brain region and remove the redundant parts and then MinMax normalization is performed in the intensity range [0,1] for each of the modalities so as to ensure model learns from spatial information instead of being biased by image intensity values. After preprocessing, all the three modalities are fed to the 3D CNN for segmentation of the tumor region.

C. Tumor Segmentation and Analysis

The processed 3D MRI volume from preprocessing stage is fed to a 3D U-Net neural network which performs multi-class segmentation. U-Net contains the encoder and the decoder part which learns hierarchical features at various layers of neural network while encoding and then upsamples the acquired information with the use of skip connections to produce accurate segmentation masks.

The segmentation process predicts three distinct classes of tumors, background, tumor core, and enhancing and edema regions of the tumors. The predicted mask from the U-Net network is then used to calculate the total volume of tumor, and subregion volumes along with the volume calculations in cm^3 using NIfTI header's voxel spacing values to enable clinically meaningful analysis of tumor volume.

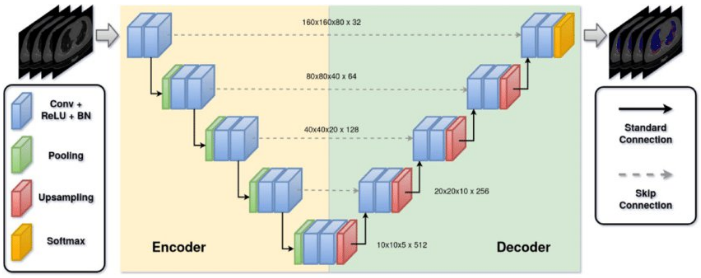


Fig.2. 3D U-Net Architecture

Random Forest classifier is then used to predict High-Grade Glioma (HGG) or Low-Grade Glioma (LGG) using the extracted features of tumor and predict the survival estimate based on tumor volume and patient's age.

D. Result Delivery

The final outputs of the pipeline consisting of segmented tumor masks, segmented tumor images, tumor grade and volume estimates and survival prediction are delivered via a backend server. The NeuroScan AI system is hosted with Node.js and Express framework on the backend to cater to the client's requests while the AI tasks are performed on the Python-based pipeline, which can be viewed through a React based frontend with an login for users to upload MRI scan and visualize the real time segmentation of tumor as overlays.

Users can observe segmentation overlays, tumor grade, tumor volume measurements and predicted survival category of the brain tumor and can take better diagnostic decisions and treatment plan accordingly.

III. PROPOSED WORK

A. Dataset

The dataset utilized in the NeuroScan AI framework comprises multi-modal brain Magnetic Resonance Imaging (MRI) volumes saved in the Neuroimaging Informatics Technology Initiative (NIfTI) format. Each patient scan includes three distinct yet important modalities: FLAIR, T1-weighted contrast-enhanced (T1CE), and T2-weighted images. The combined set of modalities provide overlapping and complementary information required for the detection and characterization of brain tumors.

The 3D volume MRIs are used in native 3D form so that the relationship of slices in 3D space is not lost. Cropping to the brain region and using Min-Max intensity normalization is done as a preprocessing step.

Final features from the segmented volumetric MRI scans—including total tumor volume, core tumor volume, edema volume, and enhancing tumor volume—are calculated using the voxel spacing from the NIfTI header and fed to the subsequent classifier.

B. Scope of Work

The NeuroScan AI system is broken down into a series of structured steps:

Requirement Analysis:

We identified a set of problems related to automated brain tumor analysis such as the challenge of finding tumors accurately, segmenting them into different sub-regions, classification of tumor type (HGG/LGG), calculation of volume, and prediction of survival rates. We then identified a deep learning architecture that is capable of processing and segmenting the volumetric MR images.

Data Preparation and Preprocessing:

The multi-modal MR images are loaded in NIfTI format, then the brain portion of MR images is extracted by cropping the volumes, and finally, the MR images are normalized using Min-Max intensity normalization technique. All the three modal MR images were stacked as channel wise to form the input tensor. The 3D convolutional neural networks were then utilized.

Model Development and Optimization:

We have designed a 3D U-Net segmentation model for tumor segmentation, and implemented a Random Forest classifier which uses the volume of tumors as features to classify between the two different types of tumors namely HGG/LGG. We have computed tumor volumes from the segmentation result and then we determined the survival estimate using a rule-based system.

Deployment and Integration:

Integration of both classification and segmentation models in the Node.js and Express backend. Furthermore, the React-based front end for the end-users to upload the MRI scans and receive the results within real-time have been implemented.

Evaluation and Validation:

Validation of the segmentation models has been done using volume measurements and comparing with the manual annotation, the classification performance is also evaluated on the set of features calculated from segmented tumor regions.

C. System Architecture

The NeuroScan AI is composed of a series of structured, multi- modal deep learning steps that convert raw MRI volumes into actionable insights in real-time. There are a total of six main components in the NeuroScan AI architecture. Here are those stages listed as input layer MRI, preprocessing module, deep learning segmentation model, feature extraction module, backend server, and output module User interface.

MRI Input Layer:

The system starts by receiving multi-modal brain MRIs in the NIfTI format. The three modalities (FLAIR, T1CE and T2) are first acquired and then aligned together to formulate a structured, multi-channel input tensor which will serve as the input to the upcoming stages of the pipeline.

Preprocessing Module:

Before feeding the volumetric MR images to the 3D segmentation model, irrelevant regions surrounding the brain are eliminated via cropping the MRI volumes. Following this, an intensity normalization technique (Min-Max) is used to normalize the voxel intensities into a common range (0-1). The 3D convolutional neural networks is then employed to segment different tumor regions.

Deep Learning Segmentation Model:

We have used a 3D U-Net architecture as a segmentation model in our framework. The encoder part consists of 3D convolution blocks that are designed to extract hierarchical features from the input. All these convolution layers are combined with pooling layers in order to decrease the dimensions of input along the length, width, and height.

The decoder part, on the other hand, mirrors the structure of the encoder and increases the dimension of input via up-sampling layers in order to construct the segmentation masks from the extracted features.

Both encoder and decoder are linked by skip connections in order to pass the low-level features of input to the decoder and this method allows in the segmentation of precise anatomical structure with appropriate gradient flow across all the layers and the encoder outputs the mask of different tumor regions (tumor core, edema, enhancing tumor, background).

Feature Extraction Module:

After segmentation the features of the tumor are extracted using the generated tumor mask. We computed the volume of each region using the amount of pixels along the length, width and height and then calculated total tumor volume, enhancing tumor volume, core tumor volume and edema tumor volume in cubic centimeters(cm^3) using voxel spacing in the NIfTI header. These volume measurements were used in subsequent parts of the model to classify the tumor type (LGG or HGG) and predict the survival rate.

Backend Processing Server:

A server using Node.js and Express frameworks handles user requests, as well as the communication between the user and the Python-based inference engine. The file upload requests, model prediction results and analysis are all managed and stored using the Mongo DB.

User Interface Output Module:

While operating the NeuroScan AI system, a user will be able to upload MRI images and view the predicted segmentation, tumor class, tumor volume, and predicted survival range on real time after all the processing is done. The results from segmentation and classification are transferred back to the server through API calls and then presented on the website interface.

The data is fed through the trained segmentation model and as the outcome a predicted segmented mask of tumors present within the brain volume are computed. These segmentation masks were then used for volume calculations of tumors, as well as they are passed to the classification model along with the other extracted tumor features to classify tumors. Patient survival is also predicted using the same features and patient's age to enhance our analysis, results are send to the backend server and to display on the interface.

The web-interface based on React allows authenticated users to submit their MR volumes along with their medical history and receive the analysis report in a real-time manner, which consists of:

- Tumor segmentation masks visualized on MRI scans,
- Tumor grade: (LGG or HGG),
- Tumor volume statistics (total, enhancing tumor, edema, core) and
- Survival prediction: a number representing the predicted survival rate of the patient.

D. Deep Learning Model

NeuroScan AI uses a 3D U-Net architecture to segment tumor volumes from MRI scans of tumor MRI datasets. The encoder part of the U-Net comprises a series of 3D convolutional blocks that learn feature from spatial relationship in the multi-modal MRI dataset. The resolution decreases and features grow deep in the encoder. Similar 3D convolutional layers as used in the encoder are implemented in the decoder to recover segmentation masks through upsampling, but the detailed information is preserved from each corresponding encoding layer through skip connections.

For tumor grading, a Random Forest classifier is utilized to predict the grade of the tumor, based on input volumetric features (such as total tumor volume, core to total tumor ratio, enhancing tumor proportion, etc.). This classifier predicts tumor type as either High Grade Glioma (HGG) or Low Grade Glioma (LGG).Survival prediction, which provides insight into patient prognosis, is estimated from the features of the tumor and patient age.

E. Training and Optimization

We train the segmentation model using labeled MRI volumes via supervised learning. To enhance accuracy for prediction on segmentation masks, we minimize a multi-class segmentation loss. We use model checkpointing for stabilization and convergence. We then train the Random Forest classifier on extracted volumetric tumor features using labeled tumor grade information. We optimize the parameters for maximum classification performance. After training, we save the optimal validation model weights to be used at run-time.

F. Inference Workflow

When a user uploads data, it is first preprocessed and then sent to the trained 3D U-Net. The output segmentation mask is produced and tumor volumes calculated. These volumes and other features are input into the classifier to determine tumor grade and then survival prediction based on tumor and patient age is performed. All of this data is then sent to the backend server to be displayed to the user on the web interface.

IV. IMPLEMENTATION

NeuroScan AI is a web-based brain tumor analysis tool which is powered by a deep learning inference backend. The system consists of an interaction of frontend for managing users and backend for segmentation, classification and serving the output.

A. User Interface

The user interface is developed using React and its related HTML and CSS components. It allows users to upload multimodal MRI scans (FLAIR, T1CE and T2). The system will render a tumor segmentation mask and overlap image on MRI scans as well as tumor grade (HGG/LGG), tumor volume and prediction of survival time.

B. Backend Server

The backend is developed using Node.js and Express framework. File upload is enabled by the multer middleware and authentication is handled by JWT. The input MRI files are stored at temporary location and then passed on to the Python script responsible for processing. User profiles and scan history is stored on MongoDB.

C. Data Preprocessing

MRI inputs are validated to be in the appropriate file format and then the volumes are loaded by Nibabel into a numeric array. They undergo brain region cropping and Min-Max normalization. Voxel spacing, extracted from NIfTI header, is used to calculate the tumor volume in cm^3.

D. Deep Learning Inference

The pre-trained 3D U-Net model is loaded in the Python script and multimodal MRIs are feed to network to generate multi-class segmentation masks. Volumetric features are computed using the segmentation mask. Tumor grade is predicted by a Random Forest classifier, whereas prediction of survival time is achieved using patient age. Output images are stored and sent back to backend for visualization.

E. Result Delivery Module

The classification results of tumor, volumetric data and prediction are generated at the backend and sent to the front-end through an API response. The system interface displays and visualizes images and numeric results.

F. Runtime operation

Upon execution of the system, the users upload the MRI scans using the interface and the data is sent to Python segmentation pipelines. Models remain in memory thus efficient inference is obtained without frequent reloading. User can interact with their images and obtain the results in real-time.

G. Development Environment

The NeuroScan AI system is developed using:

- Python for AI processing
- TensorFlow/Keras for 3D U-Net segmentation
- Scikit-learn for Random Forest classification
- NumPy and NiBabel for medical image handling
- Matplotlib for visualization
- Node.js and Express for backend server
- MongoDB for database management
- React for frontend interface
- JWT for authentication

V. RESULTS

The performance of the presented NeuroScan AI framework is evaluated based on quantitative and qualitative aspects. Multi-modal MRI scans are used as input to measure the segmentation accuracy, performance of the tumor classification and volume estimation.

A. Segmentation Performance

The tumor region, including the core, edema, and enhancing tumor are segmented by the 3D U-Net. It can be seen from the qualitative visual evaluation of segmentation mask that the boundary between tumor regions is accurately portrayed and the separation between the tumor sub-regions is also correctly represented.

The segmentation performance is analyzed based on common segmentation metrics, including Dice Coefficient (DC) and Intersection over Union (IoU). The proposed method achieved a good overlap score between the predicted segmentation mask and ground truth label, which proves the ability to localize the tumor.

$$\text{Dice Coefficient} = 2\,TP / (2\,TP + FP + FN)$$

$$IoU = TP / (TP + FP + FN)$$

(TP=True Positives, FP=False Positives, FN=False Negatives)

TABLE I
SEGMENTATION PERFORMANCE METRICS OF 3D U-NET MODEL

Metric	Whole Tumor	Tumor Core	Enhancing Tumor
Dice Coefficient	0.86	0.81	0.78
IoUScore	0.75	0.69	0.65

B. Tumor Classification Performance

The Random Forest classifier is assessed based on the features extracted from tumors, the classification accuracy obtained for differentiating between HGG and LGG is good. The integration of volume features helps to achieve more reliable grade estimation in comparing with only using image features alone.

TABLE II
CLASSIFICATION PERFORMANCE OF RANDOM FOREST MODEL

Metric	Value
Accuracy	0.81
Precision	0.85
Recall	0.80
F1 – Score	0.82

C. Tumor Volume and Survival Estimation

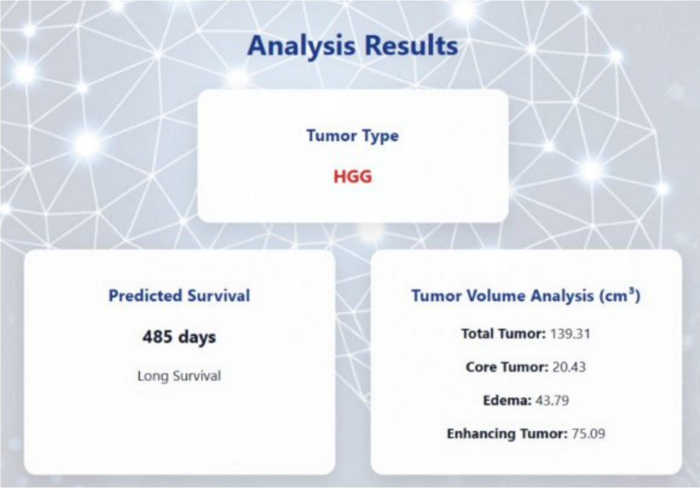
The system computes the tumor volume in cm^3 by using voxel spacing, the tumor volumes as well as sub-region volumes are computed. In survival prediction, we computed approximate days of survival by inputting tumor characteristics along with age.

D. Qualitative Analysis

Visual results show that the segmentation mask overlays are precisely made, surrounding structures of MRI images are not affected during segmenting the tumors. The representative output samples presented below demonstrate:

- Precise boundary detection for tumor segmentation.
- Accurate segmentation in three different regions of tumor.
- Clear visualization when overlay segmentation masks with tumor regions.

All the above results confirm the validity of the combined segmentation and classification model.



Analysis Results

Tumor Type
HGG

Predicted Survival
485 days
Long Survival

Tumor Volume Analysis (cm^3)
Total Tumor: 139.31
Core Tumor: 20.43
Edema: 43.79
Enhancing Tumor: 75.09

Fig. 3. Tumor grading, survival prediction, and volumetric analysis

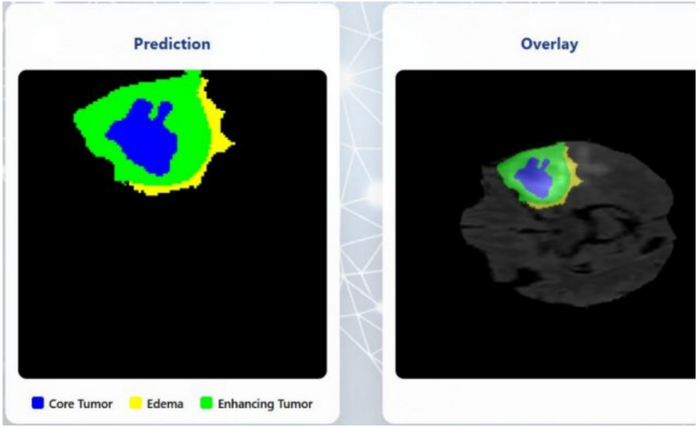


Fig. 4. Tumor segmentation mask and MRI overlay visualization.

VI. CONCLUSION

The work of this paper is the proposal of NeuroScan AI which is an automated framework based on deep learning, dealing with brain tumor segmentation, classification, volumetric assessment and prediction of patient survival. The system is a fusion of a 3D U-Net for the segmentation stage with a Random Forest classifier for discriminating the tumor in the images such as High Grade Glioma (HGG) or Low Grade Glioma (LGG) based on volumetric features.

Different from many recent studies that are limited to offline experiments, this paper proves that 3D medical images can be processed using deep learning in a real time framework that can be useful for clinician support. The outcomes obtained demonstrate that accurate tumor boundary identification can be achieved with clinically relevant volumetric measures, contributing to filling the research- clinical gap.

Some future improvements of the framework could be the inclusion of other types of images, such as CT and PET scans, and of other type of cancers, such as lung or breast tumors, after re-training the models. The performance of the system could also be improved by using hybrid CNN- Transformer architectures and using supplementary clinical information, such as genetic information and patient history. Moreover, optimization techniques like model pruning and quantization can be used to run the system efficiently in the clinical context in real-time.

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