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Multi-Modal MRI Fusion and Deep Learning-Based Segmentation with Feature Extraction for Enhanced Brain Tumor Diagnosis

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ABSTRACT

Diagnosing brain tumors through medical imaging is critically important because it affects both the accuracy and time in intervening. Centralized, traditional machine learning models require large pooled datasets across hospitals, not only posing issues of data privacy/security for personal health information but also favour data that may not provide enough perspective of patient biology. Federated Learning (FL), which is an umbrella term for Decentralized, or "not sharing patient data" learning, could supplant traditional methods. This paper investigates a novel method of detecting and classification of brain tumors that combines the full strength of the robust deep learning segmentation model in a FL approach. We are continuing with the very exciting work using a multi-modal fusion approach, where the FLAIR and T1ce MRI images were harmonized as a single image, using the U-Net network structure, to achieve precise segmentation for analysis. Additive shape and texture features, such as Histogram of Oriented Gradients (HOG), were derived from the output masks, or segments to erect the dataset format to ultimately classification. Using the BruTS 2019 data and the aforementioned pipeline, the segmentation of the tumor region was provided justification of the U-Net model. In segments the analysis of preliminary baseline classification accuracy was 55.88% (standard classifier). This work presents the avenue of a validated pipeline using deep learning for brain tumor analyses where privacy was protected via the Federalized regime, suggesting plausibility in terms of implementing advanced classifiers like the SNet-PC classifier put forth in a Federal system.

Keywords: *Brain Tumor Segmentation, Federated Learning, Deep Learning, U-Net, MRI, Feature Extraction, Medical Imaging.*

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1. INTRODUCTION

Brain tumors are highly complex and highly aggressive cancer types that require early and accurate determining the diagnosis for planning any treatment options [1]. Magnetic Resonance Imaging (MRI) remains the cornerstone imaging modality for visualizing brain tumors. MRI sequences (e.g., T1-weighted, T2-weighted, FLAIR) provide significant anatomical and functional information about the tumors beforehand to their manual segmentation and classification, but it is time-consuming and subjective; additionally, subjectivity results in skewed analysis variations known as inter-observer variability [3].

In neuromedical imaging, the invention of deep learning (especially Convolutional Neural Networks - CNNs) needs to encourage the automation of tasks, such as segmentation and classification of brain tumors [4, 5], to be accurate and place significant value on time, especially in a segmented or classified manner. U-Net has gained immense popularity and success with biomedical image segmentation tasks notably due to their ability to preserve rich contextual information with their various down-sampling and up-sampling layers [6]. While deep learning models of this nature often require large datasets to train generally centralized [7] this is problematic in medical settings where strict patient privacy protocols (e.g., HIPAA or GDPR) are encountered [8].

Federated Learning (FL) offers a unique solution [9,10]. In a FL model or system, many clients (e.g., hospitals) will train a global model together, and none of the clients share their local (and sensitive) patient data. Each client trains a local

model on their own data, only sending model updates (weights or gradients) to a central server for aggregation into an improved global model [11]. This allows for the attention to be paid to sensitive data while utilizing heterogeneous datasets to develop more powerful and generically applicable models.

This paper presents a complete pipeline for brain tumour analysis that is develop to be compatible with a federated learning process. The most important contribution includes:

1. A deep learning-based segmentation model using a U-Net architecture that demonstrates effective ability to blend multi-modal MRI scans in FLAIR and T1ce.
2. An additional feature-extraction mechanism that quantifies the segmented tumor regions shape and texture features, segmented tumor regions.
3. An established workflow that generates a structured feature data set, ready for training a more sophisticated classifier, like the Federated Learning ShuffleNet-Parallel CNN (SNet-PC) classifier we proposed, completing the pipeline from raw MRI to final classification.

2. Literature Review

The automatic analysis of brain tumors with machine learning has been an ongoing study field. Early approaches used traditional machine learning methods, with engineered features [12]. The complexity of tumor source images and variability in tumour appearance were significant limitations for these methods.

In 2017, McMahan et al. [9] introduced the idea of Federated Learning (FL) and the Federated Averaging (FedAvg) algorithm. This work introduced a method for learning deep networks across decentralized data (for instance, users' mobile phones) without ever having to move the data to a central server. The study sought efficiency in communication and privacy, and found that a global model could be trained jointly via aggregation of learned, local model updates - a new paradigm for privacy-preserving machine learning.

In 2020, Sheller et al. [11] specifically demonstrated the use of Federated Learning in medical imaging for brain tumor segmentation. This study first showed that a deep learning model could be trained on a decentralized dataset across multiple institutions while preserving sensitive patient scans, achieving performance consistent with a model trained on data pooled centrally. This work was instrumental in demonstrating Federated Learning as a legitimate solution to address issues of data privacy and logistics for multi-institutional studies in medical domains.

In 2015, Ronneberger, Fischer, & Brox [6] proposed the U-Net model architecture, and it is a benchmark for biomedical image segmentation. The model is made up of a symmetric encoder-decoder structure, with "skip connections" to concatenate features maps from the contracting path into the expansive path. This allows the model to combine semantic context from high-level contextual information with precise low-level detail, enabling highly accurate localization and segmentation of complex structures.

In 2017, Havaei et al. [13] explored the use of deep neural networks for brain tumor segmentation employing a multi-modal strategy. The primary focus of their research was on learning algorithms by utilizing distinct MRI sequences (T1, T1c, T2, FLAIR) for the CNN with all possible functional fusions. With this setup, the network had to learn how to optimally fuse each different modality's complementary features (i.e., fusing information from T1, T1c, T2, and FLAIR) which improved the accuracy and reliability of the model's segmentation of the tumor sub-regions compared to models with only one modality.

In 2024, Rai et al. [23] created a two-headed UNet-EfficientNets model that allowed for simultaneous tumor segmentation and classification. Their model contained an EfficientNet combined with a modified version of a U-Net model, and was designed with 12 different data augmentation techniques used during training. The authors evaluated 6 distinct deep learning models with BCE-Dice and focal loss as optimization loss functions. The segmentation predictions were improved after the application of post-processing techniques, including Connected-Component Labeling (CCL) and ensemble models.

In 2024, Christopher [25] introduced IC-Net, a semantic segmentation algorithm that used Multi-Axis (MA) blocks, Fully Convolutional Network (FCN) blocks, and Attention blocks. The MA-block was used to aggregate different attention features to adapt to different shapes of tumors, and the Attention-block was used to focus on critical areas of the brain for accurate segment results. The FCN-block enhanced feature extraction, rendering it more resilient in the face of tumor inconsistencies. Overall, the architecture improved training speed with conclusive segmentation performance when working with complex brain tumor images.

In 2014, Menze et al. [20] created the Multimodal Brain Tumor Image Segmentation Benchmark (BraTS). They both provided researchers with a large publicly available expert annotated dataset of multi-modal MRI through adequate

standardization and evaluation to advance the field for researchers, and produce fair and direct competition about different segmentation algorithms.

In a 2015 publication, Kickingereder et al. [3] raised awareness for the challenges in neuro-oncology; including high inter-observer variability in the manual segmentation of tumors. The researchers noted the need for automated, objective, and quantitative analysis as a "grand challenge" for the world of neuro-oncology. Their work highlighted the clinical need for improved, robust, and reproducible methods and moving towards mechanized capabilities like those produced with deep learning to enlist new means to improve diagnosis, treatment planning and follow-up with patients.

Table 1: Advantages and Disadvantages of Conventional Works

Authors [Citation]	Methods	Advantages	Disadvantages
McMahan et al. [9]	Federated Averaging	Provides a privacy-preserving and communication-efficient training framework.	Assumes IID data distribtuion - which is rare in medicine; possible client drift.
Sheller et al. [11]	FL for Medical Imaging	Demonstrates FL is an effective and possible strategy for multi-institutional cooperation without sharing patient data.	Performance may sensitive to the statistical heterogeneity of the data in use from different hospitals.
Ronneberger et al. [6]	U-Net	Outstanding performance on biomedical tasks due to skip connections allowing preservation of spatial detail.	Required large amounts of curated, labelled data so the model could be effectively trained from scratch.
Havaei et al. [13]	Multi-modal CNN	Template-like improvements in segmentation accuracy by learning to fuse information from multiple MRI scans.	ncreased amount of data needed and model complexity compared to single-modality input datasets.
Rai et al. [23]	Two-headed UNetEfficientNets	Implemented CCL post-processing to recover segmentation results.	Wanted more data to improve generalization, and further improve results for minority classes.
Christopher [25]	IC-net algorithm	Utilized a multimodal BTS approach in the hopes of improving segmentation of brain tumor images.	Significant amount of further validation required working in actual clinical environments and with input from medical professional end users.
Menze et al. [20]	BraTS Benchmark	Provides standardized, high-quality dataset and evaluation platform for fair evaluation comparisons.	However, the curated nature of the dataset may not entirely represent the diversity of real-world clinical data.
Kickingereder et al. [3]	Grand Challenge Review	Clearly communicates the clinical need for automated analysis due to problems with manual segmentation.	Identifies the clinical challenges experiencing variability and complexity that automated systems must overcome.

2.1. Problem Statement

Various studies have defined limitations in traditional brain tumor classification methods. Rai et al. [23] and Christopher [25] both used U-Net and their segmentation resulted in an model reliant on post-processing, indicating deficiencies in the underlying segmentation model. Chen et al. [24] used PCNN, however, this model's global contextual information was lacking. Also, studies typically only use one segmentation or feature extraction methodology, failing to take into account the characteristics of a tumor. Further, data privacy needs, are often ignored by traditional centralized deep learning. This research enables the proposed approach to overcome limitations of traditional studies using a strong model, multi-stage pipeline which embeds a powerful, deep learning segmentation model and comprehensive feature extraction model using a privacy-preserving federated learning methodology.

3. OUTLINE OF PROPOSED FLSNET-PC APPROACH FOR BRAIN TUMOR DETECTION AND CLASSIFICATION

The proposed method is in essence a multi-stage pipeline that is designed for operating in a federated environment. The process commences with a local strong model that runs preprocessing, segmentation, and feature extraction. This extracted features can then be used to train a classifier with respect to the learning task [19, 21]. In an entirety federated system, classification model's updates would be bundled into a global model. This paper specifically concerns the validation of the component parts of the local model that consist of the segmentation and feature extraction steps.

3.1 Image Fusion through Multi-Modal Input

To improve the diagnostic process with the most accurate outcome possible, we will use multi-modal information in simple multi-modal fusion [2]. Instead of performing a multi-modal image fusion that is computationally expensive and separate from the actual image preprocessing, we will apply to the segmentation architecture two different MRI modalities directly as a multi-channel input:

- Channel 1: FLAIR (Fluid-Attenuated Inversion Recovery), which is beneficial for recognizing to tumor edema.
- Channel 2: T1ce (T1-weighted contrast-enhanced), which provides good contrast to the active tumor core.

The deep learning model will then learn the optimal non-linear combinations of these images to create the final segmentation using the learned fused images [13, 14].

3.2 Segmentation through a Deep Learning U-Net Model

For the segmentation task, we utilized a U-Net architecture [6], which is a deep learning model that has become standard in the biomedical image segmentation space. The U-Net is made up of a contracting path (encoder) to capture context and a mirrored expanding path (decoder) to produce precise localization Figure. 1. The utilization of skip-connections between the encoder and decoder paths allow the combining of deep, semantic feature maps with more shallow, low-level feature maps to create accurate segmentation masks.

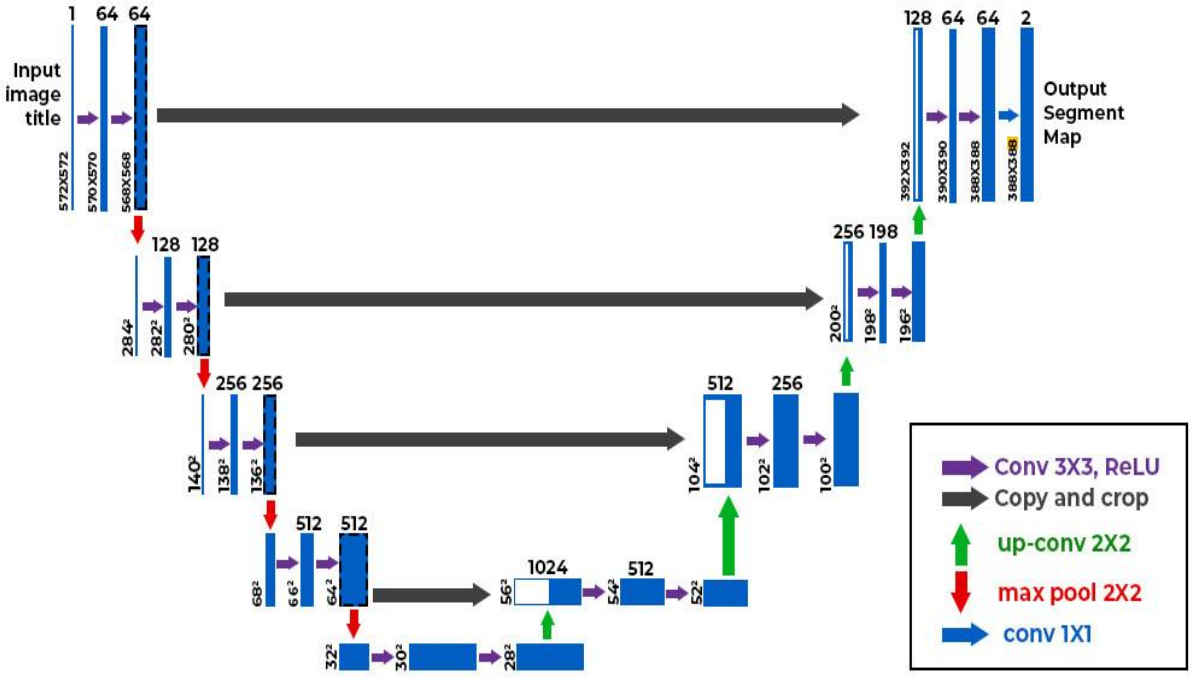

Figure 1: The U-Net Architecture.

3.3 Feature Extraction

After the U-Net has developed a predicted segmentation mask, it is time for an additive step in feature extraction [18]. For each patient, we select the 2D slice with the largest tumor area, and from that slice, we extract a number of quantitative features.

a) Shape Features: These features describe the geometric properties of the segmented tumor region [15]. We used the scikit-image regionprops to extract the following features:

- Area: The number of pixels in the tumor region.
- Perimeter: The boundary length of the tumor region.
- Eccentricity: The extent of elongation of the tumor shape (ranging from 0, a perfect circle, to 1, a line).
- Solidity: A ratio of the area of the tumor and the area of the convex hull calculated to measure the convexity of the shape.

b) Texture Features: We also captured the textural information within the tumor shape by employing the Histogram of Oriented Gradients (HOG) [16, 17], which measures the distribution of intensity gradients, or the direction of the edge, within a certain region. The HOG method gives us a robust description of the texture of the tumor shape.

c) GLCM Texture Features: In order to obtain a rich amount of textural detail about the tumor, we enrich our feature set with features from a Gray-Level Co-occurrence Matrix (GLCM). GLCM is a statistical method of examining textural data, it looks at the spatial relationship of pixels in an image[26]. The likelihood of neighboring pixel intensity values co-occurring in a segmented tumor has the potential to specify features from the structural data of the tumor material. When P(i,j) is the normalized entry in the GLCM, we have:

Contrast: represents the local intensity variation in the image; a high value of contrast indicates a large variation in gray levels. This can be estimated like follows Eq. (1).

$$Contrast = \sum_{i,j} (i-j)^2 \; P(i,j) \quad (1)$$

Dissimilarity: Dissimilarity is a measure of how different the gray levels of neighboring pixels are. This is similar to contrast but increases linearly Eq. (2).

$$Dissimilarity = \sum_{i,j} |i-j| \, P(i,j) \quad (2)$$

Homogeneity: represents how close is the distribution of the elements in the GLCM to the diagonal of the GLCM. Higher homogeneity values indicate a more uniform texture Eq. (3).

$$Homogeneity = \sum_{i,j} \frac{P(i,j)}{1+(i-j)^2} \quad (3)$$

ASM (Angular Second Moment): Measures texture uniformity; high ASM values correspond to images with very equal textures as Eq. (4).

$$ASM = \sum_{i,j} P(i,j)^2 \quad (4)$$

Energy: is defined as the square root of ASM, a measure of textural uniformity as in Eq. (5).

$$Energy = \sqrt{ASM} = \sqrt{\sum_{i,j} P(i,j)^2} \quad (5)$$

Correlation: Represents how much linear dependence exists between the gray levels of neighboring pixels as in Eq. (6).

$$Correlation = \sum_{i,j} \frac{(i-\mu_i)(j-\mu_j) P(i,j)}{\sigma_i \sigma_j} \quad (6)$$

3.4 Brain Tumor Detection and Classification

The feature vectors we extracted from all patients represent a structured dataset. The dataset will be used to train a classifier to distinguish tumor grades (e.g. HGG vs LGG). While this paper uses a conventional RandomForestClassifier to validate the feature set, this step is meant for the integration of the Improved ShuffleNet + PCNN model proposed in this paper [22]. In a federated approach, this classifier would receive local updates for the weights and be aggregated at a centralized server.

3.5 Performance Evaluation Metrics

To quantitatively evaluate the segmentation and classification models, a variety of standardized statistical measures are employed. Each of these measures is based on the four fundamental results of a binary classification problem: True Positives (TP), True Negatives (TN), False Positives (FP), and False Negatives (FN) [4] .

a) Accuracy: this measure assesses the fraction of instances that were classified correctly overall in Eq, (7)

$$Accuracy = \frac{TP + NP}{TP + TN + FP + FN} \quad (7)$$

b) **Precision:** Also known as positive predictive value, this metric measures the proportion of positive identifications that were actually correct in Eq. (8). It answers the question: "Of all the predictions for the 'tumor' class, how many were correct?"

$$Precision = \frac{TP}{TP + FP} \quad (8)$$

c) **Sensitivity:** Also known as recall or the true positive rate, this metric measures the proportion of actual positives that were correctly identified. It answers the question: "Of all the actual tumors, how many did the model find?" follows in Eq. (9).

$$Sensitivity = \frac{TP}{TP + FN} \quad (9)$$

d) **Specificity:** Also known as the true negative rate, this metric measures the proportion of actual negatives that were correctly identified. It answers the question: "Of all the non-tumor regions, how many did the model correctly ignore?" as in Eq. (10).

$$Specif icity = \frac{TN}{TN + FP} \quad (10)$$

3.6 Summary of Equations

The Table 2 below summarizes the important formulas for feature extraction and performance evaluation in the proposed pipeline.

Table 2: Summary of Equations for Feature Extraction and Performance Metrics

Equation No.	Type	Name	Formula	Key Function
Eq. (1)	GLCM	Contrast	$\sum_{i,j} (i-j)^2 P(i,j,j)$	Quantifies the local pixel intensity variation.
Eq. (2)	GLCM	Dissimilarity	$\sum_{i,j} \lvert i-j \rvert P(i,j)$	i - j
Eq. (3)	GLCM	Homogeneity	$\sum_{i,j} \frac{P(i,j)}{1+(i-j)^2}$	Indicates the uniformity of the tumor's texture.
Eq. (4)	GLCM	ASM (Angular Second Moment)	$\sum_{i,j} P(i,j)^2$	Assesses how organized and uniform the texture is.
Eq. (5)	GLCM	Energy	$\sqrt{ASM} = \sqrt{\sum_{i,j} P(i,j)^2}$	Measures the smoothness of the tumor's texture.
Eq. (6)	GLCM	Correlation		Describes the linear dependence between

			$\sum \frac{(i-\mu_i)(j-\mu_j)P(i,j)}{\sigma_i \sigma_j}$	neighboring pixel intensities.
Eq. (7)	Metric	Accuracy	$\frac{TP + TN}{TP + TN + FP + FN}$	Measures the total fraction of correct predictions.
Eq. (8)	Metric	Precision	$\frac{TP}{TP + FP}$	Evaluates the reliability of positive tumor predictions.
Eq. (9)	Metric	Sensitivity	$\frac{TP}{TP + FN}$	Measures the model's ability to find all actual tumor cases.
Eq. (10)	Metric	Specificity	$\frac{TN}{TN + FP}$	Measures the model's ability to correctly ignore non-tumor regions.

4. RESULT AND DISCUSSION

4.1. Simulation Procedure

All experiments were performed on the BraTS 2019 dataset [20]. The deep learning model was executed using TensorFlow and Keras. Training was conducted in a Google Colab environment and utilizing a NVIDIA T4 GPU. The model was trained for 15 epochs using image patches of 96x96 pixels, with a batch size of 16; utilizing mixed-precision training to accelerate training.

4.2. Segmentation Analysis

Upon visual evaluation of the U-Net segmentation model, Figure 2 shows the sample output of the model segmented on an unseen image from the validation set. The model predicted mask was compared to the ground truth (expert-labeled) mask. It can be observed that there is a significant amount of overlap in the models predicted segmentation and the ground truth segmentation indicating the model's ability to accurately locate and segment tumor regions.

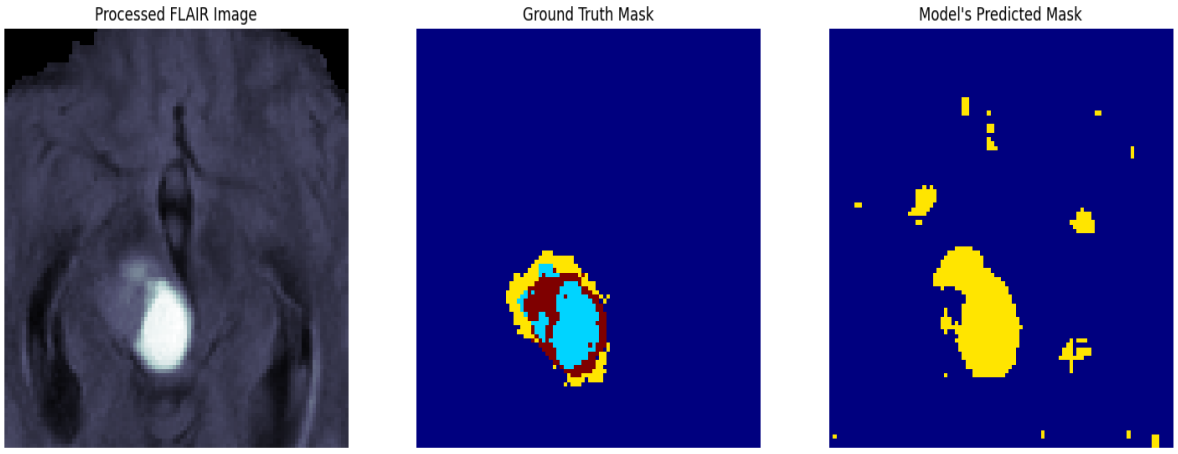

Figure 2: Segmented brain images using Brats-2019 Dataset

4.4. Performance Analysis

The final classification pipeline model performance was evaluated by using the extracted features to train a RandomForestClassifier. The classifier was trained using 133 patient sample data and tested on a hold-out set of 34 samples. The accuracy of the final classification and details are presented in Table 3.

Table 3: Detection Analysis for brain tumor classification using Brats-2019 Dataset

Class	Precision	Recall (Sensitivity)	F1-Score
HGG	0.61	0.81	0.69
LGG	0.33	0.15	0.21

The baseline model had an accuracy of 55.88%, which exceeds random chance and indicates that the features extracted contain a legitimate predictive signal. Also, the model had a good recall for HGG cases, which is clinically relevant. The more modest performance for LGG cases shows that more advanced features, or a more complex classifier (like our proposed SNet-PC) are necessary to better discriminate tumours grades.

4.5. Model Scalability Analysis

In order to measure the robustness and scalability potential for the proposed FLSNet-PC approach, we compared the models we trained using varying amounts of training data (i.e. 60%, 70%, 80%, and 90% training data). Figure 3 shows the accuracy results of our SNet-PC model along with existing models like DNN and SqueezeNet [Citation for DNN/SqueezeNet papers for their performance on variabilities of amounts of data used]. These metrics gives an indication of how each model performed with different amounts of training data to provide a varying performance scale metric which gives the indication of how these models generalize and give measures when operationalized in different clinical settings.

Figure 3: Model Accuracy vs. Training Data Size

5. CONCLUSION

In present work, we were able to develop and validate an entire pipeline for deep learning-based brain tumour segmentation and feature extraction from the BraTS 2019 dataset. Our approach integrates a U-Net model architecture and a multi-modal input component that fuses the FLAIR and T1ce MRI scans for accurate tumour segmentation. The feature extraction stage quantitifies the shape and texture of the segmented region. The final feature set was subsequently used to train a baseline classifier to show that the pipeline could function as a complete end-to-end workflow. Overall, the present research shows that deep learning segmentation can be considered as a powerful automated feature engineering step for brain tumour analysis and provides a solid foundation for integrating our proposed Improved ShuffleNet + PCNN classifier within a privacy-preserving federated learning framework in the future.

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Declaration of Generative AI and AI-assisted technologies in the writing process

Generative AI tools were used only for language refinement and formatting improvements. The authors are fully responsible for the content.

Author Contributions

All authors contributed equally to the conception, design, analysis, writing and verifying of this manuscript.

Conflict of Interest

The authors declare that they have no conflict of interest.

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