

Deep learning techniques for efficient brain cancer identification*

by

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Abstract: Magnetic Resonance Imaging (MRI) is a non-invasive medical imaging technique, which is widely used for the diagnosis and treatment of various neurological disorders, including brain tumors. Accurate segmentation of brain tumors in MRI images is essential for effective diagnosis and treatment planning. Deep learning algorithms have shown significant potential in improving the speed and accuracy of medical image analysis, while reducing human error. In this paper, a deep learning-based approach called **Deep Networks with Stochastic Depth (DNSD)** is proposed for brain tumor segmentation in MRI images. It leverages the advantages of deep convolutional neural networks, combined with stochastic depth training to enhance feature learning and reduce training complexity. The performance of the proposed technique is evaluated using a publicly available dataset and compared with state-of-the-art deep learning models, such as U-Net and ResNet. Experimental results demonstrate that the proposed method achieves improved segmentation accuracy and computational efficiency compared to existing techniques.

Keywords: deep learning, medical image analysis, convolutional neural networks, brain tumor segmentation, MRI

1. Introduction

Brain tumors are abnormal growths of cells in the brain that can damage surrounding tissues and lead to severe neurological complications, disability, and even death. Early detection and accurate diagnosis of brain tumors are essential for effective treatment planning and enhanced patient survival. However,

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identifying tumor regions in medical images remains a challenging task, due to the complex structure of the brain and the similarity between tumor tissues and surrounding healthy tissues. Magnetic Resonance Imaging (MRI) is widely used for brain tumor diagnosis, because it provides detailed information about brain anatomy and pathological structures. MRI enables the visualization of different tissue characteristics using multiple imaging sequences, such as T1-weighted, T2-weighted, and Fluid Attenuated Inversion Recovery (FLAIR). Structural brain atlases and MRI-based anatomical studies have also been widely used in the analysis of brain structures and understanding pathological conditions (see Mandal et al., 2012; Colby et al., 2012; or Tang et al., 2010). These imaging modalities assist radiologists and clinicians in identifying abnormal brain structures and tumor regions. However, manual inspection and segmentation of MRI images are time-consuming and highly dependent on expert knowledge. Recent developments in medical imaging technologies and computational methods have enabled significant progress in automated medical image analysis. Advanced imaging techniques allow researchers and clinicians to examine the anatomical and physiological structures of the brain more effectively (Ottom, 2019). Despite these advancements, analyzing large volumes of high-resolution MRI data remains challenging. Manual segmentation requires extensive expertise and collaboration among radiologists, neurologists, and medical researchers, and it is often prone to subjective errors. Artificial Intelligence (AI) and machine learning techniques have been increasingly applied in medical image analysis to address these challenges. AI-based models can learn patterns from previously labeled medical images and automatically detect abnormal structures in new datasets (see Dinov, 2018; Dinov and Velez, 2021).

These computational models are not intended to replace medical professionals but rather to support clinical decision-making by improving diagnostic efficiency and reducing human error. Medical image segmentation plays an important role in computer-aided diagnosis systems. It involves identifying and labeling specific anatomical structures or pathological regions within medical images. Brain tumor segmentation helps clinicians to accurately locate tumor boundaries and analyze tumor characteristics, which are critical for treatment planning and disease monitoring. Segmentation methods are generally classified into three categories: manual segmentation, semi-automatic segmentation, and fully automatic segmentation. Traditional machine learning approaches rely on manually annotated datasets to train classification models. In such approaches, experts create segmentation masks that identify tumor regions, and machine learning algorithms are trained to detect similar patterns in new images (Ahmad, 2013).

Although these methods can provide useful results, they require extensive manual annotation and often encounter difficulties in cases, in which tumor boundaries are unclear or when tumor tissues have similar intensity values to

those of the surrounding tissues. Machine learning and data mining techniques have also been widely applied in medical diagnosis systems for various diseases (Ottom and Nahar, 2019; Al-Issa, Ottom and Tamrawi, 2019; Kapur et al., 2014).

In order to address the limitations of existing approaches, this paper proposes a deep learning-based brain tumor segmentation technique called Deep Networks with Stochastic Depth (DNSD). The proposed model utilizes a convolutional neural network architecture with stochastic depth to improve feature learning and enhance segmentation performance in MRI images. The stochastic depth mechanism helps in reducing overfitting and improves the training efficiency of deep networks by randomly dropping layers during training. The proposed DNSD technique is evaluated using a publicly available MRI brain tumor dataset and compared with existing convolutional neural network models, such as U-Net and ResNet. Experimental results demonstrate that the proposed approach achieves improved segmentation accuracy and reliable performance in detecting tumor regions. The findings suggest that the DNSD technique can assist clinicians in automated brain tumor detection and contribute to more efficient medical image analysis systems.

2. Existing literature

Medical image analysis plays an important role in modern healthcare systems and is widely used in medical research and in clinical applications, such as computer-aided diagnosis, medical robotics, and image-based clinical decision systems (Doi, 2007; Taylor et al., 2016; Litjens et al., 2017).

In recent years, deep learning techniques have shown remarkable performance in medical image processing tasks, particularly in brain tumor detection and segmentation from MRI images. Several studies have demonstrated that deep learning models can automatically learn complex feature representations and significantly improve segmentation accuracy and reliability (Liu et al., 2023). To address the gradient degradation problem, commonly encountered in deep neural networks, researchers have proposed improved network architectures. For example, an improved Residual Network (ResNet) architecture was introduced for brain tumor segmentation to enhance feature extraction and improve segmentation performance (Aggarwal et al., 2023). Residual connections allow deep networks to be trained more effectively by enabling better gradient propagation during training. In another study, brain tumor segmentation was performed using a combination of Convolutional Neural Networks (CNN) and Probabilistic Neural Networks (PNN) (Madhupriya et al., 2019). The study compared different model architectures and observed that a CNN architecture utilizing overlapping convolution kernels of sizes 3×3 and 7×7 produced im-

proved segmentation performance by capturing both local and global spatial features from MRI images.

Machine learning techniques have also been applied for predicting clinical outcomes related to brain tumors. For instance, a Random Forest technique was used to predict the overall survival of patients, based on imaging and clinical features (Sun et al., 2019). In the 2018 Multimodal Brain Tumor Segmentation Challenge (BraTS), this approach achieved promising results, ranking 2nd and 5th among more than 60 participating teams in survival prediction and segmentation tasks, respectively. The method achieved an overall 61.0% classification accuracy in categorizing patients into short-, mid-, and long-survival groups. More recent studies have further explored the application of deep learning and hybrid learning approaches for brain tumor detection and medical image analysis. These studies demonstrate that advanced deep learning techniques can improve tumor localization accuracy and support automated diagnostic systems in clinical environments (Prasad, Saxena and Laha, 2024; Anantharajan et al., 2024).

3. The proposed system

A novel CNN architecture called Deep Network with Stochastic Depth (DNSD) is used to segment brain tumors in MRI images. The proposed method takes advantage of the unique characteristics of MRI images to accurately segment brain tumors. Although ResNet has proven to be one of the most powerful CNN architectures in many applications, one major drawback is that a deeper network usually requires weeks for training, making it practically infeasible in real-world applications. To tackle this issue, a study on Deep Networks with Stochastic Depth, is introduced in this paper, a counter-intuitive method of randomly dropping layers during training and using the full network in testing. The architecture of the proposed approach is depicted in Fig. 1.

3.1. Image pre-processing

The preprocessing stage involves normalizing and transforming the MRI scans to prepare them for analysis. It may include techniques to identify and distinguish true tumor regions from noise. This could involve setting a threshold for the size or shape of detected regions or considering the context of the surrounding regions. The respective module applies noise filtering or reduction techniques to the segmentation results as presented later on in Fig. 2. Common methods include morphological operations (such as erosion and dilation), Gaussian filtering, or median filtering. These operations help to remove isolated noise regions while preserving important tumor regions. Depending on

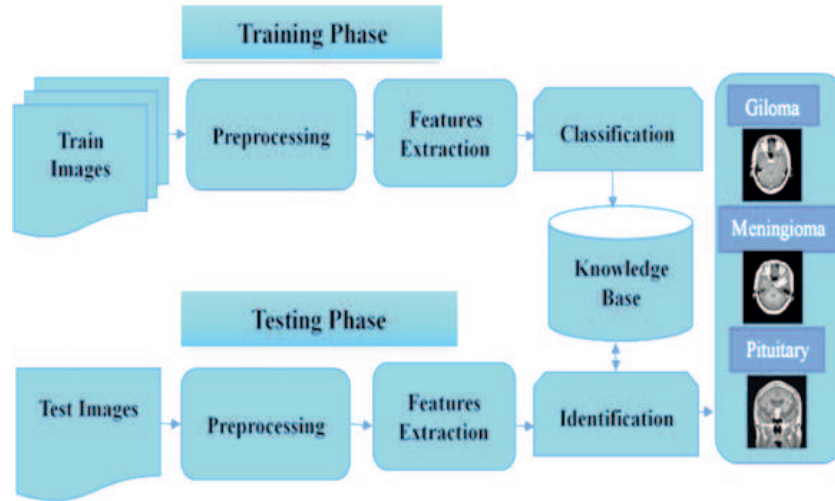


Figure 1. Architecture of the proposed method

the specific requirements, region-growing algorithms or smoothing techniques can be employed to refine the segmentation by ensuring that the tumor regions are contiguous and smooth. These techniques can help in reducing irregularities and jagged edges in the segmentation. The pre-processing steps applied to each MRI scan are detailed in Algorithm 1. These steps ensure that the input data is clean, standardized, and optimized for segmentation.

3.2. Feature extraction

Feature extraction is an important step in MRI brain tumor segmentation, as it involves selecting the most relevant features from the MRI scans that can be used to train the machine learning model. The following are the methods used for feature extraction in MRI brain tumor segmentation:

3.2.1. Intensity-based features

These features are based on the intensity values of the MRI scans and can include measures such as mean, standard deviation, and histogram features. The calculated intensity based feature values for a sample image from the dataset considered are shown in Table 1.

Algorithm 1 Preprocessing Pipeline for MRI Brain Tumor Segmentation

Input: Raw 3D MRI scan volume

Output : Preprocessed 3D MRI volume ready for segmentation

Step 1: Load MRI Volume

Read the raw MRI scan in DICOM format.

Step 2: Perform Intensity Normalization

The intensity values across all slices are normalized using z-score normalization:

$$I_{\text{norm}} = (I - \mu) / \sigma$$

where I is the input intensity, μ is the mean, and σ is the standard deviation.

Step 3: Apply Skull Stripping

A pre-trained U-Net model is used to remove non-brain tissue $I_{\text{brain}} = \text{Skull-Strip}(I_{\text{norm}})$

Step 4: Noise Reduction

Mean and median filters are applied for noise filtering and smoothing

Step 5: Resampling to Isotropic Resolution

Resampling of the volume to uniform voxel spacing (e.g., $1 \times 1 \times 1 \text{ mm}^3$) is performed using interpolation techniques.

Step 6: Export the processed volume in a suitable format for input into the segmentation model.

Table 1. Intensity based feature values for a sample MRI image

<i>Value</i>	<i>Feature</i>
132.5	Mean
29.6	Standard deviation
0.41	Skewness
1.15	Kurtosis
4.28 bits	Entropy

Table 2. Texture based feature values for a sample MRI image

<i>Feature</i>	<i>Value</i>
GLCM Contrast	16.8
GLCM Homogeneity	0.54
GLCM Correlation	0.93
GLCM Energy	0.011
GLRLM	0.13
GLSZM	42.0

3.2.2. Texture-based features

These features are based on the spatial patterns of the MRI scans and can include measures such as gray-level co-occurrence matrix (GLCM), gray-level run length matrix (GLRLM), and gray-level size zone matrix (GLSZM). The calculated texture based feature values for a sample image from the dataset considered are given in Table 2.

3.2.3. Shape-based features

These features are based on the shape of the brain tumors and can include measures such as volume, surface area, aspect ratio, compactness and mean curvature. The sample values calculated for an image from the dataset considered are shown in Table 3.

Table 3. Shape based feature values for a sample MRI image

<i>Feature</i>	<i>Value</i>
Volume	1452 mm ³
Surface Area	275 mm ²
Aspect Ratio	1.77
Compactness	0.47
Mean Curvature	0.021 / voxel

3.2.4. Multi-scale features

These features are based on the information obtained from multiple scales and can include measures such as scale-invariant feature transform (SIFT), speeded

up robust features (SURF). SURF descriptors were extracted using integral images and Haar wavelet responses, providing efficient and robust scale-space analysis. Table 4 shows the extracted values for multi-scale features.

Table 4. Multi-scale feature values for a sample MRI image

<i>Feature</i>	<i>Value</i>
SIFT Keypoints (count)	190
Wavelet Energy Level 1	0.34
Wavelet Energy Level 2	0.16
Wavelet Energy Level 3	0.06

3.3. Segmentation

The segmentation module is the crucial component in the proposed deep learning framework for MRI brain tumor analysis. The goal of this module is to automatically identify and delineate tumor regions in MRI images. In this work, a convolutional neural network (CNN) based architecture is employed to generate segmentation mask that highlights the tumor regions. Each pixel in the segmentation map represents the probability that the corresponding location in the MRI image belongs to a tumor region.

Step 1: Data preprocessing

The MRI images and their corresponding ground-truth segmentation masks are first loaded. The images are normalized to a consistent intensity range, typically between 0 and 1, to ensure stable training. All images are then resized to a fixed input dimension suitable for the CNN architecture.

Step 2: Network architecture design

A CNN-based architecture is designed for tumor segmentation. The architecture contains multiple convolution layers for feature extraction, pooling layers for spatial dimensionality reduction, and up-sampling layers for generating a pixel-wise segmentation map.

Step 3: Feature extraction and prediction

During forward propagation, the CNN extracts hierarchical features from the MRI images. Convolution operations followed by activation functions are applied to learn meaningful representations. Transposed convolution or up-sampling layers are then used to reconstruct the spatial resolution and produce a segmentation output.

Deep Network with Stochastic Depth (DNSD)

Although deep neural networks, such as, for instance, ResNet, provide truly powerful feature extraction capabilities, the increase in the network depth significantly increases both the training time and computational complexity. In order to properly address this issue, we propose in the present paper to adopt the concept of stochastic depth, where certain residual blocks are randomly skipped during training, while the complete network is used during testing. In the proposed architecture, the residual block serves as the fundamental building unit of the network. Each residual block contains a weighted transformation and an identity shortcut connection. The shortcut connection allows the input to bypass the convolutional layers, enabling efficient gradient propagation during training. During training, each residual block is assigned a survival probability, which determines whether the block remains active or is temporarily skipped. If the block is active, the input passes through both the convolutional transformation and the shortcut connection. If the block is inactive, the input only passes through the shortcut connection.

Let H_l denote the output of the l^{th} residual block and let H_{l-1} denote its input. Then, let f_l represent the nonlinear transformation, that is performed by the convolutional layers of the block. The function id , which is used here, represents the identity mapping that forwards the input without modification. The activation function, which is used in this work, is the Rectified Linear Unit (ReLU), the function that introduces non-linearity and helps the network to learn complex patterns. During training, the value of a Bernoulli random variable b_l determines whether the block is active. The output of the block is defined following equation (1) below:

$$H_l = ReLU(b_l * f_l(H_{l-1}) + id(H_{l-1})). \quad (1)$$

If $b_l = 1$, the residual block is active and performs the full transformation. If $b_l = 0$, the transformation path is skipped and the output is obtained using equation (2):

$$H_l = ReLU(id(H_{l-1})). \quad (2)$$

Since the output of the previous layer is already non-negative after the ReLU activation, the operation effectively behaves as an identity mapping, as given in equation (3):

$$H_l = id(H_{l-1}). \quad (3)$$

During testing, all residual blocks remain active. However, the contribution of each block is scaled by its survival probability p_l to maintain consistency with the stochastic training process, as this is shown in equation (4):

$$H_l = ReLU(p_l * f_i(H_{l-1}) + id(H_{l-1})). \quad (4)$$

To control the probability of skipping layers, a linear decay rule is applied to the survival probability across network depth. Earlier layers have higher survival probabilities, because they extract essential low-level features, whereas deeper layers may be skipped more frequently. The survival probability of block l is defined as in equation (5):

$$P_l = 1 - l/L(1 - P_L), \quad (5)$$

where L represents the total number of residual blocks in the network and P_L is the survival probability of the last residual block. In this work, P_L is fixed to 0.5. The input layer is treated as $l = 0$ and is never skipped. This stochastic depth strategy effectively trains an ensemble of multiple sub-networks while maintaining a deep architecture during inference. Compared to conventional ResNet training, this approach significantly reduces training time while maintaining high segmentation accuracy.

Step 4: Model optimization

The network parameters are optimized using gradient-based optimization algorithms such as Adam or stochastic gradient descent (SGD). The objective is to minimize the loss function between the predicted segmentation map and the ground-truth mask.

Step 5: Model training

The CNN model is trained using the preprocessed MRI images and their corresponding segmentation masks. During training, the loss value is monitored and model performance is evaluated on a validation set to avoid overfitting.

Step 6: Post-processing

After prediction, post-processing techniques, such as connected component analysis or morphological filtering, can be applied to refine the segmentation output.

The final result is a segmented MRI image, in which each region is classified as tumor or non-tumor tissue.

4. Experimental results

4.1. The dataset

The experiments in this study were conducted using a publicly available Brain MRI dataset obtained from Kaggle (cf. Kaggle, no date), which is widely used for brain tumor classification and segmentation research.

The dataset contains MRI images belonging to four classes: Glioma, Meningioma, Pituitary tumor, and No Tumor. From among the total number of samples, 350 images correspond to Glioma, 280 images correspond to Meningioma, 138 images correspond to Pituitary tumors, and 432 images represent the No Tumor class, resulting in a total of 1,200 MRI images. All MRI images were preprocessed before training, including normalization and resizing to ensure uniform input dimensions for the deep learning model. The dataset was divided into training, validation, and testing subsets, and so 768 images were used for training and 432 images for testing, while a portion of the training data was used for validation during model training. For experimental evaluation, different training proportions (20%, 40%, 60%, 70%, 80%, and 90%) were used to analyze the performance of the proposed model under varying training conditions. Figure 2 illustrates a case of the segmentation outputs obtained at different stages of the proposed algorithm. The preprocessing stage includes noise reduction techniques such as mean filtering and median filtering, whose effects are illustrated in Fig. 3.

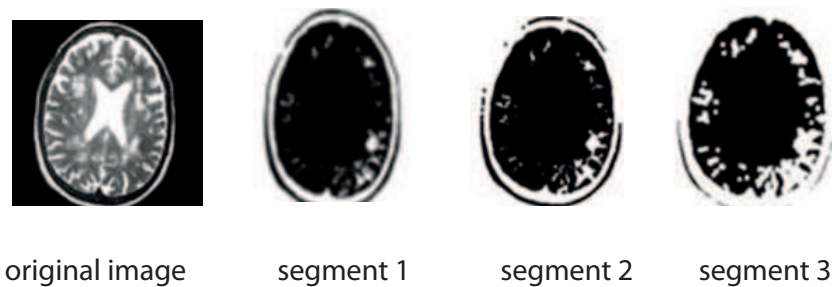


Figure 2. An illustration of segmentation results



Figure 3. An illustration of image preprocessing results

4.2. Model evaluation

In the evaluation phase various evaluation metrics are being calculated in order to quantify the model's performance, including common metrics like Dice coefficient, F1 score, precision and recall. These metrics help in quantifying the model's ability to correctly identify tumor regions while minimizing false positives and false negatives. The corresponding elaborated system module may provide visualizations of the segmentation results alongside the ground truth for qualitative assessment. These visualizations can help clinicians and researchers understand the model's performance. For a comprehensive evaluation, the module may perform statistical analysis to determine the significance of the model's performance compared to a baseline or other state-of-the-art segmentation methods.

4.2.1. Dice coefficient

Here, we define a loss function in order to measure the dissimilarity between the predicted segmentation mask and the ground truth (manual segmentation mask). A common choice for image segmentation is the Dice coefficient (DC) loss as shown in equation (6):

$$DC = \left(2 * \frac{|A \cap B|}{|A| + |B|} \right). \quad (6)$$

The terms of equation (6) are as follows:

- A is the predicted segmentation mask (binary image);
- B is the ground truth segmentation mask (binary image);
- $|A \cap B|$ is the intersection between A and B (the number of overlapping pixels);

$|A|$ is the total number of pixels in A ;

$|B|$ is the total number of pixels in B .

4.2.2. F1 Score

The F1 score is the harmonic mean of precision and recall (Hand, Christen and Kirielle, 2021). It balances the trade-off between false positives and false negatives, making it a suitable metric for imbalanced datasets, where one class (e.g., tumor) may be less prevalent than others (e.g., healthy tissue). The F1 score is defined using equation (7), in which TP , FP , FN indicate true positives, false positives and false negatives, respectively. The F1 score ranges from 0 (worst) to 1 (best), with higher values indicating better model performance.

$$F1 = \frac{2TP}{2TP + FP + FN}. \quad (7)$$

4.2.3. Precision and Recall

Precision is the ratio of true positive predictions to all positive predictions (true positives + false positives). It measures the accuracy of positive predictions. It is calculated using equation (8). Then, recall, also known as sensitivity or true positive rate, is the ratio of true positive predictions to all actual positives (true positives + false negatives). It measures the model's ability to capture all positive instances and is calculated according to equation (9):

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

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

High precision indicates that the model is making few false positive errors, which means it is correctly identifying tumor regions without including much of the healthy tissue.

4.2.4. Performance analysis

Table 5 presents the performance of the proposed DNSD model at different training levels using evaluation metrics such as Precision, Recall, F1-score, and Dice coefficient. From Table 5, it can be observed that the precision value increases as the percentage of training data increases, reaching the highest value at 90% training level. This indicates that the model becomes more reliable

in predicting tumor regions when more training data is available. The recall value also gradually increases with the training data size, reaching 1.0 at the 90% training level, suggesting that the proposed model successfully detects all tumor regions without missing positive cases. The F1-score gradually increases, as well, with the increase in the volume of training data, indicating an improved balance between Precision and Recall. This demonstrates the effectiveness of the DNSD model in accurately identifying tumor regions. The Dice coefficient measures the spatial overlap between the predicted segmentation and the ground truth segmentation. The obtained Dice values indicate a reasonable agreement between predicted tumor regions and the actual tumor boundaries.

Table 5. Performance of the DNSD model at different training levels

<i>Training levels</i>	<i>Precision</i>	<i>Recall</i>	<i>F1-Score</i>	<i>Dice score</i>
20%	0.74	0.87	0.86	0.82
40%	0.82	0.93	0.92	0.88
60%	0.91	0.96	0.95	0.91
70%	0.89	0.97	0.96	0.93
80%	0.99	0.98	0.98	0.94
90%	1.00	1.0	1.00	0.95

To further validate the robustness and generalization capability of the proposed DNSD model, 5-fold cross-validation was performed. In this approach, the dataset was divided into five equal subsets, and the model was trained and evaluated five times using different combinations of training and validation data. Table 6 summarizes the performance metrics obtained across the five folds, including Precision, Sensitivity (Recall), Specificity, F1-score, and Dice coefficient.

Table 6. Performance evaluation using 5-fold cross-validation

<i>Fold</i>	<i>Precision</i>	<i>Sensitivity (Recall)</i>	<i>F1 score</i>	<i>Dice co- efficient</i>	<i>Specificity</i>
1	0.88	1.00	0.936	0.93	0.902
2	0.90	1.00	0.947	0.94	0.913
3	0.89	1.00	0.941	0.94	0.907
4	0.87	1.00	0.930	0.93	0.895
5	0.91	1.00	0.950	0.95	0.919
Avg	0.89	1.00	0.941	0.94	0.907

The Precision values remain consistently high across all folds with an average value of 0.89, indicating that the model effectively minimizes false positive predictions. The sensitivity remains equal 1.00 across all folds, demonstrating the model's ability to correctly detect tumor regions. The average specificity value of 0.907 indicates that the model successfully distinguishes between tumor and non-tumor regions with minimal misclassification of healthy tissue. The F1-score and Dice coefficient values remain relatively stable across different folds, indicating balanced segmentation performance and reliable spatial overlap with the ground truth segmentation. These results confirm that the proposed DNSD model provides stable and reliable segmentation performance across different data splits.

Then, Table 7 presents the classification accuracy of U-Net, ResNet, and the proposed DNSD model using 5-fold cross-validation. Accuracy was computed for each fold and averaged to evaluate generalization across unseen data. The DNSD model achieved the highest average accuracy of 93.8%, significantly outperforming ResNet (74.3%) and U-Net (68.4%). This indicates that DNSD consistently provides more accurate results compared to traditional convolutional neural network architectures. Finally, Table 8 presents the comparison of U-Net, ResNet, and the proposed DNSD model across different training levels, using the accuracy metric. The results demonstrate that the DNSD model consistently achieves higher accuracy across all training levels, compared to the other CNN techniques. As the percentage of training data increases from 20% to 90%, the accuracy of the DNSD model improves significantly, from 78.25% to 95.23%, highlighting the effectiveness of the proposed model when trained with larger datasets. Figure 4 illustrates the performance comparison of the proposed DNSD model across different training levels. The chart presents the variation of evaluation metrics as the percentage of training data increases. It can be observed how the performance of the DNSD model improves as the proportion of the training data increases, indicating that the model effectively benefits from larger training samples. The figure highlights the consistent improvement in model performance, particularly in terms of accuracy and F1-score, as the training level increases from 20% to 90%. This very clear positive trend demonstrates the capability of the proposed DNSD model to effectively learn complex tumor patterns from MRI images when sufficient training data is available. Overall, the results shown in Fig. 4 confirm the robustness and reliability of the DNSD model for brain tumor segmentation tasks.

To further evaluate the performance of the proposed Deep Network with Stochastic Depth (DNSD) model, a confusion matrix was constructed to compare predicted labels with the ground truth labels, and is presented here as Table 9. The confusion matrix summarizes the classification outcomes through classification into four categories: True Positive (TP), True Negative (TN), False Positive (FP), and False Negative (FN). True Positive represents tumor images

Table 7. Accuracy metric values when using 5-fold cross- validation

<i>CNN techniques</i>	<i>Fold 1</i>	<i>Fold 2</i>	<i>Fold 3</i>	<i>Fold 4</i>	<i>Fold 5</i>	<i>Average Accuracy</i>
U-Net	66.5	68.7	69.1	67.3	70.4	68.4
ResNet	72.8	74.2	73.1	75.0	76.3	74.3
DNSD	91.5	93.1	94.2	95.4	94.7	93.8

that are correctly classified as tumor, while True Negative represents non-tumor images correctly classified as non-tumor. False Positive indicates non-tumor images incorrectly predicted as tumor, and False Negative represents tumor images incorrectly classified as non-tumor.

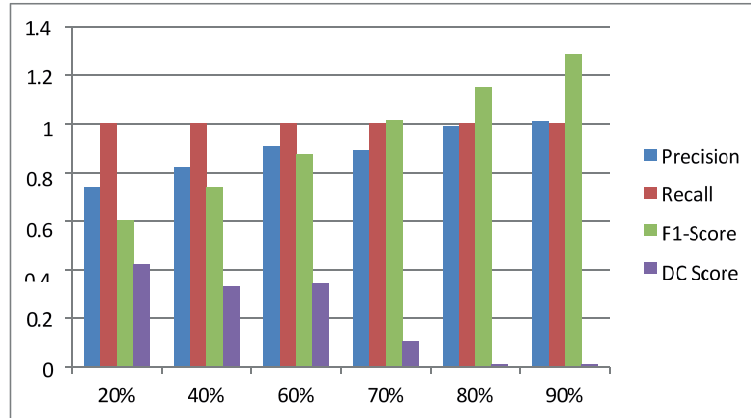


Figure 4. Performance comparison of the proposed DNSD model at different training levels

The confusion matrix results demonstrate that the DNSD model correctly classifies most tumor and non-tumor images with very few misclassifications. This supports the high precision, recall, and F1-score values obtained during evaluation and confirms the effectiveness of the proposed technique for reliable brain tumor detection. Table 9 presents the confusion matrix obtained for the proposed DNSD technique using the testing dataset. The results indicate that the numbers of correctly classified tumor and non-tumor images is significantly higher than those for the misclassified cases. The low number of false positive

Table 8. Comparison table for accuracy

<i>CNN Techniques</i>	<i>Training levels</i>	<i>Accuracy</i>
U-Net	20%	65.64
	40%	71.25
	60%	80.85
	70%	72.33
	80%	73.64
	90%	74.58
ResNet	20%	71.02
	40%	72.15
	60%	63.45
	70%	76.54
	80%	81.45
	90%	83.56
DNSD	20%	78.25
	40%	85.45
	60%	88.12
	70%	92.45
	80%	94.27
	90%	95.23

and false negative predictions demonstrates the ability of the DNSD model to accurately detect tumor regions while minimizing classification errors. Of special interest and importance is also the fact that there are much less false negatives than false positives, which has a high medical significance.

4.2.5. Model training and hyper parameters

The proposed DNSD model was trained using the Adam optimizer with a learning rate of 0.001 and batch size of 16. Training was performed for 100 epochs with a dropout survival probability of 0.9, ensuring effective regularization. Early stopping was employed to avoid overfitting. These hyper parameters were determined empirically through pilot experiments and were kept constant across all folds of cross-validation.

5. Conclusion

This study describes a Deep Network with Stochastic Depth (DNSD) technique, which is proposed and verified for the use in automatic brain tumor segmenta-

Table 9. Confusion matrix of the proposed DNSD model

	Predicted	
Actual	<i>Tumor</i>	<i>No Tumor</i>
<i>Tumor</i>	214	2
<i>No Tumor</i>	18	198

tion in MRI images. The main contributions of this work include an efficient preprocessing framework, consisting of skull stripping, noise removal, and voxel normalization, along with multi-level feature extraction techniques, incorporating intensity, texture, and shape descriptors, meant to support improved tumor segmentation. The performance of the proposed approach was evaluated using 5-fold cross-validation with the use of standard metrics such as accuracy, sensitivity, and specificity.

Experimental results demonstrate that the proposed DNSD approach achieves superior segmentation performance compared to conventional U-Net and ResNet architectures, highlighting the effectiveness of stochastic depth in improving feature learning and model generalization. The approach was trained for 100 epochs, achieving a maximum accuracy of 95.23% at 90% training data, with an average accuracy of 93.8% across the 5-fold cross-validation experiments. The evaluation metrics and visualization of automatic segmentation results on the testing dataset, as shown in Fig. 4, further demonstrate the capability of the proposed approach in accurately diagnosing and segmenting brain tumors from MRI images.

Despite its promising performance, this study has several limitations, including the relatively small dataset size, the computational cost associated with deep learning models, and the lack of real-time clinical validation. Future work will focus on expanding the dataset with multi-institutional MRI data, optimizing the DNSD model for lightweight deployment in clinical environments, and extending the proposed framework to support other medical imaging modalities.

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