

# HybridCSF model for magnetic resonance image based brain tumor segmentation

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## ABSTRACT

The human brain comprises a complex interconnection of nerve cells and vital organs, which regulates crucial bodily processes. Although neurons commonly undergo developmental stages, they may occasionally experience abnormalities, leading to abnormal growths known as brain tumors. The objective of brain tumor segmentation is to produce precise boundaries of brain tumor regions. This study extensively analyzes deep learning methods for brain tumor detection, evaluating their effectiveness across diverse datasets. It introduces a hybrid model, which is proposed by the name HybriCSF: hybrid convolutional-SVM-fuzzy C-means model combining convolutional neural network (CNN) with the classifier support vector machine (SVM) and clustering technique fuzzy C-means (FCM). The proposed model was implemented on Br35H, BraTs 2020 and BraTs2021 datasets. The suggested model outperformed the existing methods by achieving 98.6% of accuracy on Br35H dataset and dice score of 0.63, 0.87, 0.81 on BraTs 2020 dataset for enhancing tumor (ET), whole tumor (WT), and tumor core (TC), respectively. The achieved dice scores on the BraTs 2021 datasets are 0.89, 0.95, and 0.89 for ET, WT, and TC, respectively. The results show that the suggested model HybriCSF outperforms the other CNN-based models in terms of accuracy.

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## 1. INTRODUCTION

The human brain, a complex network of nerve tissues and vital organs, oversees crucial bodily functions. Neurons undergo developmental processes but can sometimes deform, leading to abnormal growths known as brain tumors [1]. These can be benign or malignant, caused by factors like radiation exposure, genetic mutations, or immune disorders. Brain tumors, with their irregular shapes and scattered borders, pose a challenge in early identification. Detecting them early is crucial for treatment and patient prognosis, as they have a low survival rate. Brain tumors falls into benign or malignant categories, impacting brain cells differently. Primary tumors originate in the brain while secondary tumors spread from other body areas [2].

Meningioma, glioma, and pituitary tumors are among the identified brain tumor types, each affecting brain and spinal cord functions differently. Gliomas, arising from glial cells, are aggressive and life-threatening. Treatment involves surgery, radiation, and chemotherapy, often aided by MRI scans for precise visualization [3], [4]. Manual brain tumor segmentation is labour-intensive, leading to the development of automated methods using deep learning, especially convolutional neural networks (CNNs). CNNs have proven effective in segmenting, classifying, and extracting features, outperforming traditional methods.

Despite requiring extensive training datasets, which can be challenging to obtain in clinical settings, CNNs offer precise predictions that are increasingly utilized in brain tumor analysis [5], [6].

In the remaining of this paper section 2 focuses on literature review. Section 3 discusses various datasets used in this study, along with investigation of models like CNN, support vector machines (SVM), fuzzy C-means (FCM) model and proposed a novel hybrid model, "HybridCSF", which combines multiple methods to achieve high accuracy and segmentation quality. Section 4 evaluates the performance of these models using the BR35H dataset, which serves as a benchmark for assessing brain tumor segmentation techniques.

## 2. LITERATURE REVIEW AND GAPS

The application of nn-UNet as the standard technique for brain tumor segmentation is described by Luu and Park [7] in their study. By employing a bigger network, group normalization in place of batch normalization, and axial attention in the decoder, the authors expanded the nn-UNet architecture. Comparing the suggested changes to the baseline, quantitative measurements showed a slight improvement.

In order to segment 2D brain tumors in magnetic resonance (MR) images, the study proposes a novel framework called Znet that makes use of data augmentation techniques together with deep neural networks (DNN). In order to generate additional training mages and reduce overfitting, data augmentation methods such as random rotations, affine transformations, horizontal and vertical flips are employed. The TCGA-LGG dataset, which includes FLAIR MRI pictures of low-grade glioma (LGG) tumors, is used to train the framework. High mean dice similarity coefficient values (dice=0.96 for training and dice=0.92 for independent testing dataset) are shown in the experimental findings [8].

In their study, Vardhman and Singh [9] introduced a fully automated method for brain tumor segmentation, leveraging deep neural networks (DNNs) alongside a mathematical model. The proposed approach involves applying the mathematical model to individual slices of the 3D brain tumor image, followed by segmentation using a 3D attention U-Net. For tumor pixel segmentation, the suggested system HybriCSF architecture provides a pixel level accuracy of 98.90%. K-means clustering and Kernel-based support vector machines (K-SVM) are used in the proposed framework. The K-means method is optimized for the segmentation stage. Discrete wavelet transform (DWT)-based texture characteristics are used for feature extraction, and principal component analysis (PCA) is used to identify important features. The suggested framework achieves metrics of 95.73% accuracy, 97.65% precision, and 98.75% recall [10].

A technique named category guided attention U-Net (CGA U-Net) has been proposed by Allah *et al.* [11]. Accurate and consistent long-range dependence in feature maps is captured by the CGA U-Net with the use of a supervised attention module (SAM) based on the attention mechanism. It uses an intra-class updating technique to aggregate pixels from the same category to recreate feature maps. Dice scores for GCA U-Net are 78.83, 89.29, and 82.32 on ET, WT, and TC, in that order.

The research presented by Raza *et al.* [12] is based on the Edge U-Net model, a Deep Convolution Neural Network (DCNN) with an encoder-decoder structure modelled after the U-Net design. It combines the primary information from brain MRIs with boundary-related MRI data to more precisely identify tumors and accomplish exact segmentation. The model's dice score values for meningioma (88.8%), glioma (91.76%), and pituitary tumors (87.28%) were all satisfactory.

In order to separate brain tumors from MRI images, a hybrid model called dResU-Net that combines the deep residual network and U-Net model has been suggested by Xiong *et al.* [13]. To solve the vanishing gradient problem, the residual network is employed as an encoder and the U-Net model as a decoder. With an average dice score of 0.8357 for the tumor core (TC), 0.8660 for the total Whole Tumor (WT), and 0.8004 for the Enhancing Tumor (ET) on the BraTs 2020 dataset, the model demonstrated promising performance.

The methodology used in the paper [14] involves an MRI-based brain tumor segmentation using a Field Programmable Gate Array accelerated neural network. They train model parameters in their method, and the model output is compared to predicted outcomes to minimize the disparity. For real-time findings, the inference process is sped up. Dice Similarity Coefficients of 0.871 and 0.882 were obtained for the BraTs19 and BraTs20 datasets, respectively. Calabrese *et al.* [15] uses an approach based on deep learning and an attention mechanism for brain tumor segmentation using MRI multi-modalities brain images. The proposed strategy has a special focus on removing insignificant regions inside the four modalities before applying them to the CNN model. The proposed model demonstrated strong performance, with Dice scores for End, Whole, and Core tumor regions increasing from originally low values to 0.8756, 0.8550, and 0.8715 respectively when preprocessing was added.

The technique used in this study [16] involves the employment of machine learning, specifically three-dimensional fully convolutional neural networks (dCNN). It includes three-dimensional convolution bottleneck residual blocks, strides convolution down-sampling, transpose convolution up-sampling, and long-

range skip connections with feature concatenation. The average Dice coefficients were  $0.64 \pm 0.20$  for glioblastomas and  $0.73 \pm 0.37$  for lower-grade gliomas. The authors of the paper used an end-to-end brain tumor segmentation model known as Multi-Inception-UNET to segment brain tumors from MRI scans.

The paper discusses a medical image segmentation method that combines CNN and Transformers in a hybrid network. Specifically, the authors proposed a method that alternates between CNNs and Transformer stages for feature extraction and makes use of a module they labelled as TSEM. The proposed method achieved an average Dice score of 86.31% accuracy on the BraTs2018 dataset [17].

### 3. METHOD AND ARCHITECTURE

In this section, diverse datasets are used for the examination of brain tumors. Furthermore, a comprehensive range of machine learning methodologies is utilized, encompassing CNN, SVM, FCM, as well as architectures such as UNet, ResNet50, EfficientNet V2, VGG16, and VGG19-RNN Model. Finally, an integrated model termed HybridCSF, amalgamating CNN, SVM, and FCM components, is introduced as a novel approach.

#### 3.1. Datasets

This study utilizes multiple datasets for the analysis of brain tumors. Specifically, BraTs 2020 and BraTs 2021 datasets are utilized from the University of Pennsylvania's Center for Biomedical Image Computing and Analytics (CBICA), which provide 3D MRI brain images along with annotations by specialists. Additionally, Br35H dataset are incorporated, sourced from Kaggle for investigation. The datasets encompass T1, T1c, T2, and FLAIR modalities, facilitating the segmentation of tumor sub-regions such as enhancing tumors, necrotic cores, and peritumoral edema. These sub-regions include the enhancing tumor, the necrotic and non-enhancing tumor core, and the peritumoral edema, as annotated. The annotations were used to produce three nested sub-regions: ET, TC, and WT. The BraTs 2020 dataset, a compilation of pre-operative MRI scans from many institutions, is used to segregate intrinsically heterogeneous brain tumors. The goal of the BraTs 2020 challenge was to evaluate state-of-the-art methods for multimodal MRI brain tumor segmentation. The collection contains 2640 mpMRI scans, or 660 occurrences. BraTs 2021 is a large-scale dataset utilized in the multimodal brain tumor segmentation challenge. The collection consists of 2,000 occurrences, or 8,000 mpMRI pictures. In every example, four different 3D MRI modalities are used: T1, T1c, T2, and FLAIR. Standardized processes like alignment, skull stripping, and resampling achieve an isotropic  $1 \times 1 \times 1$  mm resolution, with images sized  $240 \times 240 \times 155$ . The dataset splits into training (1,251 cases), testing (370 cases), and validation (380 cases). The provided image measures 240 by  $240 \times 155$ . Additionally, the Br35H dataset contains 3060 brain MR images, half tumorous and half non-tumorous, featuring, with 1500 Brain MRI Images that are tumorous and 1500 brain MRI images that are non-tumorous. These datasets enable comprehensive analysis and development of brain tumor segmentation techniques [18], [19].

#### 3.2. Convolutional neural network

CNNs are specialized models with grid-like structures, adept at processing 1D grids for time series and classification, and 2D grids for image data. These networks consist of sequential layers transferring activation volumes, comprising convolution and pooling layers. It combines two primary building blocks, where first is a convolution block containing the convolution and pooling layers and the second is a fully connected neural architecture that performs the classification task [20]. Convolutional layers apply filters to input images, reducing complexity, while pooling layers down sample feature maps. Fully connected layers are substituted for transposed convolution layers, which produce pixel-wise segmentation maps by up sampling feature maps, to segment brain tumors. Fully connected output nodes are used for the classification, Softmax activation function is used along with the output for better probability. The Softmax activation function is shown in (1) [21].

$$p(\vec{z})_i = \frac{e^{z_i}}{\sum_{j=1}^K e^{z_j}} \tag{1}$$

where  $K$  represents the number of classes. The loss, which is determined by the discrepancy between the expected and actual segmentation maps during training, is reduced using backpropagation, which adjusts the network's weights. Categorical cross-entropy loss function calculates the performance between 0 and 1. Its formula is shown in (2) [22].

$$Loss(y, \hat{y}) = -\frac{1}{N} \sum_{i=1}^N [y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)] \tag{2}$$

CNNs excel at automating brain tumor segmentation, aiding medical professionals in diagnosis and treatment planning. Their accuracy can be enhanced through parameter optimization, data augmentation, and transfer learning from pre-trained CNN models [23].

### 3.3. Support vector machine and fuzzy C-means

SVM is a classification algorithm that selects one classifier from multiple options to create a multi-class SVM. The learner extracts traits from each fingerprint picture to construct an SVM structure, which is then used to classify test data. An error-correcting output codes classifier, like SVM, simplifies learning with more than two classes by eliminating many binary classifiers. To use SVM, the first step is to train the classifier with available training data, which teaches the classifiers used in the classification process to determine the class of new test data. For the FCM calculation, the cluster centers or membership numbers in the given picture are set to random. In the segmentation method, the unique picture of the tumor is used as input to the segmentation process to limit the image's tumor area. In repeated clustering and fuzzy c-Means calculations, the main goal is to limit the weight age inside the collection part of the squared error objective function [24].

### 3.4. The proposed model

The HybridCSF model, shown in Figure 1, combines CNN with SVM classification and FCM algorithms. The reasoning behind this integration originates from the inherent strengths of each component. CNN has incredible flexibility in supporting more hidden layers, which allows for improved feature extraction, increasing accuracy and overall performance. Simultaneously, SVM is well-known for its ability to extract features with more efficiency and speed than other techniques. In the proposed model architecture, the output from the CNN's convolutional layers serves as input for the SVM classifier. This integration ensures that the retrieved features are efficiently used for classification tasks by using the complementary strengths of CNN and SVM. Furthermore, throughout the segmentation phase, the most efficient centroids from each iteration of the Fuzzy C-means method are used. These optimum centroids are critical for effectively identifying tumor areas in MR pictures. By utilizing these ideal centroids, the HybridCSF model performs an improved segmentation approach, enhancing tumor area detection precision.

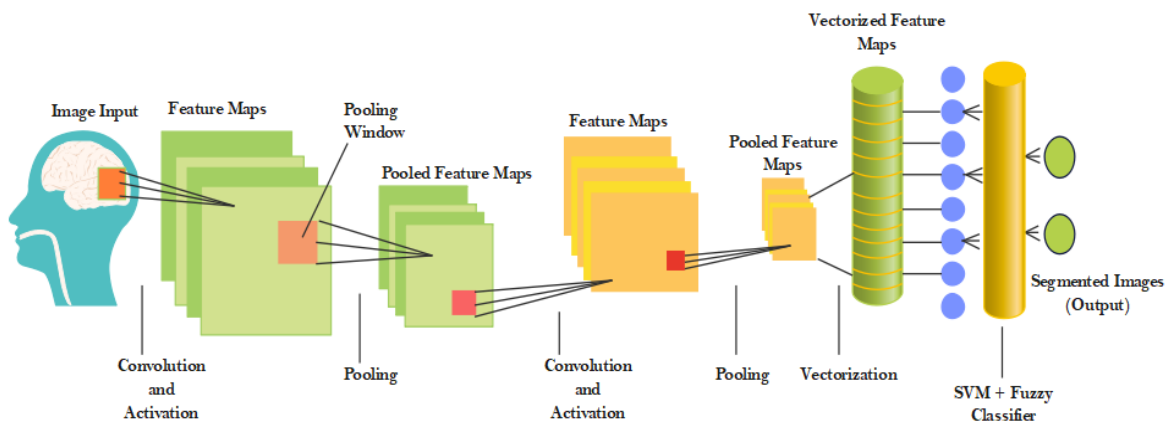


Figure 1. Architecture of proposed model

## 4. RESULTS AND DISCUSSION

This section, focuses on evaluating the performance of various models using the BR35H dataset. The BR35H dataset serves as a benchmark for assessing the efficacy of different methodologies in handling brain tumor segmentation tasks. A range of evaluation criteria are included, which allow us to comprehensively evaluate the efficacy of methodologies in handling brain tumor segmentation.

### 4.1. Evaluation criterion

Many common statistical indicators are included in the assessment criteria for both detection and classification. Table 1 showcases the standard assessment criteria for this work. Dice similarity coefficient (DSC): dice coefficient correlates in evaluating picture segmentation, if one model A outperforms Model B, the other generally agrees. Ranging 0 to 1, they depict similarity between actual and forecasted data. These metrics gauge segmentation accuracy by comparing manual and automated MR image segmentations for

exact spatial overlap with automated probabilistic fractional segmentation of MR images. These assessment criteria's helps in evaluating the efficacy of brain tumor detection and classification models by testing the models' capacity to accurately identify positive and negative samples and distinguish between various tumor types. They are frequently used to assess the efficacy of these models and contrast them with alternative strategies in clinical practice and research investigations.

Table 1. Binary classification and performance metrics

Performance Metric	Description
True positive ( $T_p$ )	The number of accurately identified positive samples (tumors) in the dataset is shown by this metric.
True negative ( $T_n$ )	The number of accurately detected negative samples (tumor-free) in the dataset.
False positive ( $F_p$ )	The number of falsely recognized positive samples (tumor-free samples) in the collection is indicated by this value.
False negative ( $F_n$ )	The total of the dataset's falsely detected negative samples (tumor-filled).
Accuracy	The proportion of the dataset's accurately known samples: $\text{Accuracy} = \frac{(T_p + T_n)}{(T_p + F_p + T_n + F_n)}$
Recall	The proportion of all the real positive samples that were correctly recognized, $\text{Recall} = \frac{(T_p)}{(T_p + F_n)}$
F1 Score	The harmonic mean of recall and precision gives equal weight to both metrics $\text{F1 Score} = \frac{2 \times (\text{Precision} \times \text{Recall})}{(\text{Precision} + \text{Recall})}$
Dice Similarity Coefficient (DSC)	Dice coefficient correlates in evaluating picture segmentation. These metrics gauge segmentation accuracy, $\text{DSC} = \frac{(T_p)}{\frac{1}{2}(2T_p + F_p + F_n)}$

4.2. Model's assessment

The suggested method opted Python free and open-source software as it offers enhanced control over implementation and visual spatial abilities. The suggested model performed well on the Br35H dataset and obtained an accuracy of 98.6%, outperforming other brain tumor segmentation models such as CNN (92.7%), VGG16 (83.1%), EfficientNet V2 (93.4%), ResNet50 (82.2%), and VGG19-RNN (98%) on the same dataset as shown in Table 2. The graphs showing the loss and accuracy for various methods along with proposed method are also shown in Figures 2-7.

Table 2. Evaluation of models on Br35H dataset

Model	Accuracy	Loss
CNN	0.927	1.633
VGG 16	0.831	1.6997
EfficientNet V2	0.934	0.492
ResNet50	0.822	0.308
VGG19-RNN	0.980	0.076
HybridCSF (Proposed model)	0.986	0.069

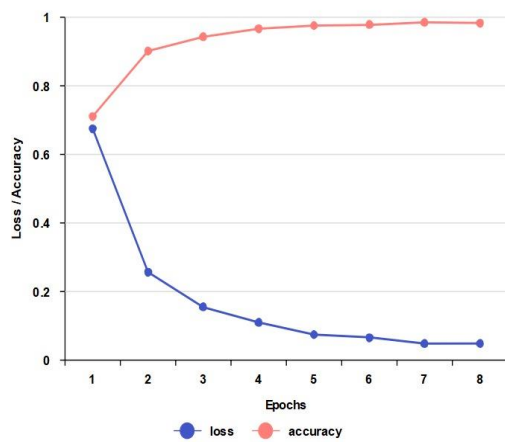


Figure 2. Loss and accuracy for CNN Model on Br35H dataset

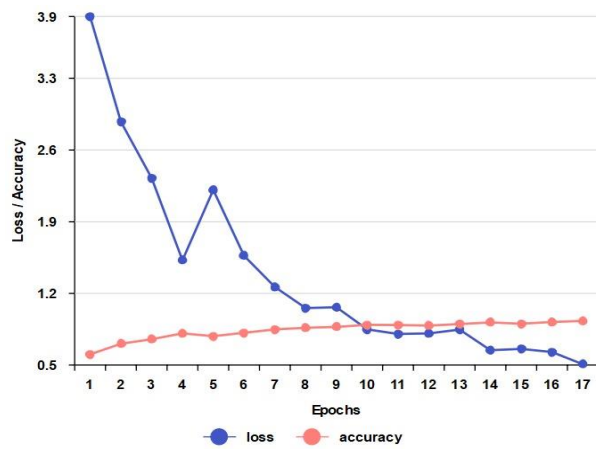


Figure 3. Loss and accuracy for VGG16 Model on Br35H dataset

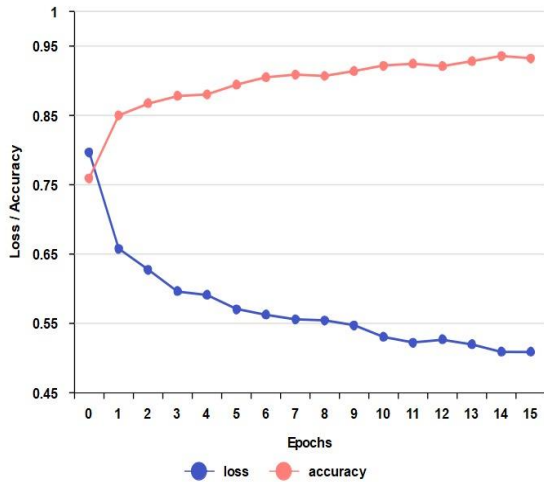


Figure 4. Loss and accuracy for EfficientNet V2 model on Br35H dataset

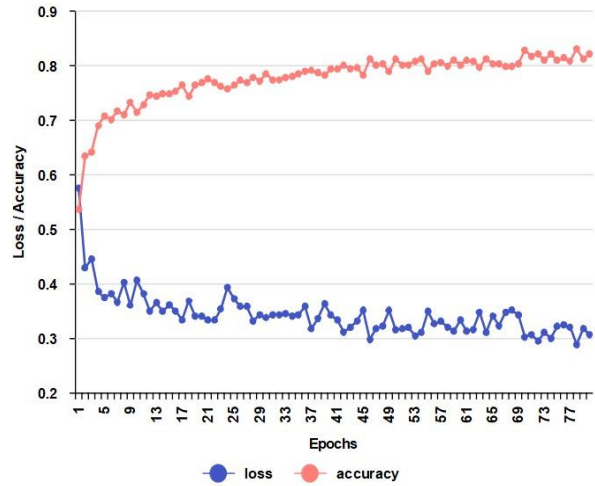


Figure 5. Loss and accuracy for ResNet50 model on Br35H dataset

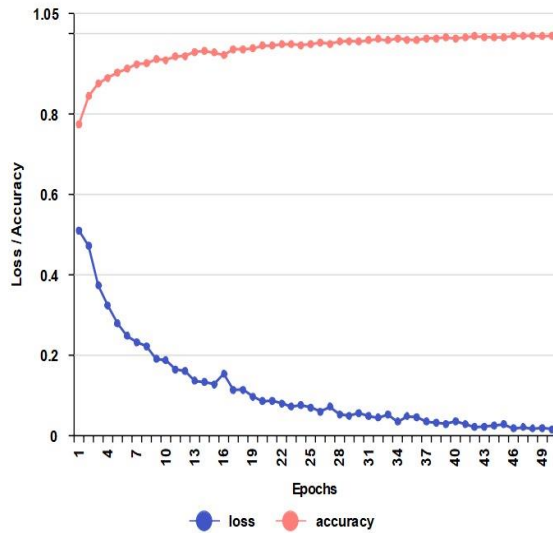


Figure 6. Loss and accuracy for VGG19-RNN model on Br35H dataset

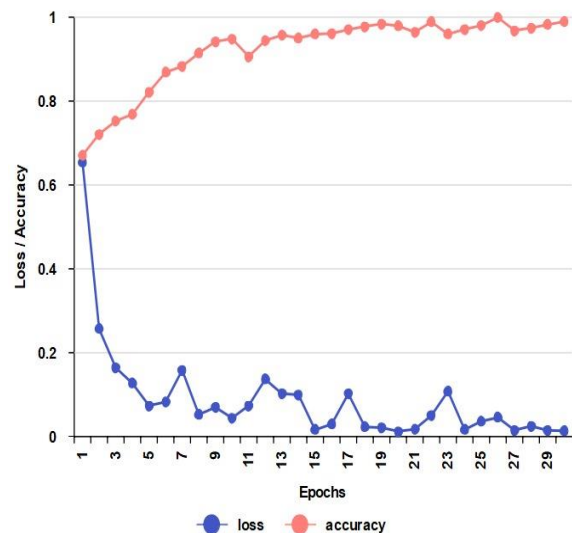


Figure 7. Loss and accuracy for HybridCSF model (proposed model) on Br35H dataset

The performance of ensemble mean Softmax, nn-3D U-Net and dual-path attention U-Net models was tested on BraTs2020 dataset. The average dice score achieved was 0.85, 0.84 and 0.80 respectively as shown in Table 3. Meanwhile, the dice score of the CSF (proposed model) achieved the highest average dice score of 0.86 for ET 0.83, WT 0.87 and TC 0.89. Table 4 presents the average dice score for BraTs2021 dataset on the models UNETR, NnUNet, HarDNet-BTS and SegResNetVAE as 0.88, 0.89, 0.89 and 0.88 respectively. The dice score of the CSF (proposed model) achieved the highest average dice score of 0.91 for ET 0.89, WT 0.95 and TC 0.89.

Table 3. Comparison of models on BraTs 2020 dataset

Model	ET	WT	TC	Average
Ensemble mean softmax [25]	0.81	0.89	0.84	0.85
nn-3D U-Net [26]	0.79	0.89	0.84	0.84
Dual-Path Attention U-Net [27]	0.75	0.88	0.78	0.80
HybridCSF (Proposed model)	0.83	0.87	0.89	0.86

Table 4. Comparison of models on BraTs 2021 dataset

Model	ET	WT	TC	Average
UNETR [28]	0.85	0.93	0.88	0.88
NnUNet [29]	0.87	0.93	0.87	0.89
HarDNet-BTS [30]	0.87	0.93	0.87	0.89
SegResNetVAE [31]	0.85	0.92	0.87	0.88
HybridCSF (Proposed model)	0.89	0.95	0.89	0.91

## 5. CONCLUSION

This article provides an overview of the topic and detailed description about the new dimensions of how various machine learning and image segmentation approaches are applied for the identification of brain tumors. By comparing the state-of-the-art and new cutting-edge methods, the deep learning methods are more effective for brain tumor segmentation using MRI images of the brain. Through rigorous evaluation of deep learning models such as 3D-UNet, CNN, ResNet50, VGG-16, and VGG19-RNN. using BraTs and Br35H datasets, this study makes a significant contribution to an entire overview of the area. In this study we have proposed a HybridCSF model, the integration of CNN with the SVM classification and Fuzzy C-means methodology for brain tumor segmentation. The proposed model was evaluated against Br35H dataset where it outperformed the rest of the models by achieving an accuracy of 98.6%. The proposed model was also tested against BraTs 2020 and 2021 datasets where the model achieved highest average dice score of 0.86 and 0.91 respectively.

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