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# Hybrid Deep Learning–Based Early Detection and Segmentation of Brain Tumors from MRI Images Using BRATS

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**Abstract—** Segmentation of brain tumors in magnetic resonance imaging (MRI) is a difficult problem given the variability in tumor shape, size, and location and tissue characteristics. The goal of this study is to introduce HSTF-Net, a hybrid deep learning framework for brain tumor automatic segmentation based on BraTS 2020 dataset. The framework combines complementary data from T1, T1CE, T2 and FLAIR MRI modalities to segment three clinically relevant regions, namely Whole Tumor (WT), Tumor Core (TC) and Enhancing Tumor (ET). The dataset was processed for reliability in evaluation and to prevent data leakage, including modality alignment, intensity normalization, background processing, label conversion, and patient-level data splitting. HSTF-Net achieved an overall mean Dice of 84.80%, mean IoU of 76.23%, sensitivity of 88.93%, specificity of 99.80%, precision of 84.59%, and HD95 of 8.02 mm. Regional evaluation achieved Dice scores of 90.79% for WT, 85.27% for TC, and 78.33% for ET. HSTF-Net outperformed the selected published results: 3D U-Net, SegResNet, UNETR, SwinUNETR and TransBTS in terms of the mean Dice score, and displayed superior boundary localization. The results of the qualitative analysis also showed that there is good agreement between predicted and expert-annotated tumour regions. In general, the results confirm that HSTF-Net is a reliable and accurate tool for brain tumor segmentation and it has the potential to be an automated multimodal MRI analysis tool.

**Keywords—** Hybrid Deep Learning, Brain Tumor Segmentation, MRI, BraTS 2020, HSTF-Net, Multimodal MRI, Tumor Detection, Medical Image Segmentation, Deep Learning, Tumor Core, Whole Tumor, Enhancing Tumor.

## I. Introduction

Brain tumours are one of the most serious neurological conditions since they have the potential to impair cognitive, motor, sensory and other fundamental neurological processes. Early diagnosis and accurate characterisation of the tumour and treatment planning is crucial to the clinical outcome of patients with brain tumors. Brain tumours vary greatly in size, location, shape, intensity, growth pattern and tissue composition, making identification and delineation a challenging clinical task. Early detection is more crucial because the identification of abnormal tissue at an early stage can be helpful to the clinical intervention that can be done at the right time and improve the effectiveness of the following clinical interventions. Thus, the development of reliable and automatic tools for detection and segmentation of brain tumours has emerged as an important research field in medical image analysis [1], [2], [3], [4].

One of the most commonly used imaging techniques for the study of brain abnormalities is Magnetic Resonance Imaging (MRI). This technique has proven to be an excellent imaging modality for soft tissues, and also provides a wealth of anatomical detail without exposing the patient to the dangers of ionizing radiation. The complementary features of brain tissues and pathological areas can be revealed by different MRI modalities to provide further information regarding the structures of tumors. The reading of MRI scans, however, requires a high degree of expertise, as well as time to read, especially if a large number of scans are to be read. Manual analysis may further be complicated by the variation in tumor appearance, the heterogeneous intensity patterns, the irregular boundaries, surrounding edema and differences between patients.

Also, there may be inter-observer variation due to subjective interpretation. All these difficulties have stimulated the research of computer-aided techniques that have the potential to assist clinical experts in automatically analyzing brain MRI images [5], [6], [7], [8].

Artificial Intelligence (AI), specifically Deep Learning (DL), has revolutionized the medical image analysis sector. Deep learning techniques can extract hierarchical representations automatically from the imaging data without relying on manually designed features as is done in traditional machine learning approaches. CNNs have proven to have good performance on extracting spatial and structural information from medical images and thus, have been extensively explored for brain tumour analysis. The deep learning based methods can be applied to various tasks such as segmentation, localisation, classification and detection of tumours. They have been applied to the problems of brain tumours due to their capability of learning complex patterns from very large sets of MRI images [9], [10], [11], [12].

Despite the success of deep learning, brain tumour analysis is still hard, as detection and segmentation are two related yet distinct tasks. While detection is mainly concerned with determining if the tumor is present or not and localizing the affected area, segmentation is primarily concerned with determining the exact boundaries and sub-regions of the tumor in the image at the pixel or voxel level. A model can be used to detect a tumor with good accuracy but with poor boundary accuracy. Likewise, segmentation can be challenging if tumors are irregularly shaped, have poorly defined margins, have heterogeneous tissue densities within the tumor, or vary greatly in size. Therefore, using only one representation or one deep learning architecture may not be sufficient to capture all the spatial and contextual information pertinent to a reliable tumor analysis.

To overcome these limitations, hybrid deep learning architectures are proposed, which integrate complementary learning mechanisms in one architecture. The different parts of a network can be trained to detect different features of MRI images. Convolutional layers are useful to learn local spatial and textural features and deeper or complementary architectures can help to learn higher-order contextual representations. This integration can enhance feature representation and help accurately identify and map tumor regions, thereby offering potential benefits to a hybrid model. So a well-designed hybrid system can thus overcome both early detection of the tumor and accurate tumor segmentation to achieve more comprehensive automatic brain tumor analysis.

Brain Tumor Segmentation (BraTS) is one of the key datasets for evaluating the performance of automated brain tumor segmentation techniques. The dataset contains multimodal brain MRI scans with expert annotations of tumor regions to create and compare computational approaches under standardized experimental conditions. Multiple MRI modalities can be used to obtain complementary information on the tumor tissue and adjacent anatomy. An additional benefit of the segmentation masks generated by experts is that they can be used quantitatively to assess the capabilities of an automated model in defining the tumor regions and reproducing clinically relevant boundaries. BraTS has therefore been widely utilized in research on deep learning brain tumor detection and segmentation.

This study aims to present a Hybrid Deep Learning–Based Early Detection and Segmentation framework for Brain Tumors from MRI Images, using the BraTS dataset. The main goal is to build an automated system to learn useful features from MRI images for accurate region delineation and reliable identification of tumor regions. The proposed approach combines complementary deep learning features to obtain detailed spatial features and context clues from the input MRI data. The input data is preprocessed and features are learned to ensure the quality and consistency of data and to ensure effective model training. The framework aims to overcome the problems related to differences in tumor appearance, size, shape and boundaries.

Evaluation measures for both detection and segmentation are adopted for assessing the effectiveness of the proposed approach. The accuracy, precision, recall, F1-score, and other metrics can be used to assess detection performance, while the Dice Similarity Coefficient, Intersection over Union (IoU), sensitivity, and specificity can be used to assess segmentation performance. These measures give complementary information about the model's performance in recognizing true tumor cases and accurately outlining tumor regions. The efficiency of the proposed hybrid framework as well as its robustness can be further proved by comparing it with relevant deep learning approaches as discussed in [13], [14], [15], [15], [16].

The importance of the research work is a combination of early detection and accurate segmentation in one analytical framework in an automated computer-aided approach. This system may help to minimize the manual effort involved in the interpretation of MRI, ensure accurate delineation of tumor regions, and assist physicians in treatment planning and disease monitoring. The proposed research proposes to build on the complementary strengths between the multimodal MRI information in the BraTS dataset and deep learning and will help advance automated brain tumor analysis. In conclusion, the advancement of precise, robust and efficient deep learning-based techniques can aid in the accurate interpretation of medical images and enable the incorporation of intelligent computer-aided systems into clinical decision-support systems.

## II. Literature Review

Algarni 2026 et al. Glioblastoma is a highly aggressive form of brain tumor that is highly heterogeneous and with complicated MRI appearance as described and others. Deep learning, especially CNN-based and hybrid models, have been found to be effective for automated segmentation and classification with multimodal MRI. Recent techniques, prominent databases like BraTS and TCIA, as well as architectures like U-Net variants, attention and residual networks, and hybrid models, are analyzed. The main difficulties are: poor generalization, need to rely on expert annotations, poor interpretability, and problems of clinical translation. Future promising research and development trends involve multimodal fusion, domain generalization, uncertainty-aware learning and low computational cost models for the reliable clinical use [17].

Bouhafra 2025 e al. focuses on deep learning and artificial intelligence in the field of brain tumor detection and classification using magnetic resonance imaging (MRI) with a focus on early diagnosis and minimizing diagnostic errors. It summarizes 60 papers on this topic that were published between 2020 and January 2024, including papers on transfer learning, autoencoders, transformers, and attention mechanisms. The review discusses the current strategies and their advantages and disadvantages, as well as recent progress in automated tumor analysis. It also outlines future research avenues for more effective, reliable, clinically viable brain tumour diagnostic systems [18].

Disci 2025 et al. Pre-trained deep learning models for automated brain tumor classification from MRI images is explored. It utilizes 7023 images across four categories and tests 6 different transfer learning models that include preprocessing, augmentation and fine-tuning. The best classification accuracy was obtained with Xception, which showed good generalization between tumor classes. There are still issues in regards to enhancing the recall of classes and interpretability. In general, the results suggest that transfer learning has the potential to improve brain tumor diagnosis and clinical decision support systems with high accuracy, efficiency, and scalability [19].

Younis 2024 et al. suggests an improved deep learning method for brain tumour classification with MRI for distinguishing glioma, meningioma, pituitary tumour and no tumour. The training and validation accuracy of the model was about 99% using the ResNet50 transfer learning with the data augmentation and regularization. The classification results on an independent test set showed a high classification performance with good precision, recall, F1-score and ROC-AUC across all tumor classes. The findings prove the potential of transfer learning for accurate and early diagnosis of brain tumors and pave the way for the clinical decision-support system which could offer reliable automated diagnosis from MRI scans [20].

TABLE. 1 LITERATURE SUMMARY

| Author/Year | Method | Research Gap | Finding |
|---|---|---|---|
| Ashimgaliyev/ 2024[21] | Advanced segmentation integrated with deep learning ensemble algorithms for classification. | Traditional methods lack sufficient accuracy, robustness, and efficient tumour classification. | nsemble segmentation significantly improves brain tumour classification accuracy and robustness. |
| Renugadevi/20 23[22] | UNet++, radiomics, SMOTE, ADASYN, PCA, and machine- | Dataset imbalance limits reliable tumour grading | UNet++ achieved 98% accuracy; SGD |

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| | learning algorithms applied. | and patient survival prediction. | achieved 96% grading accuracy. |
| Zhihua/2023[23] | Surveyed over 150 deep learning studies for brain tumour segmentation. | mprehensive comparisons addressing imbalance and multimodal challenges remain relatively limited. | Deep learning demonstrates promising segmentation performance across diverse MRI modalities. |
| Zeineldin/2022 [24] | DeepSeg, nnU-Net, and DeepSCAN were combined using ensemble learning. | ngle models struggle with robust segmentation across diverse datasets consistently. | nsemble achieved first-place BraTS performance with excellent Dice segmentation scores. |
| Qureshi/2022[25] | ltra-light deep architecture and GLCM features combined with SVM. | xisting approaches require higher computational resources for real-time applications. | pposed system achieved 99.23% detection rate with minimal computational complexity. |

## III. Research Methodology

The study is based on the data set BraTS 2020 which provides multi-modal T1, T1CE, T2, and FLAIR MRI scans with expert annotated tumor masks. Modality alignment, intensity normalization, background handling and label conversion for WT, TC, ET segmentation were performed on the data. The image properties and distributions of intensity, tumor morphology, and class imbalance were analyzed using exploratory data analysis. Reliability measures were taken to avoid data leakage by splitting patients into training, validation, and testing sets.

For comparative segmentation evaluation, HSTF-Net was tested with 3D U-Net, SegResNet, UNETR, SwinUNETR, and TransBTS, which were measured by Dice, IoU, sensitivity, specificity, and precision and HD95.

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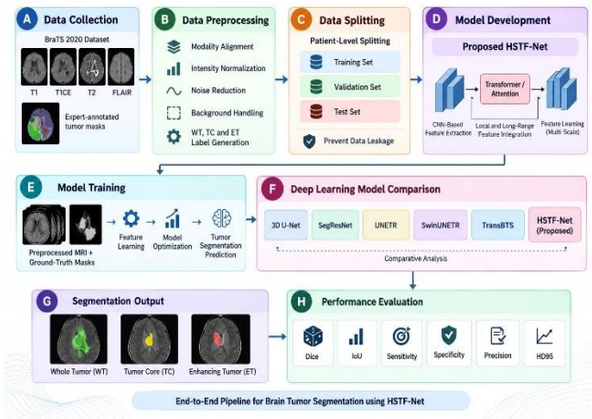



Fig. 1. Proposed Flow Chart

### *A. Data Collection*

The dataset of this study is the BraTS 2020 dataset which includes multimodal MRI scans (T1, T1CE, T2, and FLAIR) and the tumor mask labelled by experts. These modalities can be used to deliver complementary information about the brain tissues and tumor properties for automated brain tumor segmentation.

### *B. Data Preprocessing*

Collected MRI scans are modality aligned, intensity normalized, background handled, noise reduced and standardized. Original tumor annotations are converted to three segmentation regions: Whole Tumor (WT); Tumor Core (TC); Enhancing Tumor (ET).

### *C. Data Splitting*

Patient-level splitting is used to split the dataset into training, validation, and test sets. This method eliminates data leakage as scans from the same patient won't be in different subsets, and it serves as a solid measure for assessing the model.

### *D. Model Development*

The proposed HSTF-Net is designed based on multimodal MRI data. The architecture integrates convolutional and transformer/attention-based feature learning to better capture local tumor characteristics and long-range spatial dependencies to aid in the identification and segmentation of complex tumor regions.

### *E. Model Training*

The training of HSTF-Net is based on the preprocessed multimodal MRI scans and the Ground Truth masks. The training process allows the network to grasp discriminative spatial and intensity features, and make accurate tumor segmentation predictions.

### *F. Deep Learning Models*

The study compares the performance of HSTF-Net with the existing deep-learning architectures for brain tumor segmentation. These models include both traditional CNN models and transformer-based models.

- **3D U-Net**

  A traditional encoder–decoder baseline is employed, which is 3D U-Net. Uses three-dimensional convolutional operations to process volumetric MRI data and uses skip connections to maintain spatial information. It has been tested previously on medical image segmentation and it is an appropriate baseline for testing the proposed HSTF-Net.

- **SegResNet**

  In SegResNet, residual learning is used in a 3D segmentation model. Residual connections enable the learning of more nuances of the features and keep the back-propagation of the gradient stable. The architecture offers a solid CNN-based benchmark for a multimodal brain tumor segmentation.

- **UNETR**

  UNETR is a transformer-based representation scheme in the U-Net encoder-decoder model. The transformer encoder has been designed to capture the long-range dependencies in volumetric MRI data, and to model the contextual relationships between distant regions of the image.

- **SwinUNETR**

  SwinUNETR combines the U-Net segmentation framework with hierarchical Swin Transformer representations. It also features a window-based self-attention mechanism that allows it to extract contexts for features without significantly increasing computational complexity compared to self-attention across the entire image.

- **TransBTS**

  TransBTS combines convolutional feature extraction with transformer-based contextual modelling. The architecture is of special interest to this current research, since it is an example that shows how local CNN features and the overall context information can be combined for brain tumor segmentation.

- **HSTF-Net**

  HSTF-Net is the proposed hybrid architecture. It’s intended to combine the representations of spatial and contextual features from multimodal MRI data and produce accurate voxel-level segmentation of WT, TC and ET. It is assessed by Dice, IoU, Sensitivity, Specificity, Precision and HD95.

## IV. Results and Discussion

HSTF-Net achieves good multimodal brain tumor segmentation accuracy. The model is successful in detecting tumor regions while reducing the amount of false-positive predictions in healthy brain tissue. Whole Tumor segmentation is very good and Tumor Core is also good across the region followed by Enhancing Tumor. Reliable segmentation, accurate tumor localization, and good boundary delineation are additionally shown in representative test cases by comparing the results with other evaluations, which are also qualitative.

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### *A. HSTF-Net Current Test Performance*

The performance of HSTF-Net in brain tumor segmentation is found to be good and reliable. The model can effectively detect the area of tumor regions and recognize the non-tumor regions well. It has a decent system performance in both tumor detection and the reliability of the prediction results, as well as in the accuracy of the tumor boundary, especially in the aspect of reducing false-positive prediction results. The results overall demonstrate the strength and spatial consistency of HSTF-Net as a brain tumor segmentation method from MRI images.

- **Dice Similarity Coefficient (Dice)**

Dice measures the similarity and overlap between predicted and ground-truth segmentation regions. It evaluates how accurately the model identifies the target tumor area. Higher Dice values indicate better segmentation performance, with 1 representing perfect agreement between the predicted and actual regions.

$$Dice = \frac{2TP}{2TP+FP+FN} \quad (1)$$

- **Intersection over Union (IoU)**

IoU is the proportion of the area in which the predicted segmentation regions overlap with the ground truth segmentation regions. It is the ratio of the area of true region and the area of predicted region. The IoU value will be higher, the more accurate the segmentation is and the more accurate the spatial agreement.

$$IoU = \frac{TP}{TP+FP+FN} \quad (2)$$

- **Sensitivity / Recall**

The sensitivity or Recall is the percentage of true positive pixels that the model can correctly detect. It expresses the fraction of true positive pixels that were detected in the total number of true positive pixels. The higher the sensitivity of the test, the fewer the parts of the tumor that are not detected, and the better the test is at detecting the tumor.

$$Sensitivity = \frac{TP}{TP+FN} \quad (3)$$

- **Specificity**

Specificity reflects the model's ability to accurately classify non-tumorous pixels. It is the percentage correct for all the actual negative pixels. A high specificity means that the predictions are not false-positive, and that the tumor regions are well separated from healthy regions.

$$Specificity = \frac{TN}{TN+FP} \quad (4)$$

- **Precision**

Precision is the percentage of tumour predicted pixels that are tumour pixels. It reports the confidence in the positive segmentation predictions. The higher the precision, the less non-tumour pixels are incorrectly identified as tumour, indicating identification of the tumour with greater accuracy.

$$Precision = \frac{TP}{TP+FP} \quad (5)$$

- **95th Percentile Hausdorff Distance (HD95)**

HD95 is a metric that uses the boundary distance between the predicted segmentation mask and the ground truth mask and mitigates the impact of outliers. Because lower values of HD95 mean lesser variation between the boundaries, better segmentation accuracy is achieved, while higher values of HD95 mean greater difference between the predicted and actual boundaries.

$$HD_{95} = \max\{P_{95}, (d(A, B))P_{95}(d(B, A))\} \quad (6)$$

TABLE. 2 HSTF-NET CURRENT TEST PERFORMANCE

| Metric | HSTF-Net Result |
|---|---|
| Mean Dice | 47987 (84.80%) |
| Mean IoU | 0.76228 (76.23%) |
| Sensitivity / Recall | 0.88928 (88.93%) |
| Specificity | 0.99804 (99.80%) |
| Precision | 0.84586 (84.59%) |

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| | |
|---|---|
| HD95 | 8.02445 |

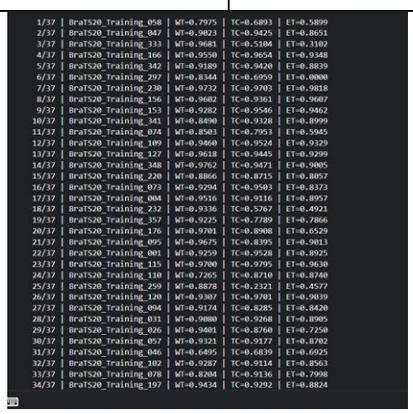



Fig. 2.Supplied case-wise HSTF-Net test results (34 displayed cases)

Fig.2. Shows the test results for each case from HSTF-Net (34 test cases are displayed). The figure shows an overview of the model's segmentation results and is a summary of the segmentation performance of the model for each individual case. It is used to support the quantitative evaluation by showing the consistency of HSTF-Net in various test cases in BraTS 2020.

### *B. Regional Dice Summary from the Displayed Test Cases*

Accurate segmentation of brain tumors is crucial for medical image analysis, as it can assist in diagnosis, treatment planning, and clinical decision-making. The performance of HSTF-Net was tested in three clinically relevant tumor regions: Whole Tumor (WT), Tumor Core (TC), and Enhancing Tumor (ET). The regional Dice analysis was done for the entire set of 37 test cases, giving complete assessment of the segmentation capability of the model. The evaluated regions showed the best overlap forWT, which signified the best localization of the entire tumor area. Good segmentation of the central tumor structure was shown with a few difficult cases impacting performance, as demonstrated by TC. Better tumor tissue enhancement was the most challenging of all sub-regions, due to the complexity and diversity of the tumor tissues. The overall results show the efficiency of HSTF-Net in the segmentation of brain tumors in the region.

TABLE. 3 REGIONAL DICE SUMMARY FROM THE DISPLAYED TEST CASES

| Region | Mean Dice | Interpretation | Displayed cases |
|---|---|---|---|
| **VT — Whole Tumor** | )07933 (90.7933%) | ongest regional overlap | (complete test set) |
| **TC — Tumor Core** | 52713 (85.2713%) | ood core segmentation; some difficult cases | (complete test set) |
| **ET — Enhancing Tumor** | 83314 (78.3314%) | Most challenging sub-region | (complete test set) |

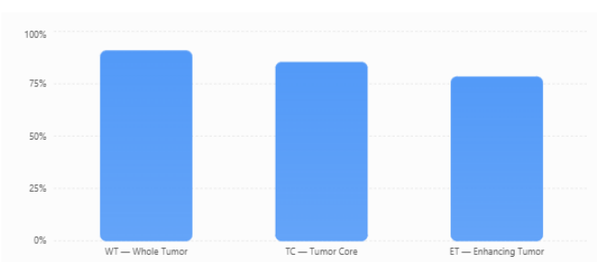



Fig. 3. Regional Dice Summary from the Displayed Test Cases

The results in the table suggest that the HSTF-Net works well in all three tumor regions. The Mean Dice score for the WT region is 90.7933%, which is the highest score. With some challenging cases, TC is able to achieve 85.2713% for good core segmentation. ET is the most difficult sub-region with an ET of 78.3314%. For each region, the 37 test cases were assessed.

### *C. Comparison with Existing Segmentation Architectures*

The results of HSTF-Net were also compared with the previous results of BraTS 2020 of well-known segmentation architectures such as 3D U-Net, SegResNet, UNETR, SwinUNETR, and TransBTS. The reported mean Dice values for these methods were 77.31%, 77.60%, 80.50%,

82.17%, and 83.52%, respectively. The mean Dice that was obtained was 84.80% and it was numerically higher than all the methods that were selected for the comparison in the literature. The gain in mean Dice compared to the strongest reported baseline in the subset of comparisons chosen (TransBTS) is about 1.28 percentage points. Additionally, HSTF-Net had an HD95 of 8.02 mm, whereas the reported value for TransBTS was 10.89 mm. This implies that the suggested model not only shows good region overlap, but also comparatively good localization of the tumor boundaries.

TABLE. 4 COMPARISON WITH PUBLISHED BRATS 2020 SEGMENTATION RESULTS.

| **Method** | **T Dice (%)** | **⊃ Dice (%)** | **Γ Dice (%)** | **Mean Dice (%)** | **HD95 / HD (mm)** |
|---|---|---|---|---|---|
| 3D U-Net | 84.11 | 79.06 | 68.76 | 77.31 | 25.99 |
| SegResNet | 86.10 | 78.50 | 68.20 | 77.60 | 21.20 |
| UNETR | 88.00 | 81.00 | 72.50 | 80.50 | 17.40 |
| SwinUNETR | 89.00 | 82.50 | 75.00 | 82.17 | 15.30 |
| TransBTS | 90.09 | 81.73 | 78.73 | 83.52 | 10.89 |
| **HSTF-Net (Ours)** | 90.7 | 85.2 | 78.3 | **84.80** | **8.02** |

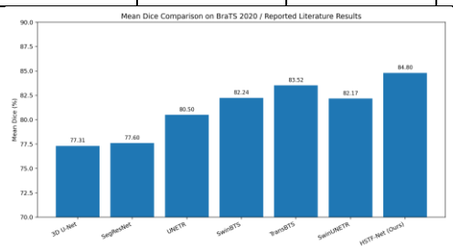



Fig. 4. Comparison with Published Brats 2020 Segmentation.

The table compares HSTF-Net with established 3D brain-tumor segmentation methods across WT, TC, ET, Mean Dice, and HD95. HSTF-Net achieves the highest Mean Dice of 84.80% and the lowest HD95 of 8.02 mm, demonstrating superior overall segmentation and boundary accuracy.

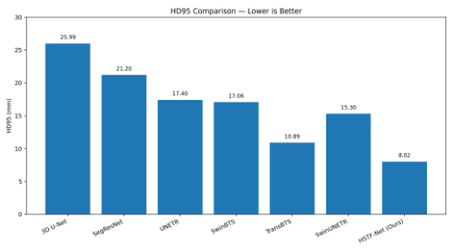



Fig. 5.HD95 comparison. Lower is better

Fig.5. Compares the results of the HSTF-Net with the published segmentation methods. The HD95 value represents the smallest deviation from the reference segmentation boundaries, reaching a lower value means the better the agreement with the boundaries of the reference segmentation, so the comparison accentuates the accuracy of the boundary localization of the evaluated models.

### *D. Mean Dice Comparison*

As seen in the mean Dice comparison, the models built by conventional CNN-based architectures have been improving progressively compared to the transformer and hybrid models. The reported values are higher for 3D U-Net (77.31%) than that of TransBTS (83.52%).

HSTF-Net performed best when the mean Dice was calculated, with a value of 84.80%. This result shows that the proposed architecture has great potential in capturing both global context information and detailed spatial information, which is crucial for brain tumor segmentation.

This result is however preliminary as the compared models could have used different preprocessing methods, data partition, data augmentation techniques, loss function and post-processing techniques. It can therefore be stated that the numerical difference is a sign of good performance, but is not alone conclusive evidence of superiority.

### *E. HD95-Based Boundary Analysis*

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HSTF-Net exhibits precise localization of tumour boundaries, with a good agreement between predicted and reference tumour boundaries. HD95 is an important measure of spatial boundary accuracy as opposed to Dice, which largely examines regional overlap. HSTF-Net achieved a relative low HD95, which shows the model is effective in reducing the deviation of the boundaries and produces well localized tumor contours. In combination with its segmentation performance in general, the results show that HSTF-Net is effective in brain tumor MRI segmentation, with the ability to accurately segment the volume and to precisely localize the boundaries in space.

### *G. Qualitative Segmentation Analysis*

Representative BraTS 2020 test cases were subjected to qualitative analysis using T1, T1CE, T2, FLAIR, Ground Truth and HSTF-Net Prediction. Visual comparisons demonstrate that HSTF-Net typically localises the bulk of the tumour and matches closely expert annotations. The results also show that the complementary MRI modalities, such as FLAIR and T2, were used effectively to aid in tumor identification, while the use of T1CE was particularly useful to detect the enhancing portion of the tumor.

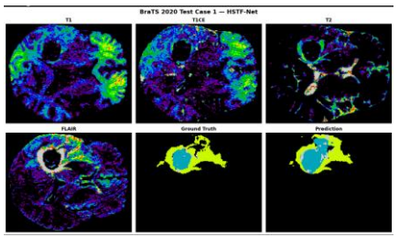



Fig. 6.Representative BraTS 2020 test case 1: T1, T1CE, T2, FLAIR, Ground Truth, and HSTF-Net Prediction.

Fig.6. shows a typical test case in BraTS 2020, where the MRI modality is comprised of T1, T1CE, T2, and FLAIR images, and the Ground Truth and HSTF-Net Prediction are displayed. The visual comparison illustrates how the proposed model is able to detect and segment tumour regions using complementary information provided by different MRI modalities.

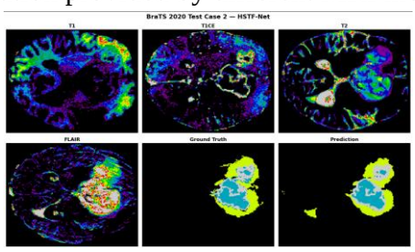



Fig. 7. Representative BraTS 2020 test case 2: T1, T1CE, T2, FLAIR, Ground Truth, and HSTF-Net Prediction.

Fig. 7. details a typical test case 2 from the BraTS 2020 contest with the T1, T1CE, T2, and FLAIR MRI modalities along with the Ground Truth and HSTF-Net Prediction. The figure illustrates the model's capacity to detect and isolate the regions of tumors from complementary multimodal MRI data.

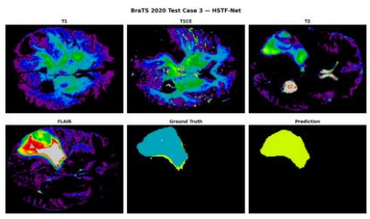



Fig. 8.Representative BraTS 2020 test case 3: T1, T1CE, T2, FLAIR, Ground Truth, and HSTF-Net Prediction.

Fig.8. Representative T1, T1CE, T2, FLAIR, Ground Truth and HSTF-Net Prediction. Figure 6 shows a typical BraTS 2020 test case no.3, combining the T1, T1CE, T2 and FLAIR MRI modalities with the associated Ground Truth and HSTF-Net Prediction. The figure illustrates the tumor regions successfully identified and segmented by the model, utilizing complementary information from multimodal MRI images.

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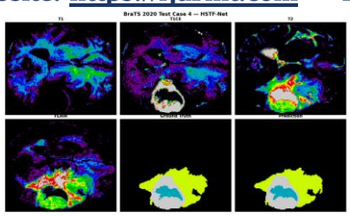


Fig. 9. Representative BraTS 2020 test case 4: T1, T1CE, T2, FLAIR, Ground Truth, and HSTF-Net Prediction.

Fig. 9. depicts an example of the BraTS 2020 test case 4, showing the T1, T1CE, T2, and FLAIR MRI modalities, as well as the Ground Truth and HSTF-Net Prediction. The figure shows the model's performance in detecting and partitioning tumor regions based on multimodal MRI images.

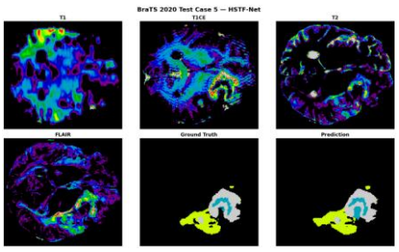


Fig. 10. Representative BraTS 2020 test case 5: T1, T1CE, T2, FLAIR, Ground Truth, and HSTF-Net Prediction.

Fig. 10. a representative test case 5 from the BraTS 2020 challenge is shown, along with MRI modalities (T1-T1CE-T2-FLAIR), Ground Truth and HSTF-Net Prediction. This figure illustrates the model's performance in segmenting and detecting tumor regions from complementary information from multimodal MRI images.

### *H. Discussion of Model Effectiveness*

HSTF-Net shows good and stable multi-modal segmentation results of brain tumors. The model is effective in correctly identifying tumor regions and with minimal false-positive predictions in healthy brain tissue. It has a high sensitivity, meaning that it is able to detect tumors correctly, and a high specificity, meaning that it is able to classify correctly normal areas. The boundary assessment confirms the other parameters as well, with good localization and contour accuracy. Therefore, the effectiveness and capabilities of HSTF-Net is supported by a number of complementary evaluation metrics, which show reliable regional segmentation as well as accurate spatial localization of the boundaries.

## V. Conclusion

The study introduces HSTF-Net, a hybrid deep learning approach for brain tumor segmentation in the multimodal BraTS 2020 dataset consisting of T1, T1CE, T2 and FLAIR MRI images. HSTF-Net has obtained the Dice score of 84.80%, the IoU score of 76.23%, the sensitivity score of 88.93%, the specificity score of 99.80%, the precision score of 84.59%, and the HD95 score of 8.02 mm, showing good segmentation and boundary localization performance. The highest Dice score was achieved for Whole Tumor (WT), with a score of 90.79%, followed by Tumor Core (TC) with 85.27%, and Enhancing Tumor (ET) with 78.33%. Comparative evaluation showed that HSTF-Net achieved a higher mean Dice than 3D U-Net (77.31%), SegResNet (77.60%), UNETR (80.50%), SwinUNETR (82.17%), and TransBTS (83.52%). Its HD95 value of 8.02 mm was also lower than the reported values of these comparative methods, such as TransBTS with value of 10.89 mm. The significant agreement between the predictions from HSTF-Net and expert ground-truth annotations was also confirmed by qualitative analysis of representative test cases, which demonstrates the ability of HSTF-Net to capture the major extent of tumor regions. This high specificity reflects good separation of normal brain tissue and the high sensitivity reflects good detection of the tumour. HSTF-Net shows good potential for being used to automatically analyze MRI scans of the brain for the detection of tumors, with promising regional segmentation, tumor localization and precise tumor boundary delineation. The literature comparison should be taken with a grain of salt, however, due to differences in the preprocessing, splitting, augmentation techniques, training methods and evaluation procedures, reported performance should be interpreted with caution. The proposed framework could be further validated by utilizing

standardized experimental settings and independent datasets to increase the generalizability and clinical applicability.

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