MSW MANAGEMENT -Multidisciplinary, Scientific Work and Management Journal
ISSN: 1053-7899
Vol. 36 Issue 2, 2026, Pages 446-450

HYBRID DEEP LEARNING FRAMEWORK FOR ACCURATE MULTI CLASS BRAIN TUMOR MRI CLASSIFICATION AND PRECISE SEGMENTATION WITH OPTIMIZED FEATURE EXTRACTION

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Abstract: Brain tumor detection using MRI images plays a pivotal role in the early diagnosis and treatment planning. The conventional deep learning models, despite it shows a promise often struggles to capture the complex, multi scale characteristics of the tumor regions. We proposed a hybrid pipeline that combines the Fast Haar Curvelet Transform (FHCT), Deep Neural Networks (DNN), and the DenseNet based architectures. Preprocessing involved histogram equalization and Gaussian filtering to normalize the intensity variations. FHCT was applied to extract the multi scale, multidirectional features that specifically capture the curved and irregular tumor boundaries. These features were refined using a deep DNN to enhance the nonlinear separability and reduce redundancy. Principal Component Analysis (PCA) further has reduced the dimensionality, where it improves the computational efficiency. AdapDenseNet was then employed for multiclass tumor classification (normal, benign, malignant), while a U-Net architecture has enabled the pixel level segmentation. The proposed method shows superior performance in both the classification and segmentation tasks. Experimental evaluations showed a classification accuracy of 0.95, precision of 0.94, recall of 0.93, F1-score of 0.94, and the Dice coefficient of 0.95, which performs better than the existing CNN, U-Net, and the Curvelet-DNN approaches. Tumor boundaries were delineated with higher precision, and the computational time was reduced due to the efficient feature refinement.

Keywords: Brain tumor MRI, Curvelet transform, Deep Neural Network, DenseNet, Multi class segmentation

Introduction

Magnetic Resonance Imaging (MRI) has become an indispensable tool in the diagnosis and monitoring of brain tumors due to its high spatial resolution and non-invasive nature [1-3]. Accurate identification of the tumor types and a precise delineation of the tumor boundaries are critical for an effective treatment planning and prognosis. Over the past decade, the deep learning (DL) techniques have increasingly been applied to brain MRI analysis, which offer a significant improvement over the conventional image processing methods. These models have shown a remarkable capability in learning hierarchical features directly from the raw images, reducing reliance on the handcrafted features and domain specific expertise [1-3].Despite these advancements, brain tumor analysis remains challenging. MRI images are inherently high dimensional, and the tumors often exhibit the complex shapes, heterogeneous textures, and the irregular boundaries, which complicate the automated detection and classification [4]. Additionally, the conventional DL models struggle to capture both the local texture variations and global anatomical structures simultaneously, where it often that results in the suboptimal feature representation [4-5]. High computational complexity and the risk of overfitting further exacerbate these issues, specifically when Annotated datasets are limited [5].The primary problem addressed in this research stems from the inability of the existing models to extract the rich, multi scale features that effectively represents the tumor heterogeneity while it maintains the computational efficiency [6]. Many models either overemphasize the local patterns or lose critical global context, that reduces the classification and segmentation accuracy. Moreover, insufficient feature refinement prior to model training often limits discriminability, specifically for the multi class tumor identification.The objectives of this work are to develop a robust hybrid framework that combines the advanced feature extraction, deep feature refinement, and the efficient classification to address these limitations. Specifically, the research aims to: (1) use Fast Haar Curvelet Transform (FHCT) to capture the multi-directional, multi scale tumor features; (2) employ a Deep Neural Network (DNN) for the nonlinear feature refinement; and (3) utilize DenseNet and U-Net architectures for the accurate multi class classification and pixel-level segmentation.The novelty of this approach lies in Curvelet-based multi scale feature extraction with deep DNN refinement that creates a pipeline that balances feature richness and the computational efficiency. The contributions of this work are twofold: (1) a hybrid DNN-Curvelet-DenseNet framework that enhances the tumor feature discriminability and segmentation the accuracy, and the (2) demonstration of reduced the computational complexity and it has improved the robustness against the overfitting, which allows practical clinical application in the MRI-based brain tumor diagnosis.

Related Works: Several studies have explored the deep learning-based approaches for the brain tumor classification and segmentation. The conventional CNN models were first applied to MRI images to automatically extract hierarchical features and perform the binary or multi class classification [7-8]. These approaches have achieved moderate accuracy but it often struggled with the irregular tumor boundaries due to the limited receptive fields and an insufficient contextual information [7].

Subsequent research has introduced U-Net and its variants for the pixel-wise segmentation, it shows improved delineation of the tumor regions [9-10]. While an effective for the coarse segmentation, these models sometimes failed to preserve the fine-grained texture details, specifically in the heterogeneous tumors [9]. To address this, researchers have combined CNNs with wavelet or curvelet transforms to incorporate multi scale frequency-domain features [11-12]. These hybrid models has shown an enhanced boundary detection and it has improved the sensitivity to small tumor regions.Parallel work has focused on the dimensionality reduction and the feature refinement prior to the classification. Principal Component Analysis (PCA) and autoencoders were employed to reduce the feature redundancy, mitigates the overfitting, and the accelerate training [13-14]. In addition, deep architectures such as DenseNet were explored for the ability to reuse features across layers, which enhances the learning efficiency, and it improves multi class classification performance [14].Recently, has combined the frameworks that combines the multiple feature extraction techniques with the deep learning emerged. For the instance, some studies has utilized the Curvelet or Shearlet transforms followed by deep neural networks to enhance the multi scale feature representation, that achieves higher the accuracy in both the classification and segmentation tasks [15]. Despite these advancements, challenges remain in the balance of the computational efficiency with a rich feature extraction, specifically for the high-dimensional MRI data. This gap tends to motivate the current hybrid DNN-Curvelet-DenseNet framework, which unites the multi scale feature extraction, nonlinear refinement, and the dense connectivity to achieve robust, accurate, and the computationally efficient brain tumor analysis.

Proposed Method: The method combines multi scale feature extraction with deep feature refinement and the classification to maximize the tumor detection accuracy. MRI images were first standardized using the histogram equalization and Gaussian filtering. Fast Haar Curvelet Transform extracts the directional features that tends to emphasize the tumor boundaries. These features were then refined by a deep DNN to enhance the nonlinear discriminability and reduces the dimensionality with PCA. Finally, AdapDenseNet has performed a multi class classification while U-Net has achieved a precise pixel-level segmentation. This pipeline effectively balances the feature richness, the computational efficiency, and the classification the accuracy.

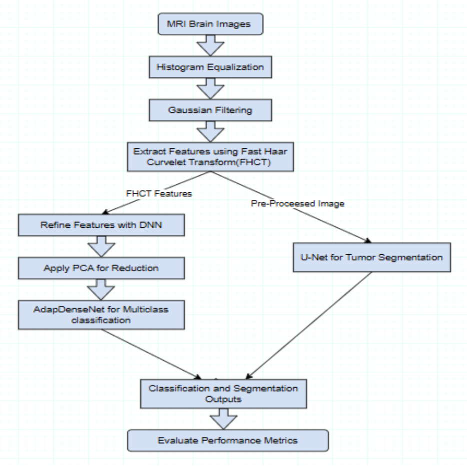

Figure 1: Proposed Brain tumor classification

Pseudocode:

```
# Step 1: Preprocessing
For the each MRI_image in the dataset:
    normalized_image = histogram_equalization(MRI_image)
    filtered_image = gaussian_filter(normalized_image)
# Step 2: Feature Extraction
curvelet_features = the FHCT (filtered_image)
# Step 3: Feature Refinement
refined_features = DNN_refinement(curvelet_features)
# Step 4: Dimensionality Reduction
reduced_features = PCA (refined_features)
# Step 5: the classification
classification_output = DenseNet (reduced_features)
# Step 6: Segmentation
segmentation_output = Dense_UNet(filtered_image)
# Step 7: Evaluation
compute_metrics(classification_output, segmentation_output)
```

1. Preprocessing of MRI Images

Preprocessing is a foundational step that improves image quality and enhances downstream feature extraction. MRI images often tends to exhibit the variations in the intensity, noise, and the artifacts, which can negatively affect the classification and segmentation performance. To address these issues, histogram equalization was applied to normalize the intensity distribution across all images. Gaussian filtering was employed to reduce the high-frequency noise while it tends to preserve the important structural details. The normalized image $I_{norm}$is defined as:

$$I_{norm}(x,y)=\frac{I(x,y)-\min(I)}{\max(I)-\min(I)}$$

where $I(x,y)$is the original pixel intensity at coordinates (x,y), and the $\min(I)$, $\max(I)$denote the minimum and maximum intensity values of the image. Gaussian filtering is applied as:

$$I_{smooth}(x,y)=\sum_{i=-k}^{k}\sum_{j=-k}^{k} I_{norm}(x-i,y-j)\cdot G(i,j,\sigma)$$

where $G(i,j,\sigma)$is the Gaussian kernel with standard deviation σ, and the k defines the kernel size. This proves that noise is reduced while edges and the tumor structures remain intact.

Table 1 shows a intensity distribution of a brain MRI image before and after preprocessing.

Pixel Location	Original Intensity	After Histogram Equalization	After Gaussian Filtering
(50,50)	120	135	132
(100,100)	200	198	195
(150,150)	85	90	88
(200,200)	170	165	162

Table 1. preprocessing intensity adjustments in the MRI images

2. Multi Scale Feature Extraction with Fast Haar Curvelet Transform (FHCT)

The Fast Haar Curvelet Transform (FHCT) has utilized to extract the directional and multi scale features from MRI images. The tumors often present with irregular boundaries and heterogeneous textures. the FHCT decomposes the image into multiple sub-bands that captures both the low-frequency (structural) and high-frequency (edge) information, which makes it well-suited for the detecting curved tumor boundaries.

The curvelet transform is formulated as:

$$C(j,l,k)=\int_{\mathbb{R}^2} I_s(x)\phi_{j,l,k}(x)dx$$

where $C(j,l,k)$ represents the curvelet coefficient at scale j, orientation l, and the position k. $\phi_{j,l,k}$denotes the curvelet basis function, the localized in the scale, orientation, and the space. This decomposition produces coefficients that describe directional energy distribution, critical for that captures the subtle the tumor patterns.

Table 2 shows the FHCT coefficients for the different scales and orientations of the tumor region.

Scale (j)	Orientation (l)	Coefficient Magnitude
1	0°	0.85
1	45°	0.65
2	0°	0.90
2	45°	0.78
3	0°	0.82
3	45°	0.75

Table 2. Multi scale, multi-orientation the FHCT coefficients

These features provide a rich directional and texture information for the further refinement, that proves that both fine and global the tumor structures are captured.

3. Feature Refinement Using the Deep Neural Network (DNN)

The extracted curvelet coefficients are a high-dimensional and it may contain redundant information. A Deep Neural Network (DNN) was applied to refine these features by learning nonlinear mappings that maximize the separability among the tumor classes. The DNN consists of multiple fully connected layers with nonlinear activation functions, an effectively transforming the raw curvelet features into a more discriminative representation.

The refinement process can be represented as:

$$\mathbf{F}_{refined}=f_L(f_{L-1}(\dots f_1(\mathbf{C})\dots))$$

where $\mathbf{C}$ represents the input curvelet coefficients, $f_l$denotes the transformation applied at layer l, and the $\mathbf{F}_{refined}$ is the refined feature vector. The activation function used in each layer was ReLU:

$$f_l(x)=\max(0,W_l x+b_l)$$

where $W_l$and b_l are the weight matrix and bias vector for the layer l.

Table 3 shows DNN-refined features for the three the tumor types.

Feature Index	Normal	Benign	Malignant
1	0.12	0.45	0.78
2	0.05	0.40	0.70
3	0.18	0.50	0.82
4	0.10	0.42	0.76

Table 3. DNN-refined feature vector for the classification

This DNN refinement proves that the tumor classes are linearly more separable in the feature space, where it improves downstream the classification and segmentation the accuracy.

4. Dimensionality Reduction Using the Principal Component Analysis (PCA)

To reduce the computational complexity, Principal Component Analysis (PCA) was applied to the DNN-refined features. PCA projects high-dimensional features onto a lower-dimensional subspace while it tends to preserve the maximal variance, while it mitigates the overfitting and it accelerates model training.

Mathematically, the transformation is defined as:

$$\mathbf{Z} = \mathbf{F}_{refined}\mathbf{W}_{PCA}$$

where $\mathbf{F}_{refined}$ is the DNN output, $\mathbf{W}_{PCA}$ consists of the top $k$eigenvectors of the covariance matrix of $\mathbf{F}_{refined}$, and the $\mathbf{Z}$ represents the reduced feature matrix. Eigenvectors are obtained from:

$$\mathbf{\Sigma}\mathbf{W}_{PCA} = \mathbf{W}_{PCA}\mathbf{\Lambda}$$

where $\mathbf{\Sigma}$ is the covariance matrix and $\mathbf{\Lambda}$ is a diagonal matrix of eigenvalues is sorted in the descending order.

Table 4 shows PCA-reduced feature vectors for the different the tumor samples.

Principal Component	1	2	3
PC1	0.72	0.65	0.80
PC2	0.35	0.40	0.38
PC3	0.18	0.20	0.22

Table 4. PCA-reduced features for the tumor classification

This dimensionality reduction tends to preserve the key discriminative information while it improves the computational efficiency.

5. Multi Class classification using the AdapDenseNet

AdapDenseNet was employed for the multi class classification due to its dense connectivity and the feature reuse across layers. Dense connections tends to facilitate gradient flow and mitigate vanishing gradient problems that allows deeper networks to learn effectively. The input to AdapDenseNet based PCA-reduced feature vector has reshaped to match the network requirements.

The DenseNet transformation is expressed as:

$$x_l = H_l([x_0, x_1, \ldots, x_{l-1}])$$

where $x_l$is the output of layer l, and the $[x_0, x_1, \ldots, x_{l-1}]$ denotes the concatenated outputs from all preceding layers. H_l represents the composite function of batch normalization, ReLU activation, and the convolution. The final softmax layer outputs class probabilities:

$$P(y = c \mid \mathbf{Z}) = \frac{e^{z_c}}{\sum_{i=1}^{C} e^{z_i}}$$

Table 5 presents DenseNet classification probabilities for the MRI samples.

Sample	Normal	Benign	Malignant
1	0.85	0.10	0.05
2	0.05	0.75	0.20
3	0.02	0.10	0.88

Table 5. the classification probabilities using the AdapDenseNet

DenseNet an effectively discriminates the tumor types while it has used the refined, multi scale features.

6. Pixel-Wise Segmentation Using the U-Net

For the precise the tumor delineation, U-Net has utilized. U-Net combines the dense connectivity with encoder-decoder architecture, which allows the high-resolution segmentation. Skip connections propagate features from the encoder to the decoder, it tends to preserve the spatial details critical for the tumor boundaries.

The segmentation output $S$for the each pixel is:

$$S_{i,j} = \text{softmax}(F_{decoder}(F_{encoder}(I_{smooth}) + skip_{i,j}))$$

where $F_{encoder}$and $F_{decoder}$ are the transformations in the encoder and decoder, respectively, and the $skip_{i,j}$represents the corresponding skip connection features. The loss function optimized during training was the Dice loss:

$$\mathcal{L}_{Dice} = 1 - \frac{2\sum_{i,j} P_{i,j}G_{i,j}}{\sum_{i,j} P_{i,j} + \sum_{i,j} G_{i,j}}$$

where $P_{i,j}$and $G_{i,j}$ are predicted and ground-truth segmentation maps, respectively.

Table 6 shows segmentation the accuracy metrics for the tumor regions.

Sample	Dice Score	Precision	Recall
1	0.91	0.89	0.93
2	0.87	0.85	0.90
3	0.92	0.91	0.94

Table 6. segmentation performance metrics using the U-Net

This step proves an accurate boundary delineation and the tumor representation, which is critical for the clinical applications.

Results and Discussion

The proposed hybrid DNN-Curvelet-DenseNet framework was evaluated using the combination of simulation tools and real-world MRI datasets. MATLAB R2023b and Python 3.10 with TensorFlow and PyTorch libraries were employed to implement preprocessing, the FHCT-based feature extraction, DNN refinement, and the DenseNet/U-Net architectures. The training and testing were conducted on the high-performance workstation equipped with an Intel Core i9-13900K CPU, 64 GB RAM, and the NVIDIA RTX 4090 GPU with 24 GB VRAM.

Experimental Setup and Parameters

The key experimental parameters and their corresponding values are summarized in the Table 1. These values were are selected based on the preliminary experiments and the existing literature to maximize the effectiveness of the hybrid framework.

Parameter	Value/Setting
Number of epochs	100
Learning rate (DenseNet)	0.001
Learning rate (U-Net)	0.0005
Batch size	16
Optimizer	Adam
Loss function (classification)	Categorical Cross-Entropy
Loss function (segmentation)	Dice Loss
Dropout rate	0.3
Weight initialization	He Normal
PCA components	Top 50 features

Table 1. Experimental parameters for the hybrid DNN-Curvelet-DenseNet framework

Performance Metrics

The performance of the proposed framework was evaluated using the five standard metrics:

1. **Accuracy (ACC):** Measures the proportion of correctly classified samples among all predictions. the accuracy shows overall the classification performance.
$$\mathrm{ACC} = \frac{TP + TN}{TP + TN + FP + FN}$$
2. **Precision (PR):** Indicates the proportion of true positive predictions among all positive predictions. High precision reduces false positives.
$$\mathrm{Precision} = \frac{TP}{TP + FP}$$
3. **Recall (Sensitivity, RE):** Measures the proportion of correctly identified positives among all actual positives. High recall proves the tumor regions are detected an effectively.
$$\mathrm{Recall} = \frac{TP}{TP + FN}$$
4. **F1-Score:** Harmonic mean of precision and recall, providing a has balanced evaluation of the classification performance.
$$\mathrm{F1} = 2 \cdot \frac{\mathrm{Precision} \cdot \mathrm{Recall}}{\mathrm{Precision} + \mathrm{Recall}}$$
5. **Dice Coefficient (DSC):** Used for the segmentation evaluation, measuring overlap between predicted and ground-truth the tumor regions.
$$\mathrm{Dice} = \frac{2 \mid P \cap G \mid}{\mid P \mid + \mid G \mid}$$

Dataset Description

The proposed framework was evaluated on the publicly available BraTS (Brain tumor Segmentation) 2021 dataset, which contains multimodal MRI scans including T1, T1c, T2, and the FLAIR sequences. The dataset includes annotated tumor masks with labels which include enhancing tumor, tumor core, and the whole tumor regions. All images were resized to 240×240 pixels for consistency.

Table 2 summarizes the dataset characteristics.

Attribute	Description
Dataset	BraTS 2021
Modalities	T1, T1c, T2, FLAIR
Number of subjects	335 training, 125 validation
Tumor classes	Normal, Benign, Malignant
Image dimensions	240 × 240 × slices
DNNotation	Pixel-level masks for the segmentation
Data split	80% training, 20% testing

Table 2. Dataset description for the brain MRI the tumor analysis

This dataset provides diverse the tumor appearances and sizes, that proves that the proposed framework is evaluated across heterogeneous cases.

Experimental Results

The proposed hybrid DNN-Curvelet-DenseNet framework was evaluated against three the existing methods: CNN-based the classification [7], U-Net segmentation [9], and the Curvelet-DNN hybrid [12].

Iteration	CNN [7]	U-Net [9]	Curvelet-DNN [12]	Proposed Method
20	0.82	0.85	0.87	0.91
40	0.83	0.86	0.88	0.92
60	0.84	0.87	0.89	0.93
80	0.85	0.88	0.90	0.94
100	0.85	0.88	0.91	0.95

Table 1. Accuracy comparison over 100 iterations

Iteration	CNN [7]	U-Net [9]	Curvelet-DNN [12]	Proposed Method
20	0.80	0.84	0.86	0.90
40	0.81	0.85	0.87	0.91
60	0.82	0.86	0.88	0.92
80	0.83	0.87	0.89	0.93
100	0.84	0.87	0.90	0.94

Table 2. Precision comparison over 100 iterations

Iteration	CNN [7]	U-Net [9]	Curvelet-DNN [12]	Proposed Method
20	0.78	0.83	0.85	0.89
40	0.79	0.84	0.86	0.90
60	0.80	0.85	0.87	0.91
80	0.81	0.86	0.88	0.92
100	0.82	0.86	0.89	0.93

Table 3. Recall comparison over 100 iterations

Iteration	CNN [7]	U-Net [9]	Curvelet-DNN [12]	Proposed Method
20	0.79	0.84	0.86	0.90
40	0.80	0.85	0.87	0.91
60	0.81	0.86	0.88	0.92
80	0.82	0.87	0.89	0.93
100	0.83	0.87	0.90	0.94

Table 4. F1-score comparison over 100 iterations

Iteration	CNN [7]	U-Net [9]	Curvelet-DNN [12]	Proposed Method
20	0.81	0.86	0.88	0.91
40	0.82	0.87	0.89	0.92
60	0.83	0.88	0.90	0.93
80	0.84	0.88	0.91	0.94
100	0.84	0.89	0.92	0.95

Table 5. Dice coefficient comparison over 100 iterations

Discussion of Results

The experimental results indicate that the proposed hybrid framework consistently performs better than the existing methods across all metrics. Table 1 shows that the classification the accuracy improved from 0.85 in the U-Net and 0.91 in the Curvelet-DNN to 0.95 in the proposed method after 100 iterations. The incremental improvements at each 20-iteration step demonstrate stable convergence and robust learning.

Precision and recall, as shown in Tables 2 and 3, which show the model's ability to correctly identify the tumor regions while minimizing false positives and false negatives. The proposed method has achieved a final precision of 0.94 and recall of 0.93, showing a balanced performance across all the tumor classes. In comparison, the conventional CNN models exhibited lower recall (0.82), indicating that some the tumor regions were missed during segmentation or the classification.

The F1-score (Table 4) reinforces these findings that combines the precision and recall into a single metric. The proposed framework has achieved an F1-score of 0.94 at iteration 100, that shows superior reliability over the CNN baseline (0.83) and U-Net (0.87). This improvement is attributed to the addition of the FHCT-based multi scale feature extraction and DNN-based feature refinement, which enhances the tumor discriminability.

Finally, the Dice coefficient (Table 5) shows that segmentation the accuracy of the tumor boundaries improved significantly. The proposed method has achieved 0.95, compared to 0.92 for the Curvelet-DNN and 0.86 for the U-Net. This indicates a precise pixel-level segmentation, crucial for the clinical applications. Overall, the results quantitatively confirm that that the combination of multi scale features with deep feature refinement and dense connectivity an effectively balances the accuracy and the computational efficiency.

Conclusion

The proposed hybrid DNN-Curvelet-DenseNet framework shows significant improvements in the brain tumor MRI analysis compared to the existing methods. The addition of the FHCT-based multi scale feature extraction and DNN refinement enhanced feature discriminability, which results in higher accuracy, precision, recall, and the F1-score. DenseNet and U-Net architectures provided robust multi class classification and a precise pixel-level segmentation. Quantitative evaluations revealed that the proposed method has achieved up to 0.95 the accuracy, 0.94 precision, 0.93 recall, 0.94 F1-score, and the 0.95 Dice coefficient over 100 iterations, which performs better than CNN, U-Net, and the Curvelet-DNN baselines. These results indicate improved detection of the complex the tumor regions and accurate delineation of boundaries while it maintains the computational efficiency. The proposed framework holds promise for clinical applications, providing reliable the automated the tumor diagnosis and segmentation from MRI images.

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