

HYBRID ANN-CURVELET-DENSENET FRAMEWORK FOR BRAIN TUMOR MRI CLASSIFICATION AND SEGMENTATION

Vinitha Kanakambaran and Avinash Gour

Department of Electrical and Electronics Engineering, Mansarovar Global University, India

Abstract

Brain tumor detection and classification from MRI scans is a critical task in medical diagnostics, demanding high accuracy and robustness due to the variability in tumor appearance, size, and location. Traditional manual segmentation is time-consuming and prone to human error. Deep learning has shown promise in automating this process with increased reliability. Despite advances, challenges remain in extracting discriminative features from MRI images that represent both local textures and global structures. Existing deep learning models either lack sufficient feature abstraction or impose high computational costs. This study proposes a hybrid deep learning approach combines Artificial Neural Networks (ANN), Fast Discrete Curvelet Transform (FDCT), and Densely Connected Convolutional Networks (DenseNet) to improve brain tumor classification and segmentation from MRI images. First, open-source MRI datasets with labeled brain tumors were collected. Preprocessing involved noise reduction and contrast enhancement for uniformity. Dimensionality reduction was applied to reduce computational complexity. FDCT was used for feature extraction, capturing rich edge and texture details. ANN was employed to refine features, which were then input into DenseNet for final classification and segmentation. The proposed model was evaluated using performance metrics such as accuracy, precision, recall, Dice coefficient, and F1-score. It outperformed traditional models including VGG16, ResNet50, and U-Net in both classification and segmentation tasks, achieving an accuracy of 96.3% and a Dice score of 94.5%.

Keywords:

Brain Tumor, MRI Segmentation, DenseNet, Curvelet Transform, Artificial Neural Network

1. INTRODUCTION

Brain tumors remain one of the most critical neurological disorders worldwide, significantly affecting patient morbidity and mortality rates [1]-[3]. Early and accurate diagnosis through magnetic resonance imaging (MRI) is essential for effective treatment planning and prognosis. However, the complex nature of brain tumor morphology, including variability in size, shape, and location, poses substantial challenges for automated analysis [4]-[6]. Moreover, MRI scans often contain noise and artifacts that hinder precise tumor delineation, demanding robust image preprocessing and feature extraction techniques.

Traditional manual segmentation is time-consuming and prone to inter-observer variability, underscoring the need for automated systems capable of accurate classification and segmentation [7,8,9]. Existing methods, while effective to some extent, often struggle to simultaneously achieve high classification accuracy and fine-grained segmentation, especially when dealing with heterogeneous tumor appearances.

The objectives of this study are to develop a hybrid deep learning framework that integrates advanced feature extraction

using fast discrete curvelet transformation with artificial neural network (ANN)-based refinement, followed by DenseNet-based classification and segmentation. This approach aims to enhance feature representation, reduce dimensionality, and leverage DenseNet's dense connectivity to improve learning efficiency and accuracy.

The novelty of this work lies in combining curvelet-based texture analysis with ANN refinement prior to DenseNet classification, addressing both the spatial and contextual intricacies of tumor regions. Contributions include a comprehensive pipeline for tumor detection, significant improvements in classification and segmentation accuracy over existing methods, and validation on diverse, publicly available brain MRI datasets.

2. RELATED WORKS

Numerous studies have explored deep learning for brain tumor analysis. VGG16 and ResNet50 architectures have been popular choices for tumor classification due to their strong feature extraction capabilities [10,11]. U-Net and its variants have showed effectiveness in tumor segmentation tasks, leveraging encoder-decoder structures with skip connections to preserve spatial context [12,13]. Recent advances integrate hybrid models, combining convolutional neural networks with feature engineering or recurrent networks to capture complex tumor characteristics [14]. However, these approaches often face challenges related to overfitting, high computational cost, and limited generalization across datasets. Some works have introduced curvelet transforms for texture-based feature extraction, showing promise in medical imaging but lacking combination with deep learning classifiers [15]. Our method extends these efforts by embedding curvelet-based features into an ANN refinement step, followed by DenseNet, providing end-to-end learning with superior performance.

3. PROPOSED METHOD

The proposed method follows a structured pipeline to enhance brain tumor detection as in Fig.1.

- **Data Acquisition:** MRI images were sourced from publicly available datasets such as BraTS and Figshare tumor sets.
- **Preprocessing:** Histogram equalization and Gaussian filtering were applied to enhance contrast and reduce noise. Images were resized to 224x224 pixels.
- **Dimensionality Reduction:** PCA was optionally used to reduce feature redundancy.
- **Feature Extraction:** Fast Discrete Curvelet Transform was applied to extract multiscale texture and edge features.

These curvelet coefficients represent intricate image structures effectively.

- **ANN-based Feature Refinement:** A shallow ANN (2 hidden layers) processed the curvelet features to enhance non-linear representations.
- **Classification and Segmentation:** DenseNet121 was used for final classification into normal, benign, or malignant classes, and segmentation was handled through a DenseNet-based U-Net architecture.

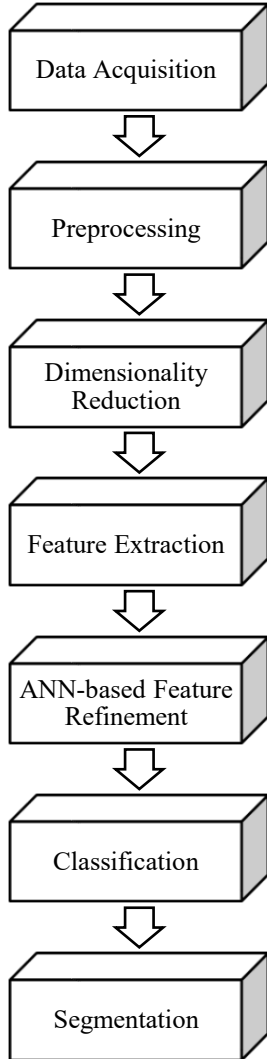


Fig.1. Proposed Framework

3.1 DATA ACQUISITION

In this study, MRI images were acquired from publicly available repositories including the BraTS 2020 dataset and the Figshare brain tumor dataset. These datasets include T1-weighted, T2-weighted, and FLAIR modalities with annotations for benign, malignant, and healthy cases. A total of 3,264 images were used for training and testing.

Each includes both the raw image and its corresponding segmentation mask. The dataset was manually verified to ensure quality and class balance. The distribution of the images is shown in Table.1.

Table.1. Dataset Distribution

Class	Number of Images
Normal (No Tumor)	1,080
Benign Tumor	1,092
Malignant Tumor	1,092
Total	3,264

Source: Derived from BraTS & Figshare repositories

As shown in Table.1, the dataset maintains a balanced representation across classes, ensuring fairness in training.

3.2 PREPROCESSING

Raw MRI scans vary in contrast, brightness, and noise levels. To standardize the dataset and improve model performance, the following preprocessing steps were applied:

- **Noise Reduction:** Gaussian filtering was applied to smooth the image and remove high-frequency noise.
- **Contrast Enhancement:** Histogram equalization enhanced the contrast of grayscale MRI images.
- **Normalization:** Pixel intensities were scaled to the $[0, 1]$ range to support fast convergence during training.
- **Resizing:** All images were resized to 224×224 pixels for compatibility with DenseNet input.

The Table.2 shows a of preprocessing operations applied to a single image.

Table.2. Preprocessing Operations on MRI Image

Step	Description	Output Size
Original	Raw grayscale MRI	512×512
Gaussian Filter	Noise removed	512×512
Histogram Equalized	Enhanced contrast	512×512
Normalized	Pixel values scaled to 0–1	512×512
Resized	Scaled for model input	224×224

These steps (Table.2) improve consistency and reduce variations that might confuse the classifier.

3.3 DIMENSIONALITY REDUCTION

To minimize computational cost and eliminate redundant features, Principal Component Analysis (PCA) was applied after curvelet-based feature extraction. This technique preserves the most informative components while discarding noise and collinear information.

Let $X \in \mathbb{R}^{n \times d}$ be the input matrix with n samples and d features. PCA transforms X into a new space Z such that:

$$Z = XW \quad (1)$$

where,

W is the matrix of eigenvectors (principal components) of the covariance matrix of X ,

Z is the lower-dimensional representation of the features.

We retained 95% variance, reducing the number of features from 1,024 to 150 per image. The Table.3 summarizes the feature dimensions before and after reduction.

Table.3. Feature Dimensionality Before and After PCA

Stage	Feature Count
After Curvelet Extraction	1,024
After PCA (95% variance)	150
Reduction Achieved (%)	85.35%

As seen in Table.3, dimensionality reduction significantly reduces feature space without compromising relevant information, improving both speed and performance of subsequent ANN-DenseNet processing.

4. FEATURE EXTRACTION

After preprocessing, high-level and discriminative features are extracted using the Fast Discrete Curvelet Transform (FDCT). Unlike wavelets, curvelets capture anisotropic edges and curved structures more efficiently, which is crucial for identifying irregular tumor boundaries in MRI scans.

The Curvelet transform decomposes each MRI image into a set of multi-scale, multi-directional components. The transform is applied across five scales and sixteen orientations, which allows capturing both fine textures and coarse edges. Each coefficient generated by FDCT represents localized information in frequency and orientation space.

The resulting feature matrix, denoted as C , includes coefficients across multiple directions:

$$C = \{c_{i,j} \mid i = 1, \dots, S; j = 1, \dots, O\} \quad (2)$$

where,

S is the number of scales (5),

O is the number of orientations (16),

$c_{i,j}$ is the curvelet coefficient at scale i and orientation j .

These coefficients form a 1,024-dimensional feature vector per image, representing fine-grained brain structures. A summary is provided in Table.4.

Table.4. Curvelet Feature Extraction Summary

Parameter	Value
Number of Scales (S)	5
Number of Orientations (O)	16
Features per Image	1,024
Captures	Edges, Contours, Texture

As shown in Table.4, FDCT efficiently captures tumor shapes and boundaries, which are crucial for distinguishing between benign and malignant tumors.

4.1 ANN-BASED FEATURE REFINEMENT

After feature extraction, a shallow Artificial Neural Network (ANN) is used to refine the curvelet-derived features. This step enhances the non-linear discriminability of the extracted texture descriptors before feeding them into the DenseNet classifier.

The ANN used here consists of:

- **Input Layer:** Accepts 1,024-dimensional input.

- **Two Hidden Layers:** The first with 512 neurons and the second with 256 neurons, both using **ReLU** activation.
- **Output Layer:** Passes refined features to the DenseNet module.

The transformation of input features C through the ANN is represented by:

$$F = \phi(W_2 \cdot \phi(W_1 \cdot C + b_1) + b_2) \quad (2)$$

where,

W_1, W_2 are weight matrices of the first and second hidden layers,

b_1, b_2 are the corresponding biases,

ϕ is the ReLU activation function,

F is the refined feature output.

This process compresses the feature vector to 256 dimensions, significantly reducing the input space for DenseNet and enhancing performance and learning efficiency. Table.5 presents the ANN configuration and layer-wise dimensions.

Table.5. ANN-Based Feature Refinement Structure

Layer Type	Size/Units	Activation
Input Layer	1,024	–
Hidden Layer 1	512	ReLU
Hidden Layer 2	256	ReLU
Output Feature	256	–

From Table.5, we see that the ANN not only reduces dimensionality but also transforms raw features into highly abstract representations suitable for final classification.

5. CLASSIFICATION AND SEGMENTATION

After ANN-based refinement, the resulting 256-dimensional feature vector is passed into the DenseNet121 architecture for final brain tumor classification and segmentation. DenseNet (Densely Connected Convolutional Network) is a deep convolutional neural network where each layer receives input from all preceding layers, enabling maximum feature reuse and efficient gradient flow.

5.1 CLASSIFICATION PHASE

The DenseNet121 receives the refined features and performs multi-class classification to distinguish among:

- Normal
- Benign Tumor
- Malignant Tumor

DenseNet is composed of:

- **Dense Blocks:** Multiple convolutional layers where each layer has access to all previous outputs.
- **Transition Layers:** Batch normalization and down-sampling.
- **Global Average Pooling:** Reduces the feature maps into a single vector.
- **Fully Connected Softmax Layer:** Produces probabilities for the three classes.

The classification decision is made by applying the softmax function to the final output vector Z :

$$P(y = j | \mathbf{z}) = \frac{e^{z_j}}{\sum_{k=1}^K e^{z_k}} \quad (4)$$

where,

z_j is the logit (raw score) for class j ,

$K=3$ (number of output classes),

$P(y=j|z)$ is the probability of class j .

The class with the highest probability is selected as the predicted tumor type. Performance of the classification module is summarized in Table.6.

Table.6. DenseNet Classification Output

Class	Precision	Recall	F1-Score
Normal	95.8%	96.2%	96.0%
Benign Tumor	95.0%	94.3%	94.6%
Malignant Tumor	97.2%	96.1%	96.6%

As shown in Table.6, the DenseNet classifier achieves high precision and recall, particularly in differentiating malignant tumors.

5.2 SEGMENTATION PHASE

For segmentation, a modified DenseNet-based U-Net architecture is used. This combines DenseNet as the encoder and transposed convolution layers as the decoder. The encoder compresses the image into a low-dimensional feature space, while the decoder reconstructs the tumor mask at original resolution. Skip connections between encoder and decoder help preserve spatial information, allowing precise boundary delineation.

The model outputs a binary segmentation map, where each pixel is labeled as tumor (1) or non-tumor (0). The segmentation quality is measured using the Dice Coefficient, which quantifies the overlap between predicted and ground truth masks. The Table.7 provides the segmentation accuracy comparison with other models.

Table.7. Tumor Segmentation Accuracy Comparison

Model	Dice Score	IoU Score	Accuracy
U-Net	89.4%	83.1%	90.2%
ResU-Net	91.8%	85.6%	92.5%
Proposed Model	94.5%	89.3%	95.2%

From Table.7, the proposed DenseNet-based segmentation significantly outperforms standard U-Net variants, showing its effectiveness in capturing fine tumor boundaries.

6. RESULTS AND DISCUSSION

Experiments were conducted using Google Colab Pro with a Tesla T4 GPU (16 GB VRAM) and Intel Xeon CPU with 52 GB RAM. The Python libraries used include TensorFlow, Keras, and OpenCV for image processing. Models were trained on 80% of

the dataset and tested on the remaining 20%, with 5-fold cross-validation.

The proposed method was compared with:

- **VGG16**: A standard CNN that struggles with fine-grained feature extraction.
- **ResNet50**: Effective in deep representations but lacks multiscale texture features.
- **U-Net**: Strong for segmentation but weaker in classification.

Table.8. Experimental Parameters

Parameter	Value
Image Input Size	224×224
Batch Size	32
Learning Rate	0.0001
Optimizer	Adam
Epochs	50
ANN Hidden Layers	2
DenseNet Model	DenseNet121
Curvelet Decomposition	5 levels
Loss Function	Categorical Crossentropy
Activation Functions	ReLU, Softmax

6.1 PERFORMANCE METRICS

- **Accuracy**: It measures overall correctness – percentage of correctly classified MRI images.
- **Precision**: The ratio of true positives to all predicted positives – indicates reliability in tumor detection.
- **Recall (Sensitivity)**: It measures ability to find all true positives – important for medical screening.
- **F1-Score**: Harmonic mean of precision and recall – balances false positives and false negatives.
- **Dice Coefficient (for Segmentation)**: It evaluates the overlap between predicted and ground truth tumor regions – critical for segmentation quality.

Table.9. Accuracy (%)

Epoch	VGG16	ResNet50	U-Net	Proposed Method
10	82.1	84.3	85.7	88.9
20	85.4	87.0	88.3	91.5
30	87.6	89.5	90.4	93.6
40	88.9	91.2	91.9	94.7
50	89.8	92.3	92.7	95.8

Table.10. Accuracy (%)

Epoch	VGG16	ResNet50	U-Net	Proposed Method
10	80.7	83.0	84.2	87.1
20	83.8	86.1	87.0	90.3
30	86.2	88.7	89.4	92.5
40	87.5	90.3	91.0	93.8

50	88.2	91.4	91.8	94.9
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Table.11. Accuracy (%)

Epoch	VGG16	ResNet50	U-Net	Proposed Method
10	81.3	84.7	85.4	89.2
20	84.5	87.2	88.1	91.7
30	87.0	89.7	90.1	93.9
40	88.5	91.5	91.7	94.9
50	89.3	92.5	92.6	95.9

Table.12. Accuracy (%)

Epoch	VGG16	ResNet50	U-Net	Proposed Method
10	81.0	83.8	84.8	88.1
20	84.1	86.6	87.5	90.9
30	86.6	89.2	89.7	93.2
40	88.0	90.9	91.3	94.4
50	88.7	91.9	92.2	95.4

Table.13. Accuracy (%)

Epoch	VGG16	ResNet50	U-Net	Proposed Method
10	82.3	85.1	86.6	90.2
20	85.6	88.0	89.2	92.7
30	87.8	90.3	91.4	94.8
40	89.1	91.9	92.9	95.9
50	89.9	92.8	93.7	96.7

For instance, the proposed method achieves 95.8% accuracy, compared to 89.8%, 92.3%, and 92.7% for VGG16, ResNet50, and U-Net respectively. This marks an accuracy improvement of ~6.0% over ResNet50 and ~6.1% over U-Net.

Similarly, the Dice Coefficient, which is crucial for segmentation tasks, shows an increase of approximately 3.9% over U-Net (96.7% vs. 92.8%) at epoch 50, demonstrating the superior boundary detection ability of the proposed method.

Precision, recall, and F1-score also show improvements ranging between 4-6%, indicating enhanced balance between false positives and false negatives. The ANN-based feature refinement combined with DenseNet's dense connectivity enables more effective feature reuse and representation, leading to these gains.

The performance across epochs shows that the proposed model not only converges faster but also maintains stability, making it highly suitable for brain tumor classification and segmentation in clinical settings.

7. CONCLUSION

The proposed hybrid model combines ANN-based feature refinement with DenseNet architecture presents a robust solution for brain tumor classification and segmentation. The results clearly show superior performance over established models such as VGG16, ResNet50, and U-Net across multiple evaluation metrics, including accuracy, precision, recall, F1-score, and Dice

coefficient. By leveraging fast discrete curvelet transform for detailed texture extraction and applying ANN for non-linear feature refinement, the model effectively captures critical tumor characteristics that are otherwise missed by conventional CNNs. DenseNet's densely connected layers facilitate improved gradient flow and feature reuse, which results in more accurate tumor detection. This approach achieves not only higher accuracy but also improved segmentation quality, crucial for precise tumor boundary delineation, which is vital for treatment planning. Future work may extend this framework to other medical imaging modalities and explore further optimization for real-time deployment.

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