

Multi-Task U-Net Architecture for Tumor Segmentation and Recognition based on Fractal Analysis and Nonlinear Reaction-Diffusion

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Abstract—This research paper introduces a novel deep learning-based cerebral tumor detection and classification framework. The proposed technique is based on an improved hybrid U-Net architecture designed for simultaneous segmentation and recognition. The developed multi-task deep network, namely PDE-Fractal-UNet, integrates successfully nonlinear reaction-diffusion based layers and attention mechanisms that are built using fractal analysis. Classical U-Net convolution blocks have been replaced by new blocks combining effectively these fractal and diffusion-based layers and using the fractal expansion. A classification branch has been also integrated in the architecture. Our PDE-Fractal-UNet model has been trained successfully on a MRI brain tumor dataset and high performance metric scores have been achieved for both segmentation and recognition tasks.

Index Terms—Brain tumor segmentation and classification, Magnetic Resonance Imaging, multi-task U-Net, fractal layers, nonlinear reaction-diffusion, fractal expansion, attention module.

I. INTRODUCTION

THE cerebral tumors are complex and life-threatening medical conditions that impact the quality of life of millions of persons worldwide. Early stage cerebral tumor detection and recognition represent critical medical tasks for improving the patient survival rates and maximizing the treatment effectiveness. Magnetic Resonance Imaging (MRI) is considered the most effective brain tumor detection modality, since it allows the detailed visualization of the cerebral structures [1].

The accurate segmentation and recognition of brain tumors from MRI, which are essential for diagnosis and treatment, still represent challenging medical image analysis tasks. Machine learning-based segmentation approaches, including the active contours [2], region growing [3] and pixel clustering models [4] achieve low accuracy, struggle with ill-defined tumor boundaries and cannot manage the complex MRI data.

Artificial intelligence, specifically through deep neural networks, have revolutionized the MRI analysis domain, locating and recognizing the cerebral tumors with high precision. Convolutional neural networks (CNN), such as U-Net model and its improved versions [5]–[11], DeepLabV3+ [12] and GSNet [13], and Vision Transformers (ViT) [14] demonstrated high brain tumor detection and classification performances. The U-Net model represents an encoder-decoder CNN specifically designed for biomedical semantic segmentation tasks [5].

Many improved variants of it have been developed in the last decade. They include U-Net++ [6] that replaces the skip connections with nested convolutional blocks, transfer learning-based versions like Res-UNet [7] and Dense-UNet [8], attention-based variants such as Attention U-Net [9] and Attention Res-UNet [10], and ViT-based models like Swin-UNet [11].

We have developed an enhanced multi-task U-Net that is applied successfully to MRI brain tumor segmentation and classification tasks. An important aim of the proposed CNN-based framework, namely PDE-Fractal-UNet, is to prove the usefulness of a combination of mathematical models based on partial differential equations (PDE) and fractal geometry in improving considerably the traditional U-Net model. Thus, the PDE-based layers of this network have been built applying a new nonlinear reaction-diffusion model, while its fractal layers are modeled using fractal analysis features. Classical U-Net convolution blocks have been replaced by network blocks combining the PDE layers to attention modules integrating the fractal layers. The structure of these blocks is based on fractal expansion, which is a fractal geometry concept [15]. A classification head has been connected to the bottleneck layer's output, to perform the recognition task.

The architecture, training and validation of PDE-Fractal-UNet is described in the next section. Brain tumor segmentation and classification results and method comparison are discussed in the third section. Conclusions of this research are drawn in the fourth section that also includes our future plans.

II. NOVEL U-NET-BASED TUMOR DETECTOR AND CLASSIFIER

The proposed segmentation and recognition framework, which locates and classifies properly the three common types of brain tumors, namely glioma, meningioma and pituitary tumors, is based on an improved multi-task U-Net architecture that is detailed here. The anisotropic diffusion and fractal analysis-based layers and attention modules are described first. Next, the construction of the fractal blocks composed of them is presented. The complete architecture, training and validation of PDE-Fractal-UNet model are then described.

A. Nonlinear Reaction-Diffusion based Layer

The PDE-based layer of this CNN, namely PDE-Layer, has been built using the next nonlinear reaction-diffusion model:

$$\begin{cases} \frac{\partial u}{\partial t} - \alpha \varphi(|\nabla^2 u_\sigma|) \nabla \cdot (\Psi(\|\nabla u\|) \nabla u) + \lambda(u - u_0) = 0 \\ u(x, y, 0) = u_0 \end{cases} \quad (1)$$

where u_0 is observed image, $u_\sigma = u * G_\sigma$, 2D Gaussian filter kernel $G_\sigma(x, y) = \frac{1}{2\pi\sigma^2} e^{-\frac{x^2+y^2}{2\sigma^2}}$, diffusivity function $\Psi(s) = e^{-s^2/k}$, $\varphi(s) = \gamma^{\frac{k+1}{\sqrt{\xi s^{k+\alpha}}}}$ and the empirically selected parameters of the model are $\alpha, \lambda \in [0.5, 4]$ and $\gamma, \beta, \xi \in [1, 5]$.

The anisotropic diffusion model (1) is non-variational, since it cannot be obtained through energy functional minimization. It is also mathematically valid, or well-posed, since it admits a unique variational (weak) solution that can be determined numerically by applying the finite difference method [16] - [18]. Therefore, we have proposed a finite difference-based approximation algorithm to solve numerically this PDE model. The following space and time quantization has been used here: $x = ih, y = jh, i \in \{1, \dots, I\}, j \in \{1, \dots, J\}$ and $t = n\Delta t, n \in \{0, \dots, N\}$.

The term $\frac{\partial u}{\partial t}$ is approximated as $\frac{u_{i,j}^{n+\Delta t} - u_{i,j}^n}{\Delta t}$ and the discrete Laplacian is $\frac{(u_\sigma)_{i+h,j}^n + (u_\sigma)_{i-h,j}^n + (u_\sigma)_{i,j+h}^n + (u_\sigma)_{i,j-h}^n - 4(u_\sigma)_{i,j}^n}{h^2}$. Next, the divergence component $\nabla \cdot (\Psi(\|\nabla u\|) \nabla u)$ is discretized as $\tau \sum_{q \in N(p)} \Psi(\|\nabla u_{p,q}^n\|) \nabla u_{p,q}^n$, where $\tau \in (0, 1]$, $N(p)$ is the 4-neighborhood of pixel $p = (i, j)$ and $\nabla u_{p,q}^n = u_q^n - u_p^n$ is the gradient magnitude in a given direction. We have considered $h = \Delta t = 1$ and thus obtained the next explicit iterative numerical approximation for (1):

$$u_{i,j}^{n+1} = u_{i,j}^n (1 - \lambda) + \alpha \tau \varphi(|(u_\sigma)_{i+1,j}^n + (u_\sigma)_{i-1,j}^n + (u_\sigma)_{i,j+1}^n + (u_\sigma)_{i,j-1}^n - 4(u_\sigma)_{i,j}^n|) \sum_{q \in N(p)} \Psi(\|\nabla u_{p,q}^n\|) \nabla u_{p,q}^n + \lambda u_0^n \quad (2)$$

The fast-converging numerical algorithm (2) is stable and consistent to nonlinear diffusion model (1). It has been implemented in PDE-Layer with a number of iterations $N = 5$. This diffusion-based layer, which is positioned at the beginning of the encoder's blocks, has the role of enhancing the image by applying the described anisotropic diffusion process that filters the noise and sharpens its edges, thus preserving the critical diagnostic details. So, PDE-Layer facilitates the capture of the fine structural details that are essential to a successful medical image segmentation.

B. Fractal-based Attention Mechanism

Fractal geometry is considered highly important for the medical image segmentation tasks, since its features allow for the quantitative representation of complex, irregular biological structures that cannot be characterized properly by classic Euclidean geometry. So, we have built a network layer, namely Fractal-Layer, by applying fractal analysis [19]-[21]. Our technique extracts and combines complex fractal geometry characteristics, such as fractal dimension [19, 20] and lacunarity [21], at multiple scales. These fractal features help differentiate between healthy and tumor tissues by quantifying tissue texture, diversity and complexity. So, integrating them into the segmentation framework enhances the tumor localization precision.

First, we have computed the fractal dimension (FD), which is a quantitative measure of branching complexity, by applying the box-counting method over $[64 \times 64]$ sliding windows with 50% overlap [19]. The considered scales (box sizes) are $\varepsilon \in \{2, 4, 8, 16\}$. For each window centered at (x, y) , we have estimated the Minkowski-Bouligand fractal dimension as follows:

$$FD = \lim_{\varepsilon \rightarrow 0} [\log N(\varepsilon) / \log(1/\varepsilon)] \quad (3)$$

where $N(\varepsilon)$ is the count of boxes at scale ε . The local fractal dimension is approximated as $FD(x, y) \approx -[d \log N(\varepsilon) / d \log \varepsilon]$. Thus, we have obtained a fractal dimension feature map that is a specialized image description where pixel intensities correspond to the local FD.

Then, we have computed the lacunarity that captures the spatial heterogeneity and gap distribution patterns. We have applied a gliding box algorithm at the same scales [21]. So, the lacunarity at scale S has been determined as:

$$A(S) = [\sigma^2(S) / \mu^2(S)] + 1, \quad (4)$$

where μ and σ return the mean and standard deviation per box at that scale. These values have been averaged across these scales to achieve a single heterogeneity map. Finally, we have combined the fractal dimension and lacunarity characteristics by concatenating their feature maps. This feature map fusion that provides a complete textural description has been implemented in Fractal-Layer. Next, this fractal layer has been integrated into a spatial attention mechanism.

Thus, we have built a hybrid fractal-based Convolutional Block Attention Module (CBAM) that fine-tunes the feature maps and named it Fractal-CBAM. Original CBAM uses 2 attention maps, mean (*Average Pooling*) and maxim (*Max Pooling*) respectively, in both Channel Attention Module (CAM) and Spatial Attention Module (SAM) [22]. Our improved CBAM incorporates Fractal-Layer directly into the spatial attention branch, and so its number of maps becomes $2N_s + 2 = 10$, since our number of scales $N_s = 4$.

This insertion of the fractal features in the attention mechanism leads to a better capture of the structural image details, which traditional approaches such as max and average pooling might discard. Statistical characteristics *mean* and *max* have been concatenated to the fractal features computed by Fractal-Layer, then a sigmoid function-based data normalization has been performed in Fractal-CBAM.

C. Fractal-based CNN Blocks

The standard U-Net convolution blocks have been replaced by more effective fractal-based CNN blocks in the proposed hybrid PDE-Fractal-UNet architecture. We have built two types of network blocks by applying the recursive fractal expansion technique [15].

The first one, namely PDE-Fractal-Block, integrates the nonlinear diffusion-based PDE-Layer and it is used only in the encoder component. The second one, namely Fractal-Block, has a similar fractal-based structure, except for the absence of the PDE-based layer, and is integrated in the bottleneck and decoder components of this network.

PDE-Fractal-Block, which has been designed to extract high-order image features, is characterized by a stochastic fractal expansion topology. First, it passes the input data through PDE-Layer, which acts as an edge-preserving denoiser. By filtering the noise in homogeneous regions while enhancing the boundaries, this diffusion-based layer ensures that the subsequent layers focus on meaningful structural characteristics rather than high-frequency noise.

A recursive expansion using a depth parameter, D , has been performed next. If $D = 1$, then we get the short path that returns the output $f(I)$ for input I , where the block acts as next layer sequence: **Conv2d** $\rightarrow$ **BatchNorm2d** $\rightarrow$ **Activation (ReLU)** $\rightarrow$ **Fractal-CBAM**. If $D > 1$, then the block expands into 2 deep recursive paths, $top_path(I)$ and $bottom_path(I)$, representing instances of itself. A final block layer performs a feature fusion combining the low-level and high-level characteristics, by merging the short and deep paths as following: $[f(I) + bottom_path(top_path(I))] / 2$. This stochastic fractal expansion approach allows this block to capture the features at multiple levels of abstraction.

D. Complete PDE-Fractal-UNet Architecture

The enhanced multi-task U-Net architecture proposed here combines four major components: encoder, bottleneck, classifier and decoder. The encoder of PDE-Fractal-UNet, which is also named contracting path and is responsible for the high-level feature extraction, is composed of a PDE-Fractal-Block sequence whose second and third block are processing the output of the previous block. At each down-sampling level, while spatial size has been decreased, the number of I/O feature channels of PDE-Fractal-Block has been increased progressively: $[3, 64] \rightarrow [64, 128] \rightarrow [128, 256]$. A $[2 \times 2]$ Max Pooling layer has been also applied to each block for spatial resolution reduction.

The bottleneck, also known as bridge, represents the central component of our network, connecting the encoder to the decoder and capturing the most compressed input image representation. The bridge contains a Fractal-Block with 512 channels that processes the deepest high-level features, and a $[2 \times 2]$ max pooling filter.

The classifier of PDE-Fractal-UNet has been created by incorporating a classification head that processes the bottleneck output. Since the bridge holds the most compressed and meaningful image version, it makes the optimal location to link the classification branch. The classification head includes Global Average Pooling (GAP) that condenses spatial data into a vector, followed by a Fully Connected (FC) layer, a Dropout with a regularization role and a linear layer receiving the number of classes as argument and outputting the classification logits. Since there are 3 tumor types and the healthy brain type, the number of classes used by our recognizer is 4.

The decoder, representing the expansive path of this deep model, restores the spatial resolution by using up-sampling layers that apply learnable 2D transposed convolutions. Each up-sampled feature map has been concatenated with the feature map from the corresponding level of encoder by using skip connections. Each output has been processed for fine-tuning by a Fractal-Block to uphold complex feature integra-

tion during reconstruction. The number of input/output channels has decreased in decoder as follows: $[512, 256] \rightarrow [256, 128] \rightarrow [128, 64]$. A final 2D convolution layer has converted the fine-tuned feature map into the segmentation map (binary mask) by collapsing the 64 channels into a single channel with a Sigmoid activation.

The described architecture of this encoder-decoder segmentation and recognition model is represented in Fig. 1.

E. PDE-Fractal-UNet Training and Validation Process

An effective cerebral tumor detection and recognition framework has been obtained by training successfully the PDE-Fractal-UNet model on a high-quality MRI brain tumor dataset. We have used the BRISC 2025 dataset for this task [23]. It contains 6,000 contrast-enhanced T1-weighted MRI brain scans and their corresponding masks, fully annotated for the segmentation and classification tasks. These medical images represent 1147 glioma tumors, 1329 meningioma tumors, 1457 pituitary tumors and 1067 no tumors (healthy brain scans).

BRISC dataset is composed of a training set and a testing set. Training set comprises 5000 images, representing 1147 gliomas, 1329 meningiomas, 1457 pituitary tumors and 1067 no tumors. Testing set contains 1000 scans, representing 254 gliomas, 306 meningiomas, 300 pituitary tumors and 140 no tumors. We have split this MRI training set into a new training set, comprising 90% of data (4500 images) and a validation set containing 10% of data (500 images).

Some pre-processing operations have been applied to the training and validation datasets. Their images and masks have been resized to $[256 \times 256]$. Next, several training and validation data augmentation and normalization procedures have been performed on them.

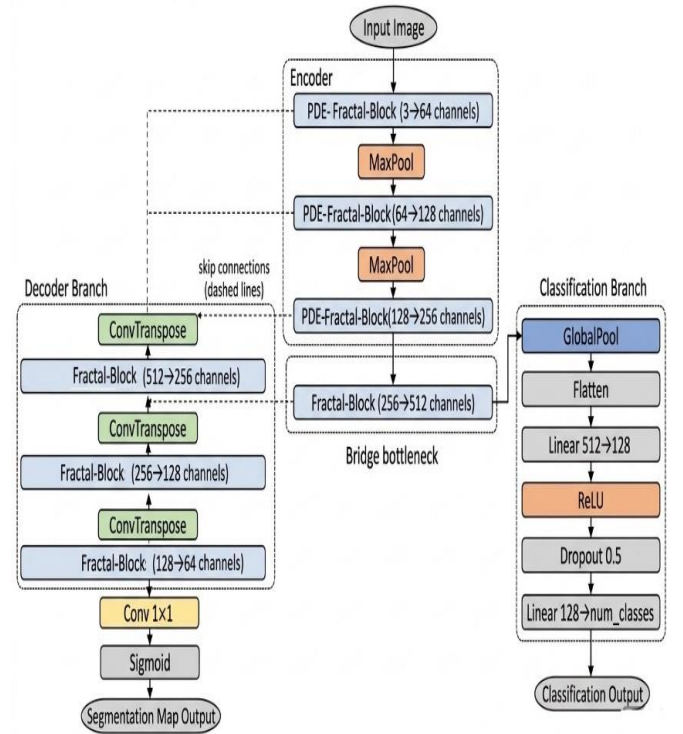


Fig. 1. PDE-Fractal-UNet Architecture

Then, some proper training options have been considered. Thus, we have used Adam (Adaptive Moment Estimation) as optimization algorithm, a learning rate of $1e-4$, a batch size of 4 and a number of 50 epochs for training. Since a multi-task training is required here, we have employed a composite loss function that balances the two objectives. So, it has been modeled as the weighted sum of the segmentation and classification losses:

$$\mathcal{L} = \lambda_{seg}\mathcal{L}_{seg} + \lambda_{cls}\mathcal{L}_{cls}, \quad (5)$$

where the segmentation loss has been determined as a linear combination of Dice loss and Binary Cross Entropy (BCE) loss, $\mathcal{L}_{seg} = \lambda_{BCE}\mathcal{L}_{BCE} + \lambda_{Dice}\mathcal{L}_{Dice}$, and the classification loss uses the cross entropy. These weights are used to prioritize a learning objective. Since we consider the detection task as more important than the classification, we have set $\lambda_{seg} = 1$ and $\lambda_{cls} = 0.5$.

This deep segmentation and recognition network has been trained and validated successfully on the corresponding datasets, as shown by the performance metric scores. An average training loss 0.106 of and an average validation loss of 0.078 have been achieved. The training process has been performed on an NVIDIA GPU and required approximately 3h. The evolution of the average training and validation losses is described in Fig. 2.

III. EXPERIMENTS AND DISCUSSION

THE brain tumor segmenter and recognizer generated by this PDE-Fractal-UNet training and validation process has been evaluated successfully on the testing MRI dataset of BRISC 2025. Our training, validation and testing experiments have been performed in Python 3.13.9, using the PyTorch library, on a high-efficiency computing environment running Windows 11 Pro on a processor Intel Core I7 12700 2.1 GHz, Turbo mode 4.9 GHz, with 32 GB (2*16GB DDR4) RAM, SSD: EMTEC X150 240 GB and video NVIDIA GeForce RTX 3070 8GB 5888.

Several examples of tumor segmentation and recognition results obtained from our simulations are described in Fig. 3. The original brain images are displayed on the first column. The ground-truth (GT) masks are depicted on the second column, while the obtained brain tumor detection and classification results are described on the third column.

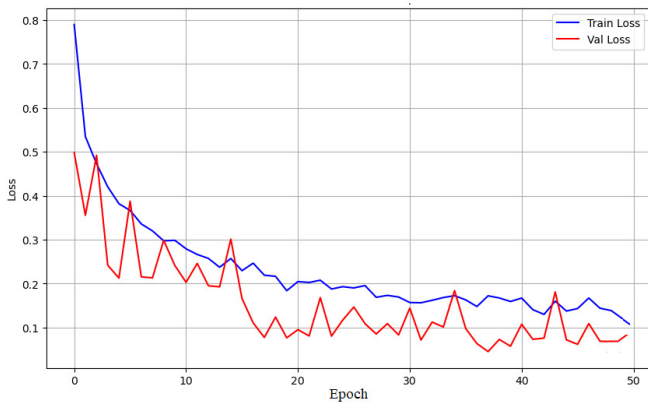


Fig. 2. Average training and validation losses

The segmentation component has been assessed by applying the performance metrics like Accuracy and Dice Coefficient, while the classification performance of our framework has been evaluated using Accuracy and F1 [24]. The high scores achieved for these measures by our PDE-Fractal-UNet model illustrate its effectiveness.

A method comparison study has been also performed here. In fact, it represents an ablation study whose results are described in Table I. As shown by these results, the proposed multi-task PDE-Fractal-UNet obtains the best performance metric scores, representing a good Dice Coefficient value and very high segmentation and classification accuracies and F1 classification score.

The framework has been compared to some ablated versions of it and with classical U-Net model, outperforming all of them. Thus, it performs slightly better than its variant using no fractal expansion in the fractal blocks, only the base path given by $D = 1$, which proves the importance of that recursive approach.

Also, the removal of PDE-Layer from the fractal-based blocks leads to an ablated Fractal-UNet with even lower, but still good, metric scores, in both fractal expansion and no fractal expansion cases. By removing the fractal features, one obtains a PDE-UNet, whose encoder has PDE-Blocks instead of Fractal-PDE-Blocks and the decoder has convolution blocks instead of Fractal-Blocks. It achieves even lower values for all performance measures, especially if no fractal expansion is used.

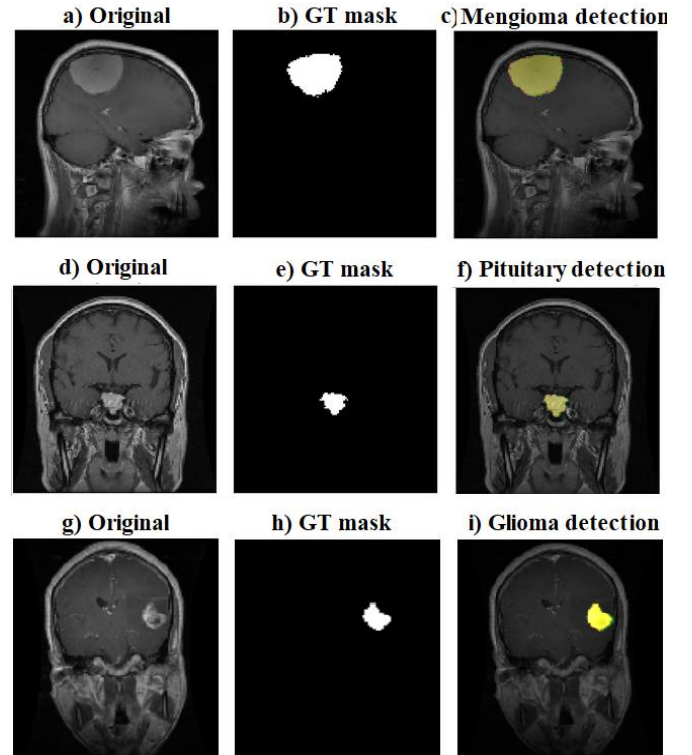


Fig. 3. Brain MRI tumor segmentation and classification results

TABLE I.
BRAIN TUMOR SEGMENTATION AND CLASSIFICATION METHOD COMPARISON

Technique	Tumor Segmentation		Tumor Classification	
	Dice score	Accuracy	Accuracy	F1 score
PDE-Fractal-UNet	0.8357	0.9979	0.9891	0.9867
PDE-Fractal-UNet w/o fractal expansion	0.8223	0.9925	0.9861	0.9857
Fractal-UNet	0.8136	0.9818	0.9812	0.9781
Fractal-UNet w/o fractal expansion	0.8061	0.9776	0.9734	0.9786
PDE-UNet	0.8014	0.9702	0.9615	0.9574
PDE-UNet w/o fractal expansion	0.7922	0.9639	0.9583	0.9590
Standard U-Net model	0.7435	0.8983	0.9106	0.9153

But even the Dice coefficient, accuracies and F1 values achieved by PDE-UNet are still high and much better than those of the standard U-Net that provides the weakest output. These results illustrate that the introduced nonlinear reaction-diffusion represents without a doubt an important asset for improving the U-Net architecture, but the fractal analysis seems to be a more valuable one. And they also show that combining anisotropic diffusion models to fractal geometry is a proven method to generate superior MRI tumor segmentation and recognition output.

However, the effectiveness of those CNN layers and blocks based on diffusion equations and fractal features can still be improved by modifying some of their parameters. For example, applying more iterations ($N > 5$) in the finite difference-based numerical scheme on which PDE-Layer is built or adding more scales in the fractal analysis process could improve the results, but would also increase the computational complexity, which leads to much longer training and validation times.

While the U-Net architecture is clearly enhanced by the introduced mathematical model-based layers, and the obtained segmentation and classification scores are very good, we admit that the proposed framework could still be outperformed by some recent state-of-the-art DL-based biomedical image segmentation techniques. Comparing it with such methods, including nnUNet [25] and the transformer-based architectures [11], will be a focus of our future research. Since this new expert-annotated MRI dataset, BRISC 2025, is expertly selected for brain tumor segmentation and recognition, and addresses the common limitations in the existing tumor databases, we consider that these results achieved on it prove the effectiveness of our DL-based approach. However, some experiments on other MRI datasets will be also considered in the future.

IV. CONCLUSIONS

A new brain MRI tumor detection and recognition framework based on an improved U-Net architecture has been described here. The proposed hybrid PDE-Fractal-UNet technique enhances considerably the standard U-Net by introducing the

multi-tasking and incorporating some improved network blocks.

Besides the image segmentation performed by classical U-Net model, PDE-Fractal-UNet also executes the recognition task, since its architecture incorporates a classification branch. The encoder, decoder and bottleneck components have been enhanced by the new blocks integrating CNN layers and attention modules based on anisotropic diffusion and fractal analysis, which use the recursive fractal expansion technique and replace the standard U-Net 2D convolution blocks. The novel deep network developed by us achieves much better tumor segmentation results and classifies glioma, meningioma and pituitary tumors very well, as shown by its performance metric scores achieved on the MRI dataset, and it is also computationally efficient.

The mathematical models based on nonlinear diffusion equations and fractal geometry, which have been used to construct the layers and attention mechanisms of PDE-Fractal-UNet, represent the main contribution of this research work. While nonlinear PDE models represent effective MRI enhancement tools, the fractal features are very useful for brain tumor analysis since they can quantify the structural complexity and chaotic, irregular growth, which the classical Euclidean geometry cannot. The main purpose of our research, which is to show how the partial differential equations and fractal features can be combined successfully to build an upgraded U-Net based cerebral tumor segmentation framework, has been fulfilled properly.

Our future research plans in this domain will focus on further improving this PDE-Fractal-UNet framework and applying it to other types of medical tumors and lesions. Thus, we intend to develop more performant nonlinear diffusion-based models for the PDE-based layers. Also, we are going to extend the fractal analysis, in order to build more effective fractal-based layers and Fractal-CBAM modules. Therefore, we consider adding more fractal features in this process, including the wavelet-based fractal features [20], succolarity, fractal entropy and the multifractal spectrum. And we also consider extending this DL-based framework for the 3D brain MRI segmentation tasks [26].

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