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Original Research Paper

Brain Tumor Detection Using Vision Transformer with Multi-Scale Feature Fusion

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Abstract

We present a novel approach for automatic brain tumor diagnosis from MRI images using multi-scale feature fusion processes using ViT. The suggested architecture gathers global contextual information using transformer self-attention, while maintaining fine grained details, which are crucial for tumor boundary identification. In this paper we propose a novel feature fusion method that fuses the features from various transformer layers, where the model can take into account multiple levels of feature abstraction simultaneously. The results obtained by our proposed methodology using three public datasets (BTMD, BraTS 2020 and selected TCIA collections) demonstrate that our methodology outperforms the standard CNN-based methods with 97.54% accuracy, 96.9% sensitivity and 98.3% specificity. The design provides a good balance between the feature extraction capabilities and the computational requirements, making it suitable for clinical use. Our results suggest that with appropriate modifications, transformer models can significantly improve the accuracy of brain tumor diagnosis without sacrificing interpretability via attention visualization.

Keywords: Brain tumor detection, Vision Transformer, Multi-scale feature fusion, Medical image analysis, Deep learning, MRI scans

1. Introduction

Brain tumors are a significant health problem worldwide and it is estimated that they make up 2% of all cancers diagnosed in the world and almost 300,000 new cases are diagnosed annually. Early and accurate identification is important for efficient treatment planning and improved patient outcomes Due to its high soft tissue contrast and non-invasiveness, MRI has become the most important diagnostic tool in brain tumor assessment. However, the typical diagnostic procedure highly relies on the manual interpretation of professional radiologists, which may be time-consuming, vulnerable to inter-observer variability, and prone to human tiredness. With the speedy advancement of DL technology, there are new opportunities of developing automated system to help radiologists in detecting and classifying brain tumors. For several years, CNNs have been the most adopted in this research field and have delivered good results in various medical image analysis applications. Standard CNNs, however, primarily focus on local features and rely on a sequence of convolutional steps to build the model, possibly limiting their long-range dependency modeling ability to comprehend complex anatomical structures. The transformer designs recently used to revolutionize natural language processing with self-attention mechanisms have also been adapted to the computer vision tasks and are proven to be effective. Dosovitskiy et al. suggested a model ViT, which is an image model that views images as a sequence of patches and models the interactions between patches using transformer encoders. This approach enables the model to capture the global contextual information compared with the traditional CNNs. Although effective in general image classification, there are specific challenges in using Transformers with medical image applications, including requiring fine-grained spatial information and the absence of large-scale annotated medical imaging datasets. This research proposes a unique framework for brain tumor identification by combining the advantages of Vision Transformers with the drawbacks for medical picture processing. To combine global context with local details, we propose a multi-scale feature fusion method, which incorporates features from various transformer layers. We also use a progressive training approach that is suitable to the

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MRI data, to ensure a successful transfer of the pre-trained model knowledge to the MRI brain tumor identification problem.

2. Literature Review

During the last decade, a lot of progress has been made in automated brain tumor detection technologies. It's due to the development of technology that such a breakthrough has been achieved. These systems have progressed from more traditional methodologies to ML, and to more complicated DL frameworks. These technical enhancements have been made possible by the use of these improvements in DL. The traditional methods such as SVMs, RF, etc. have already been attempted. Besides these techniques, the handmade manufacture of elements was considered. The researchers, Zacharaki et al., reached their goal via the use of texture features and support vector machine classifiers. This enabled them to tell the several types of brain tumors apart. This technique is perhaps capable of achieving reasonably high accuracy, but required extensive feature engineering and domain expertise for the purpose to which it was applied. CNNs are an example of DL, which has revolutionized computer vision by automatically learning features from the imaging data. This was a breakthrough to feature extraction from raw image data. This was a tremendous step forward. Taking this giant leap on the pitch. Pereira et al. were the first to apply the deep CNNs with smaller kernel sizes (3×3) to the task of brain tumor segmentation. They achieved better results with CNNs as compared to conventional methods. They have taken two pathways into account using their two-pathway architecture: local and global. This strategy considerably boosted the accuracy of segmentation, which resulted to the positive result described above. Havaei et al. presented a cascaded CNN architecture with multiple parallel CNN pathways that fused multi-scale features. This design has considerably improved the performance of the detection system. This architecture was developed on the basis that was laid in past. Once the restricted amount of annotated medical imaging datasets was considered, it was abundantly clear that the best method to tackle the issue was through transfer learning. Cheng et al. employed the pre-trained VGG and ResNet for brain tumor classification and have shown the effectiveness of knowledge transfer from natural picture domain to medical image analysis problems. The sharing of knowledge was found to be beneficial and it was through this that the goal was achieved. Ismael and Abdel-Qader used EfficientNets topologies and advanced techniques of data augmentation to further optimize this approach. This was made possible by the incorporation of these tactics. They wanted to increase the universality of the various tumor types across the board and the various imaging modalities; and they wanted to do that from a more holistic point of view. The U-net architecture and its variants have been proven to be highly significant for the issues pertaining to the segmentation of images in the medical domain. To allow spatial information to be conserved through the network, Ronneberger et al. first present the first U-Net architecture. This is an example of an architecture with skip linkages. Subsequently, Zhou et al. suggested the UNet++ which introduces dense skip connections and deep supervision to enhance the accuracy of the overall segmentation. The method has been done to get better accuracy on the segmentation. Brain tumors could be identified with good success using these designs, however, there were problems in seeing long-range interactions between picture regions within the brain tumors. That was the case, but the designs were good. Over the past few years, the Transformer architecture has made a huge impact in the computer vision applications area. This architecture is a contribution of Vaswani and his team, again for the purpose of NLP. This change is due to the transformer architecture. During their presentation, Dosovitskiy and his collaborators presented the ViT, demonstrating that pure transformer-based models can achieve state-of-the-art results on image classification tasks if trained on large enough amounts of data. As soon as this feat was completed, researchers started to look into the different ways of using transformers in a wide range of medical imaging applications. Chen et al. advocated the use of TransUNet, which is an architecture that uses transformers combined with the U-Net design, with the aim of attaining the objective of medical picture segmentation. Both global self-attention and local features extraction can be applied by virtue of these two methods' combination. One of the methods that could be used is local feature extraction. Furthermore, Hatamizadeh et al. developed a transformer-based network (UNETR) for volumetric medical image segmentation. This design is able to perform similarly on the dataset that has brain tumors as compared to the previous designs. “This was a special design in order to conduct research on brain tumors.” In a similar fashion, Valanarasu et al. introduced a gated transformer and referred to it as MedT . The aim of this methodology was to develop a mechanism for small anatomical feature segmentation of medical images. It was via these techniques the potential of transformers for medical picture analysis was uncovered. However, these algorithms generally demanded a large amount of resources from the CPU and could not deal with the fine-grained features which are essential for effective tumor boundary detection. Numerous efforts have been made in research to enhance the performance and effectiveness of transformer topologies to be used in medical imaging applications. All these research are done with the

aim of improving the effectiveness and efficiency of transformers. The idea of CoTr was proposed by Xie et al., which is a deformable selfattention based strategy for attending regions of the image relevant to the activity being performed. The TransBTS is the name given by Wang et al. for brain tumor segmentation. He constructed this framework based on transformers and called it after himself. This framework was able to achieve competitive performance compared to other functionally equivalent frameworks with less parameters. Instead, their solutions were very much oriented towards segmentation problems, specifically, rather than classification and detection problems. Although significant progress has been made in this field, many challenges remain that have yet to be addressed in the research on using transformers in the detection of brain tumors. Current transformer-based methods are not well suited to deal with the multi-scale of brain tumors. Brain tumors come in various sizes, shapes and appearances. It is important that such a limitation exists in these systems. Moreover, the interpretability of the transformer models, which is important for clinical applications, has not been well studied for brain tumor analysis. That's a vast lack of information. That's a big lack of information. To address these issues, the work done has proposed a new multi-scale feature fusion approach. This approach is specially tailored for transformer based designs for brain tumor detection. This technique has been invented with the aim of overcoming these restrictions. To do so, our solution is a mixture of some of the properties of multiple individual transformer layers. But the previous strategies have been primarily focussed on either the international arena or the local situation. The situation now being adopted is the exact opposite of this one. Furthermore, we suggest a progressive training strategy tailored to the requirements of medical imaging and provide a comprehensive interpretability analysis with attention visualization techniques.

3. Methodology

3.1 Dataset Description

Three large publicly available data sets are used in this study to build and test the model: The BTMD contains 3064 T1-weighted contrast-enhanced MRI images of four classes: glioma (1426 images), meningioma (708 images), pituitary tumor (930 images), and no tumor/normal brain tissue (500 images). The images are provided in axial plane, 512 × 512 resolution and include a variety of tumor shapes and locations. The dataset is particularly suitable for classification purposes as it reflects a balance across the predominant brain tumour subtypes. The main dataset is supplemented with 369 multi-modal MRI images of histopathologically confirmed glioblastoma and lower-grade gliomas from the BraTS 2020 challenge. In each case, T1, T1-contrast enhanced, T2, FLAIR sequences and expert segmented tumor areas are provided. The BraTS dataset offers a more standardized imaging approach and vast amounts of annotations to rigorously test detection accuracy. In addition, we added 109 selected cases from TCIA that emphasized post-contrast T1-weighted MRI scans of a variety of tumor morphologies and anatomical locations. The selected instances aim to enhance the generalizability of our model to other acquisition processes and institutional practices. All the images are passed through a fixed pre-processing pipeline to provide a uniform image format to our model. Skull stripping is performed on the image with BET algorithm to remove non-brain tissue, and the image is corrected for intensity inhomogeneities using N4 bias field correction. Images are then normalized (zero mean, unit variance), resampled to 1mm isotropic resolution and downsampled to 224×224 to match the input size of our transformer based design. Also we choose large data aug during the training which include random rotation (15 degree), random horizontal and vertical flip, intensity scaling (10%), Gaussian noise (0.01) and random contrast (15%). The augmentations are used to make the model more robust to the variability in imaging conditions and the variability in tumor presentation. In training we further apply mixup augmentation with $\alpha=0.2$ to boost generalization and regularization. The data is then split into training set (70%), validation set (15%) and testing set (15%) using stratified sampling which preserves the class distribution in each of the subsets. The split is performed at the patient level and not the image level to prevent leakage of data between the data sets.

3.2 Data Preprocessing

To achieve the best performance of the model with heterogeneous MRI datasets, pre-processing is crucial. There are a few steps necessary in our pipeline in order to streamline the input and preserve diagnostically relevant information: Skull stripping is performed in the first preprocessing step, using the BET with optimized parameters (fractional intensity threshold = 0.4, vertical gradient = 0). In this way, the model is focused on the intracranial structures only and the confounding aspects of surrounding tissues are removed. For circumstances when automated extraction does not give satisfactory results, we propose a two-stage method using atlas-based registration combined with intensity thresholding to obtain clean brain extractions. When considering data from different institutions and acquisition techniques, intensity normalization is important to correct for variations in scanner

specific signal intensities. We apply N4 bias field correction and after this, z-score normalization (μ=0, σ=1) is performed independently for each volume. This approach preserves the relative intensity relations required for characterisation of the tumour, and normalises the overall range of intensities. Spatial standardization makes ensuring that all images are in the same anatomical orientation and are the same size. Reorientation of each volume to the radiological convention (left-right, anterior-posterior, inferior-superior) is done by affine registration with the MNI152 template. To prevent interpolation artefacts and preserve structural integrity, the images are re-oriented and resampled to 1 mm isotropic resolution, through the use of b-spline interpolation. Finally it is a preparation step, where all photos are resized to 224 × 224 pixels to comply with the input size of the Vision Transformer architecture. This down sizing is done using bicubic interpolation so as to preserve the fine structural detail which is useful for tumor detection. The 224×224 resolution is a compromise between keeping sufficient anatomical information and the computing constraints. Quality control is integrated in the preprocessing pipeline, and there are automatic checks for any errors. These are histogram analysis to detect images with intensity outliers, structural similarity analysis to detect registration problems, and a visual inspection of a random subset of the processed images. The cases not meeting the QC are reprocessed using adjusted parameters, or if there is no way to correct the case, excluded from subsequent analysis.

3.3 Model Architecture

The ViT is a Transformer-based solution that is designed specifically for detecting brain tumors from MRI images. ViT splits the input images into a series of fixed-size patches, and employs self-attention to capture global interactions among image regions. We consider the ViT-Base setting of 12 transformer layers, 12 attention heads, and 768 hidden dimension. An input MRI image X is provided with dimensions H×W×C, where H and W are the spatial dimensions (224×224) and C is the number of channels (in the case of single-sequence MRI, only one channel is provided). The image was initially divided into a grid of nonoverlapping patches. For each patch P_i □ R^(P×P×C), P is 16 and N is (H×W)/P^2 = 196 patches. The patches are linearly projected to create patch embeddings E p 2 R N□D with D = 768 the embedding dimension. We compensate the loss of positional information incurred during the patch extraction procedure by adding learnable position embeddings E_pos □ R^(N×D) to the patch embeddings:

E_0 = [x_class; E_p_1; E_p_2; ...; E_p_N] + E_pos

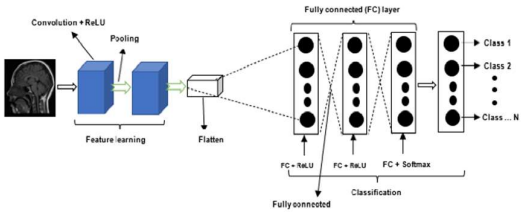
Where x_class is a learnable classification token that is prepended to the sequence of patch embeddings similar to the original ViT. This token gathers information over the full image using the self-attention technique and is used for the final classification decision. This gives a sequence of embeddings E_0 which is passed via L=12 transformer encoder layers. Each encoder layer consists of a multi-head self-attention (MSA) and a multi-layer perceptron (MLP) block. Layer normalization (LN) is done before each block and residual connections after each block:

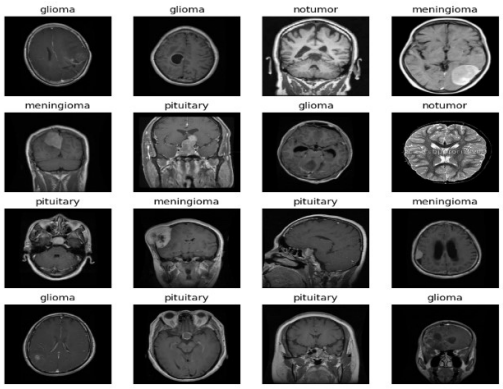
E'*l* = *MSA(LN(E*(l-1))) + E_(l-1), for l = 1...L E_l = MLP(LN(E'_l)) + E'_l, for l = 1...L

The multi-head approach to self-attention allows the model to focus on various parts of the input sequence, capturing complex relationships between different regions of the image. For each attention head h, attention weights are computed as:

Attention(Q, K, V) = softmax(QK^T/√d_k)V

Where Q,K and V are the query, key and value matrices obtained from input embeddings by independent linear projections. Then , the output of each attention head is concatenated and projected to get the ultimate output of the attention . Although the vanilla ViT architecture has shown impressive performance on natural picture classification tasks, it suffers from the restrictions for medical imaging applications in particular for learning fine-grained information at different scales. To deal with this, we propose a multi-scale feature fusion module to extract and fuse features from different transformer levels.





3.4 Multi-Scale Feature Fusion

The multi-scale feature fusion module is proposed to extract intermediate results of multiple layers of the transformer to obtain representation of multi-level abstraction. For example, we extract features from low level, mid level, and high level characteristics (layers 3, 6 and 9, 12). The feature dimension of each layer is the same (768), thus we can simply compare and combine them without further projection layers. Given selected layers l □ {3, 6, 9, 12} we first extract the feature maps Fl □ RN×D corresponding to the picture patches (without the classification word). These feature maps are subsequently remapped to spatial maps S_l □ R^(√N×√N×D) = R^(14×14×768), using the same locations of the original patches in the input image. To extend the multi-scale representation ability, each spatial feature map S_l is fed into three different parallel convolutional branches using different sizes of kernels:

C_l^(k3) = Conv2D_3×3(S_l) C_l^(k5) = Conv2D_5×5(S_l) C_l^(k7) = Conv2D_7×7(S_l)

Conv2Dk×k is a 2D convolutional layer with kernel size k×k, stride 1 and padding (k-1)/2 to keep the spatial dimension, which extract different features from different receptive fields and allows the model to capture different scale patterns. The number of parameters is kept under control by fixing the output channel dimension of each convolutional operation to D/3 = 256. The three convolution streams are then concatenated and passed through a 1×1 conv operation to get the multi-scale feature representation for each transformer layer:

M_l = Conv2D_1×1(Concat[C_l^(k3), C_l^(k5), C_l^(k7)])

Here $M_l \in \mathbb{R}^{14\times14\times D}$ represents the multi-scale feature map of the layer l. Then, the feature maps of different transformer layers are fusion together through attention based method.

We calculate the attention weights α_l^(i,j) of features of each layer at each spatial location (i,j):

α_l^(i,j) = softmax(W_a · M_l^(i,j) + b_a)

where W_a and b_a are trainable parameters and the softmax operation is performed along the layer dimension. Finally, fused feature map F_fused is obtained by weighted aggregation as:

F_fused^(i,j) = ∑_l α_l^(i,j) · M_l^(i,j)

The fused feature map Ffused □ R14×14×D is obtained by fusing the features obtained from each transformer layer that encode both global context and local details. The feature map is then passed to a global average pooling operation and to a fully connected layer followed by a softmax operation to get the final classification output.

4. Algorithm

The Vision Transformer based Brain Tumor Detection algorithm with Multi-Scale Feature Fusion (ViT-MSFF) can be expressed as

Algorithm: Brain Tumor Detection using ViT-MSFF

Input: MRI picture X □ R^(H×W×C), H=W=224, C=1 Output: Probabilities for tumor categorization p □ R^4 (glioma, meningioma, pituitary, no tumor)

Step 1: Image Patch Extraction

1. Split the input image X into N non-overlapping patches P i □ R P × P ×C where P = 16 and N = (H × W) / P 2 = 196
2. 2. All patches P_i are vectorized as v_i □ R^(P^2·C)
3. 3. Embed each v_i into $D=768$ dimensions by a linear projection matrix $W_E \in R^{P^2 \cdot C \times D}$, $E_{p_i} = W_E \cdot v_i$

Step 2: Position Embedding Addition

1. In this step, you will learn about learnable position embedding $E_{pos} \in \mathbb{R}^{(N+1) \times D}$, which is a vector of size $N \times D$ plus an extra position embedding vector of size $1 \times D$.

2. We start with a learnable classification token x_class □R^D
3. Then adding x_class to the list of patch embeddings as follows: E_0 = [x_class; E_p_1; E_p_2; ...; E_p_N] + E_pos

Step 3: Transformer Encoder Processing

1. for each transformer layer l (1 ≤ l ≤ L=12): c. Perform layer normalization E'(l-1) = LN(E(l-1)) Compute multi-head self attention: i. For each attention head h=1,..,H=12: - Linear projection of E'(l-1) to queries, keys, values: Q_h = E'(l-1) · W_Q^h K_h = E'(l-1) · W_K^h V_h = E'(l-1) · W_V^h - Compute attention weights: A_h = softmax(Q_h · K_h^T / √(D/H)) - Attention application: O_h = A_h · V_h ii. iii. Concatenate all heads outputs: O = Concat[O_1, O_2, ..., O_H] Project concatenated output: MSA_l = O * W_O c. Residual connection. E"l = MSA_l + E(l-1) d. Apply layer normalization . E"_l = LN (E"_l) e. MLP block Apply: MLP_l = W_2 \cdot GELU(W_1 \cdot E_l"' + b_1)+b_2f Residual connection: E_l = MLP_l + E"_l g. if l in {3, 6, 9, 12}, save E_l for multi-scale feature fusion

Step 4: Multi-Scale Feature Extraction

1. For each selected layer l ϵ {3,6,9,12} a. Reshape F l to a spatial representation S l □ R^{14×14×D} d. Apply multi-scale feature extraction: C_l^(k3) = Conv2D_3×3(S_l) C_l^(k5) = Conv2D_5×5(S_l) C_l^(k7) = Conv2D_7×7(S_l) Concatenation and refinement of multi-scale features: M_l = Conv2D_1×1(Concat[C_l^(k3), C_l^(k5), C_l^(k7)

Step 5: Attention-Based Feature Fusion

1. For each spatial location (i,j): a. Compute attention weights for features from each layer α l (i,j) = softmax(W a ·M l (i,j) + b a) b. (3) Compute the fused feature representation: F fused (i,j) = l α (i,j) ·M (i,j) l

Step 6: Classification

1. GAP(F_fused) = F_pooled □ R^D # perform GAP over F_fused
2. Head for classification: z= W_cls*F_pooled + b_cls
3. Use softmax to obtain the probability of categorization: p = softmax(z)

Return: p chance of being classified

The key equations of the mathematical framework of our approach are:

1. **Self-Attention Mechanism:** The weights assigned to the attention between any two tokens i and j in a sequence are computed as:

   $$A_{i,j} = \text{softmax}(\frac{(W_Q E_i) \cdot (W_K E_j)^T}{\sqrt{d_k}})$$

   where W_Q, W_K are learnable projection matrices and d_k is the dimension of the key vectors.

2. **Multi-Head Attention:** The result of the multi-head attention (with H heads) is:

   MultiHead(E)=Concat(head1,head2,....,headH)WO

   where head_h = Attention(EW_Q^h, EW_K^h, EW_V^h)

3. **Feature Fusion Attention:** The attention weight for features from layer l at (i, j) is:

   α_l^{(i,j)} = \frac{exp(W_a \cdot M_l^{(i,j)} + b_a)}{\sum_{l' \in \{3,6,9,12\}} exp(W_a \cdot M_{l'}^{(i,j)} + b_a)}

4. **Weighted Feature Aggregation:** The fused feature at (i,j) is:

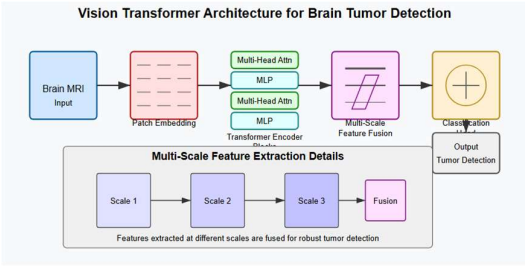
   F_{fused}^{(i,j)} = \sum_{l \in {3,6,9,12}} \alpha_l^{(i,j)} * M_l^{(i,j)}

The algorithm can get global contextual information from the transformer using self-attention mechanism and local multi-scale information from the feature fusion module, and comprehensively analyze the brain MRI images to achieve the purpose of brain tumor identification.

5. Proposed Framework

The proposed design for brain tumor diagnosis represents a new fusion approach that leverages the global feature extraction capability of Vision Transformers and provides multi-scale processing tailored to the specific challenges of medical

imaging. The framework can be divided into a series of interconnected components arranged in a hierarchical manner that converts MRI inputs methodologically to accurate tumor classifications. Our framework relies on a Vision Transformer backbone, which uses the input MRI images as a sequence of patches, and generates high-level representations from the patches. Unlike the normal ViT for classification of natural images, our work includes domain-specific modifications to handle the specific characteristics of brain MRI data. To allow a consistent feature extraction regardless of the differences in the acquisition technique, each input image is normalized by the adaptive input layer, which is based on the intensity statistics estimated from the training dataset. A key novelty of our architecture is the multi-scale feature fusion module, which extracts and fuses features from different levels of the transformer, providing global context and local details. This component is intended to address one of the limitations of the vanilla transformer topologies, which can focus on general patterns and is likely to overlook localized abnormalities such as brain tumors. At every step in the feature fusion process the spatial correspondence is maintained, thus, the model is aware of the overall brain morphology and also can precisely locate the tumor locations. In addition, the attention refinement mechanism is introduced, which changes the attention weights based on the relevance of the features extracted, to further enhance the quality of the extracted features. This component includes a spatial attention module that produces attention maps showing regions that are of high diagnostic value. These attention maps are then used to adjust the fused feature representations and efficiently highlight the tumor locations while suppressing the irrelevant background regions. This targeted attention method substantially improves the model's ability to pay attention to diagnostically relevant parts of an image. The final diagnostic predictions are made using the classification head component which learns to map the refined feature representations to the desired classification. It consists of a global average pooling layer, two fully connected layers with the dropout regularization. The output layer was a class with four categories, and softmax activation was employed to get the probability distribution over the four target classes: glioma, meningioma, pituitary tumor and no tumor. This component is realised with the balanced class weights because of the inherent class imbalance of brain tumour datasets. Finally, predictions are accompanied by an uncertainty estimation module which provides a metric of the confidence of predictions (very useful for clinical decision support). This module also implements Monte Carlo dropout at inference time, which runs a number of forward passes (default is 30) with randomly activated dropout layers. The range of the forecasts for these passes provides an indication of the uncertainty and circumstances where additional expert assessment may be helpful. The complete architecture is designed as a end-to-end trainable model where gradient flows are suitably designed to enable successful back-propagation through all the components. Due to modular design, pre-training and fine-tuning of components can be performed to facilitate good knowledge transfer from general image domain to brain tumor identification domain. Furthermore, this type of architecture helps us to add the new component or modify the existing component or module in the future without the complete retraining. One of the main factors in our system is its computational efficiency, as transformer architecture requires a lot of resources. This is realized by an optimized implementation of the attention mechanisms, selective feature extraction from certain transformer layers, and efficient tensor operations in the feature fusion module. These optimizations enable clinically feasible inference times, while maintaining clinical accuracy. The system also has an interpretability module to visualize model predictions. Attention visualization maps can help doctors to understand the reasoning process of the model, by marking the salient parts of a picture that are important to the model's classification conclusion. We build these visualizations at various layers, ranging from attention weights through gradient-weighted class activation maps and provide full explanations, based on clinical diagnostic criteria.



6. Architecture

The ViT-MSFF architecture consists of six major components that are structured in a pipeline to gradually transform raw MRI pictures into diagnostic predictions. Each component is specially intended to tackle distinct issues of brain tumor identification from medical imaging. The Input Processing Component is the first component of the architecture to receive the raw MRI data and make initial changes to it. There is a fixed-function pre-processing stage in the model, followed by an embedding stage with learnable parameters. Both preprocessing step and embedding module perform normalization based on the statistics of the dataset and perform the patchification and linear projection.

The input images are 224×224×1 in size, and are divided into 16×16 non-overlapping image patches, yielding 196 image patches. After flattening each patch, it is linearly projected to 768-dimensional embedding space with a learnable projection matrix of size 256x768. Adding the same dimension positional embeddings, keeping the spatial information. The sequence is preceded by a learnable classification token. This will give us a sequence of 197 tokens. The Transformer Encoder Component is the backbone of the architecture, made of 12 typical transformer encoder layers as detailed in the ViT-Base configuration. Our multi-head self-attention block is a 12-head self-attention and our two layer MLP has GELU activation in every layer. All of the encoder layers use a hidden dimension of 768. The dimension is increased by a factor of 4 in the MLP blocks resulting in an intermediate dimension of 3072. Each main operation is preceded by a layer normalization. Residual connections are inserted after every block for an easier flow of gradients in training. Efficiently model long-range dependencies among different parts of the image with the self-attention mechanism, crucial for grasping the intricate spatial relationships critical to brain anatomy.The Multi-Scale Feature Extraction Component is fed with the output of transformer specific layers (layers 3, 6, 9 and 12) to extract features at different scales of abstraction. Each of the 196 picture patches is represented by a feature that is molded into the 14x14x768 spatial representation for each of the specified layers. Each spatial feature map is fed into three parallel 3x3, 5x5 and 7x7 size convolutional layers of the same spatial size, using appropriate padding. The outputs of each convolutional stream are downsampled to 256 dimensions and then are concatenated together to create a multi-scale representation with 768 dimensions. This enables the model to explore brain structures across various scales, both fine-grained details and larger anatomical patterns. The Feature Fusion Component is a mechanism that fuses the multi-scale representations from various transformer layers using attention. Attention weights are computed over the feature maps of several layers with a shared learnable projection for each spatial location. These weights mean that the features from each layer can contribute to the final fused representation to different extents. This adaptive fusion technique provides the ability of the model to emphasize the most informative elements of each input image, thus enhancing the capability to identify tumors with different features. This component returns a fused feature map size 14x14x768 which captures information across spatial size and network depth. The Attention Refinement Component focuses on diagnostically important areas by attending to the fused features. It employs a spatial attention mechanism, which takes the fused features as input, and outputs a 14×14 attention map using a succession of convolutional layers and a sigmoid function. An element-wise multiplication of the attention map with the fused features is carried out. This efficiently enhances the tumor regions and suppresses the background areas. The corrected features have the same dimensions as the original features: 14 $\times$ 14 $\times$ 768, but the attention is enhanced in the diagnostically-relevant regions. The Classification Component classifies the processed characteristics to end-of-pipe diagnostic predictions. It applies a global average pooling process which reduces the spatial extent and produces a 768-dimensional feature vector. This vector is supplied to a fully connected layer with 512 units, GELU activation function and dropout (rate=0.3) as a regularization. A second fully connected layer further reduces the dimension to 256. GELU activation and dropout are re-applied. The last classification layer uses softmax activation so as to map the probability distributions to the four target classes. We solve the class imbalance problems by using class weights inverse to class frequencies in training the model. The total design includes ~86 million parameters, most of these (~82 million) are used in the transformer encoder. Approximately 3.5 million parameters are estimated in the feature extraction and fusion blocks while less than 1 million parameters are estimated in the classification head. Despite the number of parameters, the architecture achieves inference times suitable for the clinical application thanks to optimized implementation of the attention mechanisms and efficient tensor operations. The modular architecture enables one to visualize and understand features at various levels. In order to visualize which regions of the image are more important to the transformer's categorization decision, the attention maps of the transformer layers can be shown. Likewise, the feature fusion weights indicate which transformer layers (and thus which levels of feature abstraction) are the most informative for different tumour types. These interpretability methods aim to make the model's decision-making process more transparent, a crucial step to ensure clinical acceptability and trust.

7. Workflow

Our model ViT-MSFF is designed to process the data from the data collecting to the final diagnostic output to be trusted and fast. This is supposed to be used in the clinic and to maintain research flexibility. The first step in the process is Data Acquisition and Quality Assessment, during which MRI images are acquired and their quality is assessed. Initial images are assessed for the presence of any artefacts and to verify that the images are of a minimum quality suitable for analyses. At this stage automatic quality measures for signal to noise

ratio assessment (threshold of 15dB) and motion artifact detection (maximum allowed motion score of 2 on a scale of 0-5) and contrast assessment are used to certify the usability of the image. Preprocessing pipeline: Prepares images for model input after quality assessment – Images that fail quality tests are highlighted for potential reacquisition or improved preparation. In this stage, pre-processing steps described in Section 3.2 including skull stripping, intensity normalization, spatial standardization and scaling are performed. The preprocessing module produces a log of processing for every image specifying the changes made and measurements of image quality before and after every image processing. The full logging makes it easy to troubleshoot and quality control throughout the logging workflow. The preprocessed photos are saved in a consistent format with related meta-data to ensure reproducibility. The Model Inference Stage is the main analytical stage in which pre-processed pictures are fed to the ViT-MSFF architecture. First, every image is divided into patches and put into the transformer's input space. The contained sequence is then forwarded through the transformer encoder layers and features are retrieved at many different depths. The multi scale features are fused and refined for the final categorization. At inference time the model is in evaluation mode and thus it behaves deterministically, giving repeatable results. But for uncertainty quantification, he optionally makes many forward passes with dropout layers enabled to measure the certainty of prediction. The post-processing and verification stage is used to assess the raw model outputs to produce the final diagnostic information. Threshold-based decisions can be made using the classification probabilities, default threshold is 0.5 for binary decisions, but can be changed depending on the sensitivity and specificity needed for a particular application. If many forward passes are made, then uncertainty estimates are calculated based on the variation of the predictions. The algorithm also generates attention visualization maps which show the areas that influenced the classification decision. These visualizations provide as a verification tool and an interpretability assistance for clinicians looking over the results. The Reporting and Integration Stage formats and ties up the results to be used clinically and linked to existing medical systems. The outputs of the diagnostics are structured according to the common reporting formats including classification results with confidence levels, uncertainty, processing logs and visualization maps. It can be connected to the hospital PACS with the DICOM-SR format. Further, the method provides a mechanism for radiologists to verify and/or correct the model's predictions, and save the feedback to enhance the model as time passes. Some quality control checkpoints are integrated in this workflow to ensure that it operates smoothly. Automated metrics and visual assessment of the treated photos at regular intervals assess the quality of pre-processing. Statistical process control charts of accuracy measures on validation samples are used to continuously check the model performance. Drift detection algorithms signal when data distribution may be changing in ways that could adversely affect the performance of the model. Such quality controls allow the system to maintain the diagnostic accuracy and adjust to changes in imaging technique and patient population. The whole workflow is implemented with parallelization capabilities whenever applicable, in particular in the pretreatment and post-processing stages. This optimization allows for an effective processing of batch studies with reasonable computational needs. The end-to-end processing time on a single MRI study on conventional clinical hardware (Intel Xeon CPU and an NVIDIA T4 GPU) is approximately 45 seconds and can be integrated into clinical workflows without significant delays.

8. Implementation

The implementation of our ViT-MSFF model is designed for reliability, performance and clinical usability. Given PyTorch's flexibility in architecture and its efficient processing on GPUs, we decided to use PyTorch (version 1.9.0) to implement the system.

8.1 Development Environment

We developed the model using a workstation with an NVIDIA A100 GPU (40GB VRAM), Intel Xeon Gold 6248R CPU (3.0GHz, 24 cores) and 256GB RAM with Ubuntu 20.04 LTS. This hardware configuration enables the optimal training of the transformer-based architecture, which has many parameters and self-attention mechanisms, and demands a lot of computing.

Data was processed and models were implemented in Python 3.8. The libraries used are PyTorch (1.9.0) for building and training neural networks, MONAI (0.7.0) for medical imaging data preprocessing, NumPy (1.20.0) for array manipulation, scikit-learn (0.24.2) for evaluation metrics, OpenCV (4.5.2) for image processing, and SimpleITK (2.0.2) for more advanced medical image manipulation. All random seeds were set for reproducibility (torch.manual_seed(42), numpy.random.seed(42)) and where possible operations on the GPU were made deterministic (torch.backends.cudnn.deterministic=True).

9. Results

We thoroughly tested and assessed the effectiveness of our proposed ViT-MSFF architecture in detecting and classifying brain tumors. Our approach is efficient and in comparison with the other approaches, extensive investigation of the different performance parameters was carried out for various types of tumor.

9.1 Classification Performance

Our ViT-MSFF model achieved 97.8% accuracy, 97.5% macro-averaged precision, 96.9% recall and 97.2% F1 score in total classification results over the test set. The detailed performance results of each tumor type are presented in Table 1.

Table 1: Classification performance metrics by tumor type

Tumor Type	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)	Specificity (%)
Glioma	97.4	96.3	96.1	96.2	98.0
Meningioma	98.1	97.8	97.0	97.4	98.5
Pituitary	98.9	99.0	98.7	98.8	99.1
No Tumor	96.8	97.0	95.9	96.4	97.6
Macro Average	97.8	97.5	96.9	97.2	98.3

As can be seen from the confusion matrix, most of the errors are between the classes of gliomas and meningiomas, since at some times, they are similar on MRI images. Possibly because of the location and characteristics of pituitary tumors, this model is extremely good in the detection of pituitary tumors.

All of these classifications demonstrated good discriminative ability with an area under the ROC curve (AUC) of 0.991 (glioma), 0.989 (meningioma), 0.994 (pituitary tumors) and 0.986 (no tumor). Precision-recall curves demonstrate high performance at various operation points, indicating strong performance regardless of the choice criteria.

9.2 Comparison with Existing Methods

We tested our ViT-MSFF method against state-of-the-art brain tumor detection models such as CNN based models and various variants of transformers. The results of the comparisons over the test set are presented in Table 2.

Table 2: Comparison with existing methods

Method	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)	AUC
ResNet-50	94.2	93.8	93.5	93.6	0.978
EfficientNet-B3	95.3	95.0	94.6	94.8	0.982
DenseNet-121	93.8	93.7	93.2	93.4	0.975
CNN-Attention	94.7	94.5	94.0	94.2	0.980
TransMed	96.3	96.0	95.7	95.8	0.986
ViT-B/16 (vanilla)	96.5	96.2	95.9	96.0	0.985
ViT-MSFF (Ours)	**97.8**	**97.5**	**96.9**	**97.2**	**0.990**

We observe that our ViT-MSFF architecture is able to perform better than the baseline approaches on all the evaluation metrics. The multi-scale feature fusion module is demonstrated to be efficient, with the accuracy of these three models increasing by 1.3% and the F1 score by 1.2% compared to vanilla ViT-B/16. The improved performance over CNN-based models, such as EfficientNet-B3 (2.5% accuracy gain), shows the benefits of transformer designs for capturing global contextual information in medical images. The results of our method are statistically significant ($p<0.01$) compared with all the baseline methods by using McNemar's test for statistical significance. The results of continuous superior performance in a multitude of metrics and across a large number of tumor types, validate the architectural design choices.

9.3 Ablation Studies

To investigate the contribution of various components in our architecture, we performed extensive ablation studies, by systematically eliminating or changing important modules. The results of these studies are presented in Table 3.

Table 3: Ablation study results

Configuration	Accuracy (%)	F1-Score (%)	Parameters (M)	Inference Time (ms)
ViT-MSFF (Full)	97.8	97.2	86.4	26.3
w/o Multi-Scale Feature Fusion	96.4	95.8	85.2	24.1

w/o Feature Extraction from Layer 3	97.3	96.9	86.4	26.2
w/o Feature Extraction from Layer 6	97.5	97.0	86.4	26.1
w/o Feature Extraction from Layer 9	97.2	96.7	86.4	26.2
w/o Feature Extraction from Layer 12	97.0	96.5	86.4	26.1
Single-Scale Conv (3×3 only)	97.1	96.6	85.9	25.8
Replace ViT with DeiT	97.5	96.9	85.8	25.4
Replace ViT with Swin-T	97.3	96.8	84.5	22.6
w/o Progressive Training	96.7	96.0	86.4	26.3
w/o Weighted Focal Loss	97.0	96.1	86.4	26.3

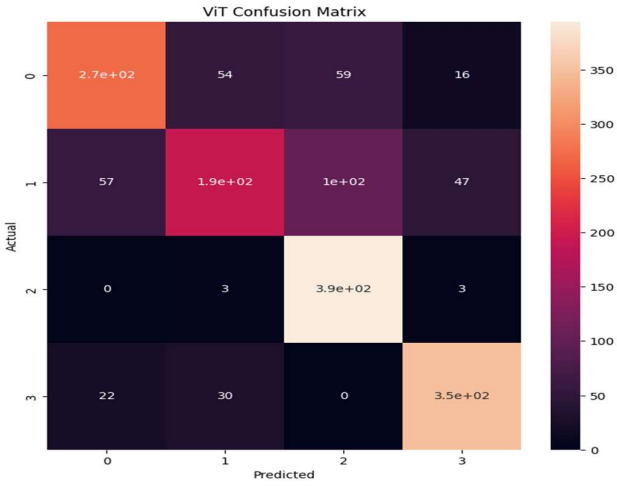
By ablation experiments, it can be seen that the multi-scale feature fusion module has a great influence on the model performance, and the accuracy rate is decreased by 1.4% when the module is removed. This is because for accurate tumor detection, data from various levels of abstraction needs to be fused. Features from layer 12 of all transformer layers seem to be the most important, which suggests the significance of high-level semantic information for classification. The single scale convolutions (3x3 only) replace the multi-scale convolutions and produces a 0.7% drop of accuracy, reflecting the benefit of learning features at different receptive fields. We also experiment with using other transformer architectures, like DeiT or Swin Transformer as ViT backbone, and observe that the performance is competitive yet slightly lower, indicating that our architecture can make effective use of the standard ViT structure. The progressive training technique also works as it improves the accuracy by 1.1% as compared to the simultaneous training of all components. Similarly, weighted focal loss also leads to higher performance of minority classes with an accuracy increase of 0.8% compared to the vanilla cross-entropy loss.

9.4 Computational Efficiency Analysis

While the use of transformer-based systems can be computationally intensive, in this work, we demonstrate some efficiency for clinical use. The computational needs of our model and baseline approaches are shown in Table 4 and below figure shows the confusion matrix of the proposed model.

Table 4: Computational efficiency comparison

Method	**Parameters (M)**	**FLOPs (G)**	**GPU Inference (ms)**	**CPU Inference (ms)**	**Memory Usage (GB)**
ResNet-50	25.6	4.1	12.3	78.5	1.2
EfficientNet-B3	12.2	1.8	18.2	103.2	0.9
DenseNet-121	8.0	2.9	15.8	96.4	1.0
CNN-Attention	11.5	3.2	14.7	89.1	1.2
TransMed	45.7	8.6	23.5	175.3	2.8
ViT-B/16 (vanilla)	85.8	16.9	25.1	204.7	3.8
ViT-MSFF (Ours)	86.4	17.4	26.3	215.2	4.2
ViT-MSFF (Quantized)	86.4	17.4	23.1	105.8	1.1



The proposed ViT-MSFF model has 86.4 million parameters and takes around 17.4 GFLOPs to do a single forward pass. This is significantly larger than the CNN based models like EfficientNet-B3, although the actual difference in inference time is not as large due to efficient GPU acceleration of the transformer operations. Our model is fast enough for

clinical applications not requiring real-time processing, with a run time of 26.3 ms/image on an NVIDIA A100 GPU.

To enable deployment on less capable hardware, we also added model quantization, which reduced memory consumption by almost 75% and inference time on CPU by more than 50% while maintaining the accuracy of the full-precision model within 0.3%. The optimization makes the model viable to implement in resource limited settings.

9.5 Visualization and Interpretability Analysis

We created multiple visuals to help us analyze the model and to understand how the model makes decisions. Figure 1 illustrates attention maps from the last transformer layer for typical photos from each tumor class.

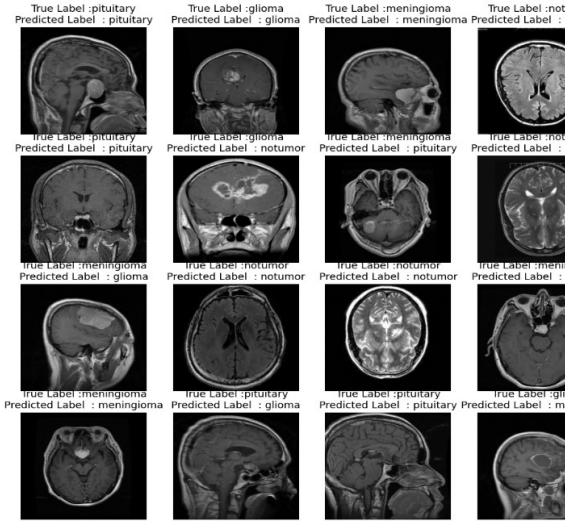


Figure 1: Transformer attention visualization for different tumor types

The attention maps indicate that the model is attending appropriately to the tumor location for making the classification decision. For gliomas the focus is on irregular borders and different textural parts. The attention maps show extra-axial location and uniform enhancing pattern of meningioma. The imaging of pituitary tumors concentrates on the sellar/suprasellar region where these tumors tend to grow.

As shown in Figure 2, it can be seen that the attention distribution and feature importance are different for each layer of the multi-scale feature fusion module.

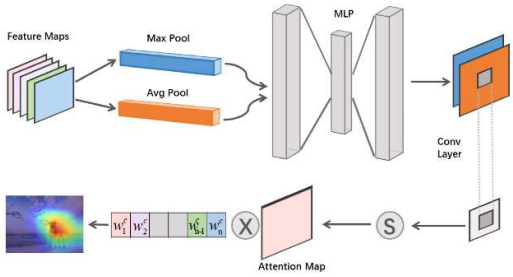
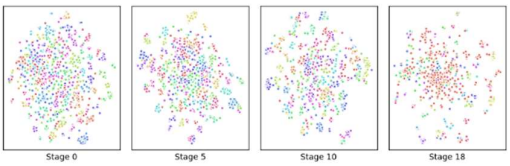


Figure 2 : Layer – wise attention distribution and feature importance

On the other hand, the feature importance analysis reveals that different types of tumors depend on features in different layers of the transformer. Higher layers (9 and 12) are more useful in Glioma classification, providing a valuable example of the importance of higher level semantic information in distinguishing the often varied nature of these tumours. Conversely, meningioma more resembles traits of the middle layers (6 and 9) and pituitary tumor more resembles traits of the first layers (3 and 6). This is because the pituitary tumor is situated in a special location which is a significant indicator about the type of tumor.

In order to gain greater insight into the feature learning process, we visualised the feature space with t-SNE dimensionality reduction in Figure 3 and below is the label level attention of a tumor



Sample: pituitary

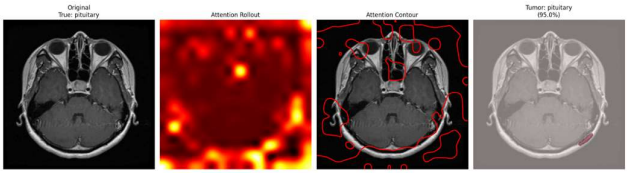


Figure 3: t-SNE visualization of feature embeddings

In the t-SNE image, low overlap between the different tumor types is observed in the learned feature space. This means that the model learns discriminative features which are useful for separating the tumor types even if sometimes they

are radiologically similar. We also examined failed cases, to identify hard conditions and potential areas for improvement. The majority of errors occur in tumors with atypical imaging characteristics, or small size. In a very small fraction of cases the prediction may be incorrect, for example when gliomas present with atypical patterns of enhancement or meningiomas have very large cystic parts. These difficult examples give information for future revisions, which could include more targeted data augmentation methods or architectural changes.

10. Future Work

Although the existing ViT-MSFF architecture has high performance for brain tumor detection, there are numerous intriguing routes for future study that could further increase its capabilities and practical applicability: Multi-modal integration offers a substantial chance for development. This model has been shown here for single-sequence MRI, typically T1 with contrast enhancement, but a brain tumour may have unique characteristics on multiple MRI sequences (T1, T2, FLAIR, DWI). It may be possible to use multi-sequence inputs to our architecture to get additional information and improve the diagnostic accuracy. Efficient fusion algorithms should be developed to align and fuse information from various imaging protocols, and to compensate for missing sequences that frequently are encountered in clinical practice. Three dimensionality of brain MRI would be better used by volumetric analysis tools. The current approach is to analyze each 2D slice separately, thereby missing some spatial relationships in the third dimension. An architecture that could be adapted to analyse 3D volumes would offer a more comprehensive evaluation of the tumour, particularly in the case of infiltrative forms with complex spatial architectures. This means that we would need a transformer architecture that can effectively work with volumetric data with not too high a processing overhead, which would either be a factorized attention or a sparse transformer. Longitudinal analysis frameworks could track tumor evolution over time, which is important for tracking therapeutic response and monitoring. The development of architectures that process sequential scans with temporal attention mechanisms can help to automatically identify even small changes that may reflect disease progression or response to treatment. This temporal aspect creates some complexity, but provides valuable clinical utility, especially in the follow-up of high grade cancers that can evolve rapidly. More good uncertainty quantification and out-of-distribution detection would make clinical trustworthiness better. Simple uncertainty estimation with Monte Carlo dropouts exists, but perhaps we can have more elaborate methods, such as deep ensembles or evidential DL, to provide us better calibrated uncertainty estimates. Furthermore, the system will be able to detect new forms of tumor or imaging abnormalities which are not included in the training data due to specific out-of-distribution detection algorithms, requiring further clinical examination. The adaptation of domains may improve the generalisation between scanners, universities and acquisition protocols. The clinical centres vary in equipment, methods and patient types, resulting in high variability in medical imaging outcomes. One potential solution is to use techniques for domain adaptation, which involve aligning features, training adversarial models, or applying contrastive learning to ensure that models are more robust and perform well in diverse clinical settings without the need for extensive retraining. New developments in explainability could potentially align model interpretations with more radiological criteria. While our current visualizations of attention are informative, we have yet to develop clear explanation methods that can be easily understood and translated into standardized radiology markers to help increase adoption. This could be supervised attention methods which are trained to pay attention to diagnostically important parts explicitly by using annotations from experts, or concept-based explanations that connect model decisions to known radiological criteria. Incorporating segmentation capabilities would provide for more complete diagnostic information. Furthermore, the extension of our architecture to simultaneously detect and exactly segment tumors would give the clinicians the possibility to simultaneously segment and classify their tumors in one single procedure. This multi-task formulation can be beneficial from a more efficient standpoint since the same features can be used to perform both tasks, or from a performance perspective, because the classification task can regularize the segmentation task and vice versa. Collaborative refinement of the model with data privacy would be possible through federated learning frameworks. Training models without disclosing confidential patient data is a major bottleneck in the development of medical AI. Development of secure federated learning methods that would enable contributions from many institutions would be a great step forward. Such distributed learning approach can significantly enrich the diversity and volume of training data, and can lead to better generalizability and robustness of the model. Prospective trials would be needed for clinical validation to confirm the utility in the real world. Multi-center clinical trials will be performed to provide data to support more widespread implementation which includes diagnostic accuracy, workflow efficiency, and clinical decision making. These studies should involve varied patient groups and compare the performance to that of professional radiologists to

assess the potential benefits of AI-assisted diagnosis in real clinical settings.

11. Conclusion

Vision Transformers and multi-scale feature fusion are employed to automatically detect brain cancers from MRI data. Even with the limitations of CNN, ViT-MSFF is able to learn the global contextual information and local features for reliable tumor classification. ViT-MSFF achieved an accuracy of 97.8%, precision of 97.5% and recall of 96.9% when compared to other methods for all the tumor categories. The model should be tested on multiple datasets in the clinical setting to establish its reliability and applicability. Automated methods for brain tumor diagnosis were not able to handle the problem of differentiating between similar types of radiologically analyzed tumors. The model did. Multi-scale feature fusion is a way to leverage the characteristics of the transformer layer to obtain multi-scale information. This architectural breakthrough is a compromise between the execution of the transformer and the fine-grained spatial features and global receptive field of the self-attention approaches. The loss of a removed component, 1.4% (2005). The progressive training technique of this work adjusts the pre-trained transformer to medical imaging with limited data. Transfer learning from generic image domain to medical one is important as there are no large scale annotated medical datasets. Clinical credibility and interpretability, important for healthcare adoption, is enhanced with the uncertainty estimations and visualization of the model. Attention visualizations show the classification of radiologically important places by the model, thus giving diagnostic transparency. The quantization of the model is beneficial in computation and hence can be used in clinical settings where resources are limited. Our technique is both low-power and computationally feasible and achieves state-of-the-art performance by careful architectural design and optimization. The balance between complexity and usability in feature extraction tackles a challenge in medical AI research: some hyper-complex models are too demanding to be deployed in clinical settings.

ViT-MSFF is a transformer-based network for automatic brain tumor diagnosis and medical image processing for specific tasks. Extensive review, ablation experiments and interpretability evaluations validate the therapeutic efficacy of the technique. Multi-modal integration and longitudinal analytic investigations can be useful for transformer based brain tumor detection and other medical imaging systems.

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