An Ensemble Deep Learning Approach for Enhanced Classification of Pituitary Tumors

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Abstract—Tumor detection has emerged as a significant aspect of neuro-oncology and neuroradiology, with critical importance in improving patient survival rates. Tumors, whether benign (non-cancerous) or malignant (cancerous), can result in severe morbidity, and their accurate detection is very important for treatment. In recent years, medical imaging modalities such as Magnetic Resonance Imaging (MRI) and Computed Tomography (CT) have been extensively utilized for non-invasive tumor detection. These imaging techniques provide in-depth information about the tumor's location, size, and morphology, which is pivotal for diagnosing and planning therapeutic interventions. However, the manual interpretation of these imaging modalities is time-intensive and susceptible to human inaccuracies. Moreover, the subtle features of tumors can be easily missed in the manual assessment. Hereby, we propose an ensemble deep learning approach to classify pituitary tumors, based on the weighted average technique that incorporates three base deep learning models: ResNet 152, DenseNet 201, and VGG 16. Moreover, we implement the Segment Anything Model (SAM) to perform segmentation to our dataset and then execute the ensemble model to classify pituitary tumors from normal/healthy brain images. We compare our proposed approach using segmented data and non-segmented data, finding that the segmented data outperforms the non-segmented data by a margin of 1.77%.

Index Terms—pituitary tumor, ensemble technique, segment anything model

I. Introduction

Pituitary tumors are common lesions ranking as the second most prevalent type of primary brain tumor [1]. According to [2], these tumors are uncommon abnormalities that form within the pituitary gland, an organ approximately the size of a pea located at the base of the brain, behind the nose. These tumors can disrupt the normal hormone production of the pituitary gland, leading to an excess or deficiency of certain hormones that regulate vital bodily functions. The majority of pituitary tumors are benign, meaning they are not cancerous. These noncancerous tumors are also known as pituitary adenomas. Most adenomas remain localized and their growth tends to be slow.

Pituitary tumors encompass approximately 10-15% of all tumors within the adult population's brain. While they are typically non-cancerous and grow slowly, they can produce symptoms by affecting hormone levels or exerting pressure within the sellar region. At least one-third of pituitary tumors are linked to various health issues, including diabetes mellitus, heart disease, fertility problems, sexual dysfunction, mood disorders, visual impairments, and hypertension [3]. Diagnostic imaging techniques like magnetic resonance imaging (MRI) are crucial in identifying tumors originating in the pituitary gland [4]. The MRI examination is highly beneficial in examining the brain and spinal cord and is widely recognized as the most effective method for detecting pituitary tumors. The images produced by MRI are typically more detailed than those obtained through CT scans [5]. However, manual evaluation of these images by medical professionals can sometimes lead to inaccuracies due to factors such as fatigue, lack of expertise, and limited information available in the images. This can happen if the tumor is too small to be visible or if it merges with certain brain areas, making it difficult to distinguish from healthy brain tissue [6]. Besides, numerous diseases occur in the pituitary area, for example, Hypopituitarism, Cushing's Disease, Pituitary carcinoma, etc. It is very important to differentiate pituitary tumors from other diseases. Considering all these points and mitigating these diagnostic inaccuracies, this study proposes an ensemble deep learning approach followed by an automatic segmentation model to enhance pituitary tumor classification accuracy.

The contributions of this study are (1) to segment the pituitary tumor MRI images applying Segment Anything Model (SAM), (2) to propose an ensemble deep learning technique based on DenseNet 201, ResNet 152, and VGG 16 to classify pituitary tumors from the segmented images, and (3) to conduct comparative analysis on the ensemble model using data with segmentation and data without segmentation.

II. Related Work

The process of detecting a brain tumor is time-consuming and depends largely on the proficiency and expertise of the radiologist. Researchers devised algorithms that can both identify and classify brain tumors quickly and accurately. In recent times, Deep Learning (DL) techniques have gained popularity for developing automated systems adept at diagnosing or segmenting brain tumors in a reduced timeframe [13]. DL leverages the power of pre-trained Convolutional Neural Network (CNN) models, specifically designed for categorizing medical images related to brain cancer.

TABLE I

SUMMARY OF WORKS DONE ON DIFFERENT TYPES OF BRAIN TUMORS SEGMENTATION AND CLASSIFICATION

Author(s) and year	Segmentation Method	Classification Method	Dataset(s)	Result(%)
Anita and Kumaran, 2022 [7]	Morphological segmentation approach: morphological dilation and morphological erosion	VGG-16	Nanfang	Sen.=99.1, Spe.=99.5 Seg. Acc.=99.4, Class. Acc.=99.2
Ragupathy et al., 2023 [8]	Morphological operation	Anisotropic diffusion filtered CNN-SVM	-	Sen.=96.01 Spe.=99.41, Acc.=99.22
Muezzinoglu et al., 2023 [9]	-	PatchResNet	Kaggle Brain Tumor MRI	Dataset 1: Acc.=98.10, Rec.=98.15 Pre.=97.91, F1-Sc.=98.01
Aggarwal et al., 2023 [10]		Improved ResNet	BraTS2020	Sen.=79.89,Spe.=92.06 Acc.=91.30
Kishanrao and Jondhale, 2023 [11]	density peak cluster with Social Ski-Driver optimization	Hybrid Deep CNN with Deer Hunting framework	Brats 2015, 2017, and 2019	Brats2019: Acc.=99.8, sen.=98.1, spe.=99.6, pre.=97.4 F1-sc.=98.6
Kaplan et al., 2020 [12]	-	nLBP(feature extraction) + KNN	Nanfang	Acc.= 95.56
ZainEldin et al., 2022 [13]	3D U-Net	Inception- ResnetV2	BRaTS 2021 Task 1	Acc.=99.98, Sen.=99.98 Spe.=99.98,F1-Sc=99.98
Farajzadeh et al., 2023 [6]	Hybrid U-Net with Hyper kernel and Attention layers	-	BraTS'20	Segmentation: Acc.=98.81,Pre.=98.99 Rec.=98.63,F1-sc=98.81 Class. acc.=98.93
Sobhaninia et al., 2023 [14]	Multiscale Cascaded Multitask Network	-	Figshare	Pre.=97.98
Ruba et al., 2023 [15]	Attention Res-Unet with Joint gate attention mechanism based deep learning architecture	-	BRATS 2015 and 2019	BRATS2015: Acc.=94.99, Sen.=87.34 BRATS=2019: Acc.=93.69, Sen.=84.21
Faragallah et al., 2023 [16]	OTSU, K-means clustering	-	58 different datasets	K-means Clustering: Acc.=98.58,Sen.=99.01 Pre.=99.40,Spe.=94.62
Indriani et al., 2023 [17]	-	Custom CNN	Kaggle	Acc.=98.93
Yousaf et al., 2023 [18]	-	CNN based integrated model	BRATS 2015 and ISLES 2015	Acc.=99.56, Spe.=99.99 Sen.=0.9987,Pre.=99.59 F1-Sc.=99.57

Abbreviation: Sen. = Sensitivity, Spe. = Specificity, Acc.= accuracy, Rec. = recall, pre. = precision, F1-sc. = F1 score, Class.=classification, Seg.=segmentation

A. Deep Learning Methods

ZainEldin et al. [13] propose Brain Tumor Classification Model based on a CNN that optimizes its hyperparameters using an Adaptive Dynamic Sine-Cosine Fitness Grey Wolf Optimizer algorithm. This process includes hyperparameters optimization and training using the Inception-ResnetV2 model. Anita et al. in [7] present a method for detecting and segmenting meningioma brain tumor images using a CNN approach. Brain MRI images are initially decomposed via the discrete wavelet transform, and the resulting sub-bands are combined using an arithmetic fusion technique. The images have been classified, and then the tumor region in the malignant brain image is segmented using a connection component analysis algorithm. The segmented brain image is then compressed using a lossless compression technique. Muezzinoglu et al. discuss an automated brain tumor classification model named PatchResNet in [9] using CNNs to enhance image classification performance. This model utilizes patch-based deep feature engineering and employs patches of different sizes for high classification performance. It uses two layers of pre-trained ResNet50 for feature extraction. Classification is achieved through k nearest neighbors (kNN), with iterative hard majority voting (IHMV) determining the overall classification accuracy. Using a Hybrid Deep Convolutional Neural Network with Deer Hunting optimization, a grade-based brain tumor classification technique is presented in [11]. The process starts by pre-processing MRI brain images using normalized bilateral filtering and density peak clustering with Social Ski-Driver optimization for effective segmentation. Several features are extracted, including a pyramid histogram of oriented gradients (PHOG), gray level co-occurrence matrix (GLCM), intensity-based features, and modified local binary pattern (MLBP). The proposed method is employed for classification into normal, low-grade, and high-grade images. Ruba et al. in [15] introduce a new and simple network design, the JGate-AttResUNet, aiming to provide a robust and reliable brain tumor segmentation system. The model yielded competitive results when tested on the BraTS 2015 and 2019 datasets, achieving mean dice values of 0.896 and 0.913, respectively. Sarala et al. [19] introduces a Dual CNN method for Glioma

brain tumor detection where the first CNN extracts features from brain images, and another CNN classifies these features. Also, they proposed a Histogram-Density Segmentation Algorithm (HDSA) to segment the Tumor Region of Interest (RoI) in the Glioma image. The Histogram of Gradient (HOG) technique is used in [20] to extract neural features from MRI images for tumor detection. Modified ResNet50 model is implemented, paired with an enhanced layered architecture for optimal computational efficiency. A two-phase deep learning-based framework is proposed by the authors in [21] to detect and categorize brain tumors in MRIs. In the first phase, the researchers propose a deep-boosted feature space and ensemble classifiers (DBFS-EC) scheme that uses customized deep CNNs to detect tumor MRIs from healthy images. In the second phase, they introduced a hybrid feature fusion-based approach for classifying different tumor types using static and dynamic features. Hu et al. [22] introduced Consensus Dice loss, a novel loss function designed for the mutual learning of multiple 3D brain tumor segmentation networks. The proposed method is based on two famous baseline models: Single-Pathway DeepMedic and Unet. The authors in [23] evaluate seven deep CNN models, including a generic CNN model and six pre-trained models, for brain tumor classification. Various preprocessing strategies were applied to the input MRI images before training the models. The evaluated CNN models include Generic CNN, ResNet50, InceptionV3, InceptionResNetV2, Xception, MobileNetV2, and EfficientNetB0. [24] proposes an ensemble learning method to classify brain tumors (glioma, meningioma, pituitary adenoma) and lesions from autoimmune diseases (multiple sclerosis) using MRI images. A support vector machine (SVM) classifier serves as the base learner, with a majority voting prediction model.

Meta AI research team has developed an image segmentation process called SAM [25] along with a dataset of 1 billion masks on 11 million images, and it has been observed that this model's zero-shot performance is remarkable. He et al. [26] have investigated this model on 12 medical image segmentation datasets and have found that it underperforms in these datasets compared to the state-of-the-art deep learning techniques. Also, it has been noted that this model performs better in 2D medical images. Ma and Wang [27] and [28] also agree that the performance of SAM is limited for medical images due to complex modalities, wide range of object scales, and complex object boundaries. [27] have presented a tool for segmentation targeting medical images named MedSAM, which outperforms SAM. [28] have evaluated SAM for the segmentation of large medical image datasets. They have investigated the two modes of SAM: *Everything* mode and *Promt* mode, and have made a conclusion that *everything* mode is not suitable for most medical images.

B. Ensemble Deep Learning Approaches

The author in [29] introduces a novel ensemble deep learning approach that integrates ResNet-152 and DenseNet-121 in order to detect Covid-19 cases from chest X-ray images. Xue et al. [30] propose a deep learning ensemble framework model
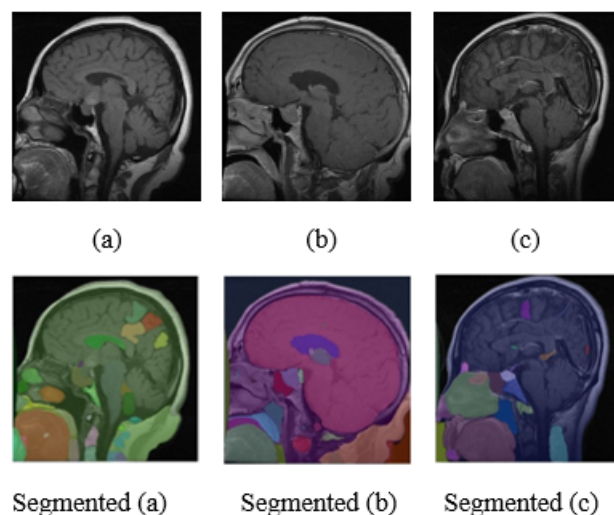

Fig. 1. Original MRI image (upper line) and Segmented Images[lower line]

based on ResNet152, VGG16, ResNet50, and DenseNet121 in order to detect Covid-19 and pneumonia using CT scan and X-ray images. Barsha et al. in [31] introduce two ensemble models designed for the detection and grading of Invasive Ductal Carcinoma (IDC), a type of breast cancer. The first model harnesses DenseNet-121 and DenseNet-169 to identify IDC. For the grading of IDC, the authors propose another ensemble model that integrates four pre-trained architectures: DenseNet-121, DenseNet-201, ResNet-101v2, and ResNet-50. Another ensemble deep learning system has been proposed to detect breast cancer at an early stage in [32] that is composed of four CNN models: DenseNet201, ResNet-101, ResNet-50, and AlexNet. The binary Support Vector Machine model is applied to each CNN to determine malignant or benign scores. To determine skin cancer from seven types of skin lesions (Melanocytic nevi, Melanoma, Benign keratosis, Basal cell carcinoma, Actinic keratosis, Vascular Lesions, and Dermatofibroma), the authors in [33] have implemented different deep learning methods: Resnet-50, VGG-16, Densenet, Mobilenet, Inceptionv3, and Xception. Besides, they have developed five different stacked models: inceptionv3-inceptionv3, Densenet-mobilenet, inceptionv3-Xception, Resnet50-Vgg16, and stack-six. They have found that these stacked models perform (78%) less than the existing models. Xie et al. [34] have done research on identifying defective carrots by applying an ensemble approach based on five classical CNN: Densenet-121, ResNet-50, Inception-V3, VGG-16, and VGG-19. They fixed ResNet-50, integrated the other two models, and found that ResNet-50, VGG-16, and DenseNet-121 performed best. Vallabhajosyula et al. [35] have proposed a weighted ensemble of deep neural networks in order to detect disease in plant leaves. They have evaluated different ensemble models based on ResNet 50, ResNet 101, InceptionV3, DenseNet 121, DenseNet 201, MobileNetV3, and NasNet and have found that ensemble models outperform other pre-trained models. A weighted average ensemble deep learning model has been proposed
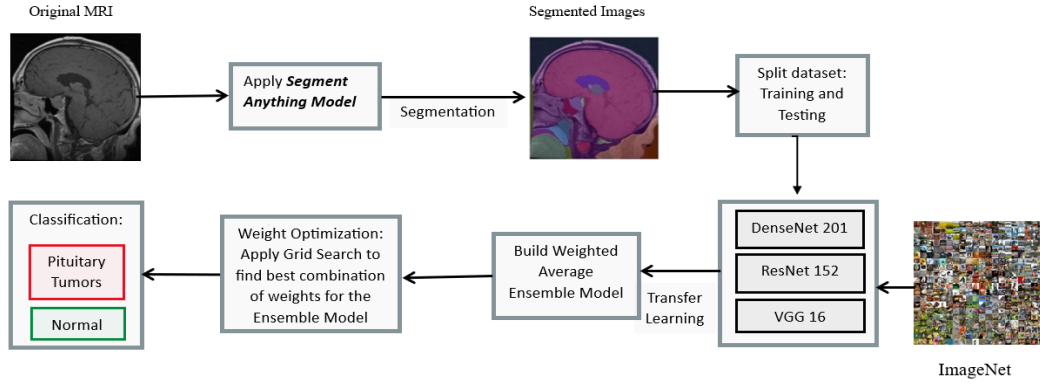
Fig. 2. Proposed System Architecture

by Anand et al. [36] to detect brain tumors in MRI images where VGG19, CNN with augmentation, and CNN without augmentation models have been considered, and the best combination of weights for those models have been obtained using grid search technique. A weighted average ensemble-based semantic segmentation process has been proposed by Shaga Devan et al. [37] where five base learners models (ResNet34, InceptionV3, VGG19, EfficientNet-B4, and SeResNet34) have been evaluated by providing weights obtained from Grid-CV search and best three models have been chosen for the ensemble approach.

III. METHODOLOGY

A. Overview of Dataset

We use pituitary tumor MRI images and healthy/normal brain MRI images from four publicly available datasets: Kaggle brain tumor classification MRI [38], Figshare [39], BR35H [40], and Kaggle brain tumor detection [41] and create a custom dataset of two classes. We have a total of 3287 images, of which 1857 are pituitary tumor images and 1430 normal/healthy brain images.

B. Proposed Methodology

First, we apply SAM to the custom dataset and generate segmented images. Then, we implement different deep learning techniques: DenseNet-201, InceptionV3, ResNet50, ResNet-101, ResNet-152, MobileNetV2, EfficientNetB0, Xception, VGG-19, VGG-16 and NasNet-Large. Among these models, the best three (i.e. ResNet 152, VGG 16, and DenseNet 201) have been selected for the ensemble model.

Segment Anything Model
SAM [25] has the capability to produce masks for any object present in any image or video, even if it includes object types and image categories that it wasn't exposed to during its training phase. It can identify and create masks for every object within an image autonomously. This model has three components: Image Encoder, Prompt Encoder, and Mask Decoder. Mask autoencoder pretrained vision transformer [42] has been used in image encoder component. Two categories of prompts have been considered: sparse (points, boxes, text) and dense

(masks). The mask decoder is designed to effectively generate a segmentation mask by mapping the image embedding, prompt embeddings, and an output token to the final mask. Prompt self-attention and cross-attention mechanisms have been used in this decoder in order to update the embeddings.

DenseNet 201
Huang et al. [43] introduce a dense convolutional network (DenseNet), a model that establishes connections between each layer and all other layers in a feed-forward manner. While conventional convolutional networks with *n* number of layers have *n* connections, each connecting a layer to its immediate subsequent layer, this model exhibits a significantly higher number of direct connections, specifically *n(n+1)/2* connections. In this network, every layer takes the feature maps from all the preceding layers as its inputs, and its own feature maps are employed as inputs for all the subsequent layers. Considering a single image x_0 passed through a convolutional network where the network includes *n* layers, each implementing a non-linear transformation $H_n(.)$. Here, *n* indicates the sequence of layers. The nth layer receives the feature-maps of all preceding layers, $x_0, x_1, \ldots, x_{n-1}$, as input:

$$x_n = H_n([x_0, x_1, \ldots, x_{n-1}]) \tag{1}$$

Here, $x_0, x_1, \ldots, x_{n-1}$ represents the combination of feature-maps generated in layers 0 through $n - 1$, achieved through concatenation. DenseNet-201 is a specific variant of the DenseNet architecture where the number "201" in the name refers to the total number of layers in this variant.

ResNet 152
Residual Network (ResNet) is an efficient CNN architecture that was introduced in order to solve the problem of vanishing gradient through the 'skip connection' technique [44]. It allows one or more layers to be passed over by transferring activation from one layer and supplying it as input to another layer [45]. Resnet 152 is a variation of ResNet which has 152 layers.

VGG 16
The VGG-16 model, developed by the Visual Geometry Group at the University of Oxford [46] emphasizes network depth and convolutional layers. The architecture comprises 16 layers,

TABLE II
EVALUATION TABLE

Evaluation Metrics	Resnet 152	Dense-net 201	VGG 16	Proposed Model(with segmented data)	Ensemble (Non-Segmented)
Recall	1.0	0.9448	1.0	0.9899	0.9676
Precision	0.9391	0.9418	0.9391	0.9881	0.9739
F Score	0.9686	0.9433	0.9686	0.9889	0.9707
Accuracy	0.9391	0.8843	0.9389	0.9885	0.9708

Fig. 3. Performance Comparison (Accuracy)

TABLE III
WEIGHTS OBTAINED FOR BASE MODELS

w1	w2	w3	Accuracy
0.1	0.1	0.8	0.9627
0.1	0.2	0.7	0.9539
0.2	0.2	0.6	0.9655
0.2	0.3	0.5	0.9741
0.3	0.2	0.5	0.9803
0.3	0.3	0.4	0.9757
0.4	0.1	0.5	0.9741
0.4	0.2	0.4	0.9753
0.5	**0.1**	**0.4**	**0.9885**
0.5	0.2	0.3	0.9836
0.6	0.2	0.2	0.9424
0.6	0.3	0.1	0.9737
0.7	0.1	0.2	0.8717
0.8	0.1	0.1	0.9465

with 13 convolutional and three fully connected layers. It employs small 3x3 convolutional filters and organizes layers into blocks with max pooling. Early blocks capture basic features, while later ones discern complex patterns. VGG-16's impact lies in revealing deep networks' potential for image recognition, underlining depth's role in neural architecture, and leveraging small filters for intricate pattern learning.

Ensemble Model

We apply SAM to our dataset and generate segmented images. A few examples of segmented images are in figure 1. We employ transfer learning on the three base models (Resnet 152, Densenet 201, and VGG 16) so that we can use the pre-trained model, which is trained by imagenet dataset. Thus, we reduce the training time of our models. Then, we build the proposed ensemble deep learning model based on the weighted average technique, which is an ensemble machine learning approach that fuses predictions from several models where each model's input is scaled according to its competence or proficiency, resulting in a combined output [47]. Next, we apply the grid search technique for weight optimization to get the optimum combination of weights for the three base models. Finally, the resultant ensemble model is applied, and pituitary tumors have been classified. Figure 2 shows the proposed system.

IV. EXPERIMENT ANALYSIS

Our experiment considers *accuracy*, *precision*, *recall*, and *F1-score* as the evaluation metrics [48]. We set the following hyper-parameters: Learning rate = 0.0001, Train-test split ratio = 80:20, Batch Size = 32, Number of Epochs = 50 and Image size = (224, 224).

At first, we implement the three base models individually using the segmented data and receive 0.9391, 0.8843, and 0.9391 for Resnet 152, Densenet 201, and VGG 16, respectively. Then, we form the ensemble model based on the weighted average technique and apply grid search to get possible all combinations of weights for these three models (Table III). We find that the ensemble model gives the highest accuracy (0.9885) for weights w1 = 0.5, w2 = 0.1, and w3 = 0.4. Here, w1, w2 and w3 indicates weights for ResNet152, Densenet201 and Vgg-16 respectively. This ensemble model with optimum weights is once again implemented with original MRI data without segmentation, and we obtain 0.9708, which is 1.77% less than the previous result (Figure 3). Therefore, we can say that segmented data provides 1.77% better performance than the original data.
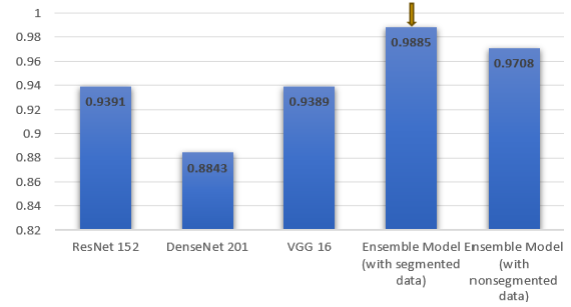
V. CONCLUSION

Our study introduces a weighted average ensemble deep learning model in order to classify pituitary tumors from MRI scans. This research uses a custom pituitary tumor MRI dataset and employs the SAM automated segmentation process. A grid search technique is used to identify the optimal combination of weights for base models: ResNet 152, DenseNet 201, and Vgg 16. The proposed ensemble model surpasses the individual models in terms of accuracy, achieving 98.85%. Moreover, We conduct a comparative analysis between data with and without segmentation. We attain 1.77% better results with segmented data. This model demonstrates remarkable efficacy, particularly in the context of smaller tumors, such as those found in the pituitary region.

VI. FUTURE WORK

We will apply the SAM in other MRI and CT scan datasets, for instance, multiple sclerosis, skin lesions, chest CT scans, etc., and conduct a comparative analysis to investigate the performance of SAM to enhance classification methods.

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