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# An integrated hybrid U-Net and EfficientNetV2-S approach for brain tumor segmentation and classification

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**ABSTRACT**

Brain tumors involve the uncontrolled proliferation of cells either inside or adjacent to brain tissue, which frequently results in poor patient outcomes. Accurate diagnosis and early identification are vital for effective treatment planning. In this study, we develop a sequential deep learning pipeline for automatic brain tumor segmentation and classification using the publicly accessible Figshare dataset, comprising 3,064 images from 233 patients. We present a double hybrid encoder model based on the U-Net architecture, which combines complementary feature extractors to improve segmentation performance. The model achieves a loss of 0.047, an intersection over union (IoU) of 86.89%, and a Dice score of 95.27%, surpassing the performance of conventional U-Net and U-Net++ architectures. For classification, we utilize a modified EfficientNetV2-S, which is lightweight and achieves a 99% F1-score and 99% accuracy, while being less computationally intensive and faster to train than deeper frameworks such as ResNet50V2. Model performance was evaluated using cross-validation, which included fault detection to improve reliability. We propose that our framework can reliably and efficiently analyze brain tumors and serve as an important component in clinical decision-making in neuro-oncology.

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## 1. INTRODUCTION

Brain tumors are a deadly disease that causes numerous deaths worldwide annually [1]. Based on their activity, brain tumors are frequently divided into two primary categories: benign, which are less aggressive, and malignant, which are invasive and potentially fatal. The benign type is non-life-threatening but does not migrate to surrounding tissues, while malignant tumors extend to other tissues and are harmful. Early identification is crucial for patients' clinical preparation. Detection can be done via diagnostic imaging techniques or histopathological examination; each method presents advantages and limitations. Practitioners use both aggressive and non-aggressive methods, including experimental imaging techniques like computed tomography (CT) and magnetic resonance imaging (MRI) [2]-[4]. The MRI is a significant tool for detection and safety due to its lack of toxic radiation.

Deep learning techniques [5] has significantly outperformed traditional machine learning methods. In various functions, including brain tumor grade classification [6]. In medical image analysis, convolutional

neural networks (CNNs) [7], are especially beneficial at segmenting [8] and classifying images [9]. Researchers have employed pre-trained CNN architectures [10] and improved them, while others have developed new models from scratch and proposed modern architectures. CNNs excel in object detection and navigation support tasks.

The U-Net architecture has emerged as a predominant framework within medical image segmentation applications [11]-[13]. This model effectively extracts both localized and broader features through encoding and decoding pathways. Skip connections preserve vital spatial information during reconstruction, making the U-Net architecture well-suited for delineating complex anatomical structures such as brain tumors in MRI scans. In the domain of brain tumor region identification and delineation, Nguyen-Tat *et al.* [14] developed an advanced segmentation approach that integrates a modified 3D U-Net architecture with Transformer technology for precise MRI-based tumor detection. Their framework utilizes self-attention mechanisms, incorporating contextual transformer and double attention components, to exploit complex MRI image features, achieving an 85.2% Dice score in the Brain Tumor Segmentation Challenge 2019 dataset. Additionally, Almufareh *et al.* [15] investigated the application of a you only look once (YOLO)-based deep learning framework for both the segmentation and classification of brain tumors, focusing on pituitary, glioma, and meningioma types. YOLOv5 and YOLOv7 performed exceptionally in identifying pituitary tumors, gliomas, and meningiomas. The meningioma class showed the highest recall, with recall scores continuously exceeding 0.78. These results confirm the accuracy of classifying brain tumors across different types and highlight the potential of YOLO models for detection. Kordnoori *et al*. [16] introduced an automatic model for identifying three main brain tumors—pituitary adenomas, gliomas, and meningiomas—in MRI images. The model features a shared encoder for feature representation, a segmentation decoder, and an MLP-based classifier, achieving a significant accuracy of 97% in both segmentation and classification tasks.While Bhimavarapu *et al*. [17] presents an improved segmentation of MRI images utilizing the fuzzy C-means clustering method, focusing on extracting morphological, textural, and chromatic features to reduce complexity. The extreme learning machine has a 99.25% recall, 99.14% precision, and 98.56% accuracy rate when classifying tumors. On the Figshare dataset, the enhanced algorithm demonstrated performance metrics of 98.47% for accuracy, 98.59% for precision, and 98.74% for recall, while evaluation using the Kaggle dataset yielded superior results with 99.42% accuracy, 99.75% precision, and 99.28% recall.

This paper emphasizes the development of an efficient model that can help in the precise identification of tumors automatically. We present a dual hybrid encoder model for the extraction of richer features and obtaining more accurate segmentation images. Two encoders can extract more complicated patterns from input data through various convolution rates, which in turn improves performance. Our segmentation model achieves more accurate results than U-Net and U-Net++. For the classification phase, we introduce fine-tuning for the lightweight EfficientNetV2 network, which achieves accurate classification compared to ResNet50V2 and Dense169 architectures. This framework might be used as the main detection method for an early diagnosis.

This study is organized as follows: section 2 presents the suggested framework for segmentation and classification and explains the data set, preprocessing, dual hybrid encoder model for segmentation, EfficientNetV2-S tuning model for classification, and data augmentation. Section 3 displays experimental findings and section 4 concludes the study and recommends further avenues of investigation.

## 2. METHOD

### 2.1. Dataset

Contrast-enhanced MRI (CE-MRI) scans comprise the Figshare dataset. Cheng [18] which served as an evaluation platform for the recently developed brain tumor model. This collection encompasses 3,064 T1-weighted contrast-enhanced MRI images from 233 patients, including 708 slices of meningioma, 1,426 slices of glioma, and 930 slices of pituitary tumors. It features detailed annotations such as labels, patient IDs, image data, tumor boundaries, and tumor masks. Data allocation across model training, hyperparameter validation, and performance evaluation phases is illustrated in Figure 1.

### 2.2. Data pre-processing

Extracting tumor regions from brain-relevant structural information using MRI remains a difficult task because of irregular contrast, irregular intensity distributions, and noise artifacts. Data pre-processing is crucial and requires careful processes. To begin, smooth MRI masks and images using a bilateral filter [19], maintain edges, and reduce noise. Resize filtered photos, crop, convert to grayscale, and normalize all images by dividing image matrix values by 255 to fall between 0 and 1 to facilitate model training.

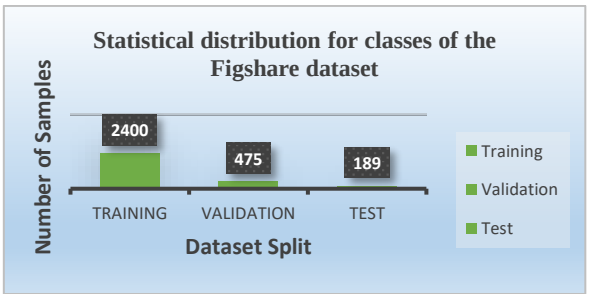



Figure 1. The data distribution for model training

### 2.3. Data-augmentation

Data augmentation in machine learning and deep learning is a procedure that expands the training dataset's size, enhancing the generalization and strength of learned models. So, augmentation is employed to enhance outcomes on a limited dataset, utilizing techniques like rotation and flipping to enable the architecture to comprehend changes while training. Our proposed image augmentation method is seen in Figure 2.

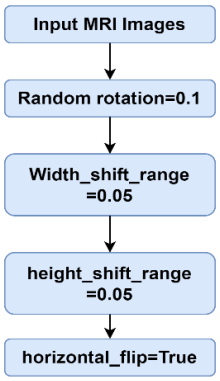



Figure 2. The augmentation technique of our proposed architecture

### 2.4. A suggested model for segmenting brain tumors

The encoder involves five blocks, the first block containing a 3×3 convolutional layer with a 32 filter size, a batch normalization layer, followed by another convolutional layer with 3×3 kernels, a ReLU activation, a dropout layer with a 0.2 ratio, and then a 2×2 max pooling layer is added at the end of the block. Subsequently, we expanded the convolution layers and filters up to 64, 128, 256, and subsequently 512, with almost the same size of the filter, i.e., 3×3. As the total number of filters increases, these little patterns are combined to form larger patterns like squares, circles, and so forth. The second encoder has the same architecture of blocks, but we start filtering size with 16, then 32, 64, 128, up to 256. As shown in Figure 3, the MRI input image is fed in parallel to the two encoders. So, features are extracted at different levels of convolution. The expansive path's decoder layers upsample feature maps from two encoders and perform convolutional operations. Extra skip connections preserve spatial information lost in the contracting path, enhancing the accuracy of feature location by the decoder layers.

### 2.5. Proposed model for brain tumor classification

CNNs' most vital accomplishment is transfer learning, employed when employing a limited data set, such as the situation under study. "In this research, EfficientNetV2-S was used for feature extraction, while ResNet50V2 and DenseNet169 were employed to compare classification results with those obtained from the EfficientNetV2-S model. To create a better design, we fine-tune by adding layers corresponding to the classes of the desired brain MRI data. A layer of global average pooling was added. To prevent overfitting, a dropout layer with a 0.4 factor is added after that. Finally, a dense layer with three neurons activated by SoftMax is used to classify the output for one of three distinct categories (pituitary, meningioma, or glioma). The proposed classification model, EfficientNetV2-S with fine-tuning, is illustrated in Figure 4.

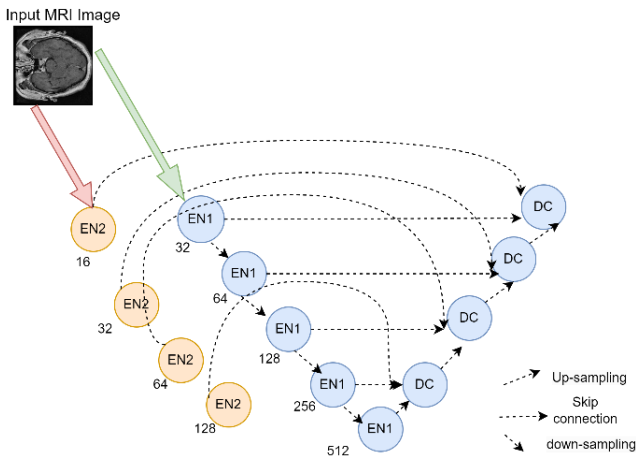



Figure 3. The proposed segmentation model

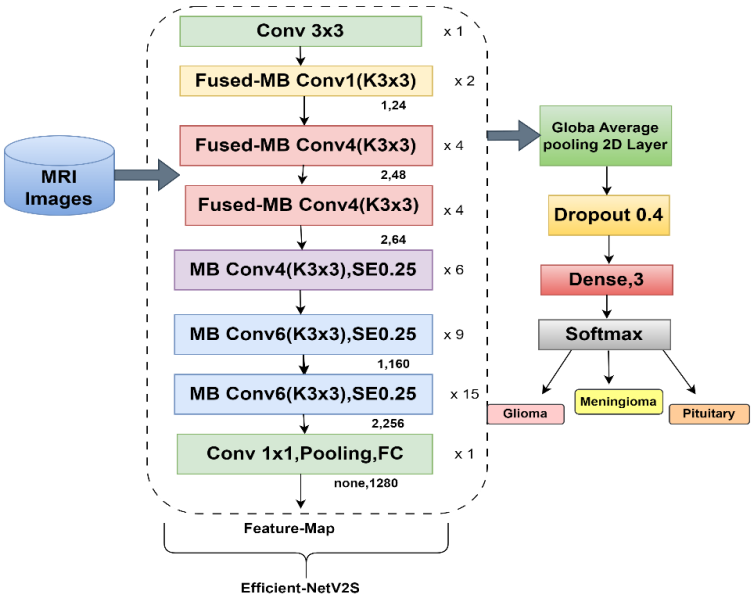



Figure 4. Fine-tuned EfficientNetV2-S architecture for brain tumor classification

## 2.5. Evaluation matrices

### 2.5.1. Evaluation matrices for segmentation

Several performance metrics, including Dice similarity coefficient (DSC), accuracy, precision, and intersection over union (IoU), were used to gauge the model's efficacy. These measures, which have the following mathematical definitions, offer insights into the segmentation quality of the model:

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \tag{1}$$

$$Precision = \frac{TP}{TP+FP} \tag{2}$$

$$Sensitivity = \frac{Tp}{Tp+FN} \tag{3}$$

$$IoU = \frac{Tp}{Tp+Fp+FN} \tag{4}$$

where TP denotes true positive, FP is false positive, TN represents true negative, and FN represents false negative.

#### 2.5.2. Evaluation matrices for classification

To evaluate the proposed classification model, "Finetuned Efficient-NetV2S," a range of evaluation metrics is utilized, including accuracy, precision, recall, and F1-score, to compare our findings with previous studies. The formulas for recall and F1-score are defined as (5) and (6):

$$Recall = \frac{TP}{TP+FN} \tag{5}$$

$$F1 - score = 2 \times \frac{Recall \times Precision}{Recall + Precision} \tag{6}$$

## 3. RESULTS AND DISCUSSION

### 3.1. Environmental setup and model training

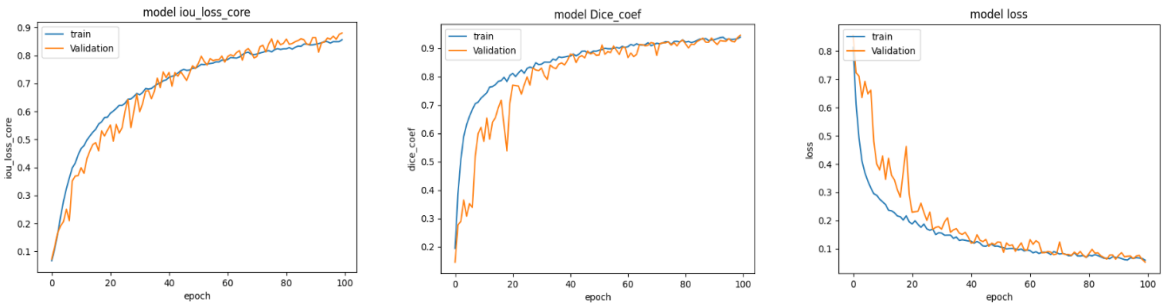
The suggested brain classification and segmentation framework was trained on a Colab GPU with a Tesla NVIDIA K80 with 12 GB. Our models are implemented using the Keras library, with TensorFlow serving as the backend. The hyperparameters used for both the segmentation phase and classification phase are presented in Table 1.

Table 1. Hyperparameters for training segmentation and classification models

| Classification | Segmentation | |
|---|---|---|
| Hyperparameter | Value | Value |
| Optimization algorithm | Adam | Adam |
| Initial learning rate/LR | 0.0001 | 0.0001 |
| Mini-batch size | 64 | 4 |
| Epochs | 50 | 100 |
| Loss function | Categorical_crossentropy | Binary_crossentropy |
| Activation | softMax | sigmoid |

### 3.2. Segmentation results

Figure 5 presents the performance metrics of the proposed segmentation model during the training and validation phases over 100 epochs. The proposed method reaches a 95.27% Dice coefficient on the test set, while for the IoU score, it achieves 86.89 and a minimum loss of 0.047. Figure 5(a) shows the IoU score for both training and validation phases, while Figure 5(b) illustrates the Dice coefficient, and Figure 5(c) presents the loss curves over 100 epochs. The dual hybrid encoder segmentation model is compared with U-Net and U-Net++ architectures. As indicated in Table 2, the designed model outperforms U-Net and U-Net++. Segmentation Dice score can be improved from 93.40% on U-Net to 95.27%, and minimize loss from 0.0532 to 0.047. Also, increase the Dice score with a 4.98% factor over U-Net++ and minimize the loss by 0.05823.




(a) (b) (c)

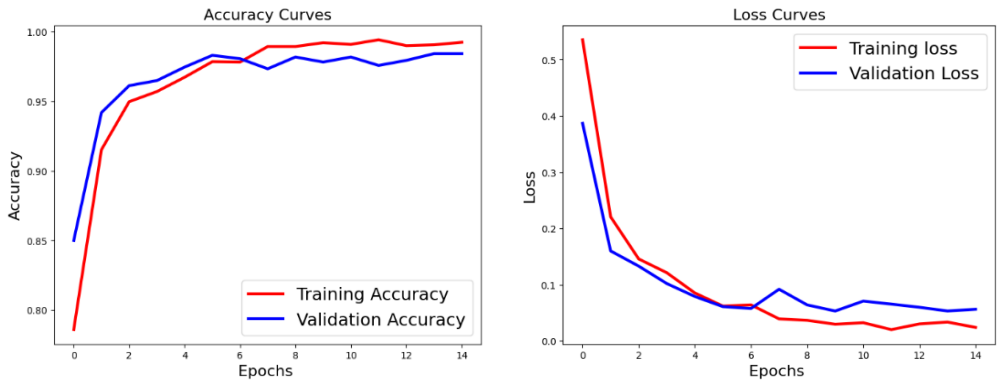
Figure 5. Performance metrics for the proposed model during the training and validation phases over epochs; (a) IoU score, (b) Dice coefficient, and (c) loss curves for training and validation

Table 2. Comparison of the constructed model for segmentation with the U-Net and U-Net++ models

| Model | Dice coefficient | IoU | Loss |
|---|---|---|---|
| U-Net | 93.390 | 86.85 | 0.0532 |
| U-Net++ | 90.287 | 92.31 | 0.1053 |
| Proposed dual hybrid encoder | 95.27 | 86.89 | 0.047 |

### 3.3. Classification results

Figure 6 presents the performance evaluation of the EfficientNetV2-S network compared with ResNet50V2 and Dense169 architectures during the training and validation phases. Figure 6(a) illustrates the accuracy curves for the training and validation phases, while Figure 6(b) shows the corresponding loss curves. The suggested model achieves a remarkable 99% accuracy on the test set with a minimum loss of 0.0390, demonstrating its ability to correctly classify most test instances with minimal misclassifications. To further demonstrate the model's effectiveness, it was compared with ResNet50V2 and Dense169 architectures. Table 3 exhibits a comprehensive analysis of the evaluation metrics for each brain tumor category with the three models. The suggested EfficientNetV2-S model has the best F1-score, precision, and recall of about 99%, while Dense169 achieved 98.31% and ResNet50V2 achieved 98.64% for F1-score, precision, and recall, respectively. To demonstrate the model's exceptional accuracy in consistently retaining accuracy with true labels. Figure 7 shows a confusion matrix with diagonal elements indicating properly predicted cases and off-diagonal elements signifying misclassifications. Finally, Table 4 compares our suggested classification and segmentation model framework with the most recent models reported on Figshare. Top performance indicators for classifying and segmenting brain tumors were obtained from the created frameworks.




(a) (b)

Figure 6. Performance evaluation of the EfficientNetV2-S network during training and validation phases; (a) accuracy curves and (b) loss curves

Table 3. Comparison of the classification performance metrics report for EfficientNetV2-S

| Model | Class | Precision | Recall | F1-score |
|---|---|---|---|---|
| Dense 169 | Glioma | 98.31 | 98.31 | 98.31 |
| | Meningioma | 98.31 | 98.31 | 98.31 |
| | Pituitary | 98.31 | 98.31 | 98.31 |
| ResNet50V2 | Glioma | 98.64 | 98.64 | 98.64 |
| | Meningioma | 98.64 | 98.64 | 98.64 |
| | Pituitary | 98.64 | 98.64 | 98.64 |
| EfficientNetV2-S | Glioma | 99.0 | 99.0 | 99.0 |
| | Meningioma | 99.0 | 99.0 | 99.0 |
| | Pituitary | 99.0 | 99.0 | 99.0 |

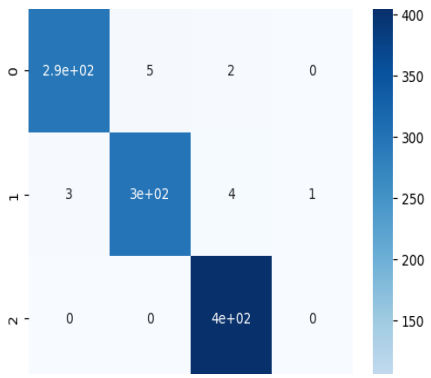



Figure 7. Confusion matrix for EfficientNetV2-S predicted labels

Table 4. Comparison with the most advanced existing techniques for categorizing and segmenting tumors on the dataset from Figshare

| Reference | Classification technique | Segmentation method | Accuracy (%) | Dice score (%) |
|---|---|---|---|---|
| [20] | Parallel deep CNN | -- --- | 98.13 | --- --- |
| [21] | --- --- | Lightweight U-Net | -- -- | 93.0 |
| [22] | CNN + SVM | --- ----- | 95.82 | ---- ---- |
| [23] | MAG-Net | MAG-Net | 98 | 74 |
| [24] | --- --- | Deeplabv3+ResNet18 | -- -- | 91.23 |
| [25] | | Multimodal deep pre-trained model | | 86.02 |
| [26] | Hybrid pre-trained (GN-AlexNet) | | 99.1 | -- -- |
| [16] | multi-layer perceptron | Encoder-decoder U-Net | 97 | 92 |
| [27] | VGG16+23-layer CNN | -- -- | 97.8 | -- -- |
| [28] | YOLO2+transfer learning | U-Net+residual net backbone | 97.0 | 90.11 |
| [29] | VGG16+ResNet50 | -- -- | 98.98 | -- -- |
| [30] | ---- ------ | EfficientNetB4 encoder+Multiscale attention U-Net | | 93.38 |
| This work | Efficient-NetV2S | Double hybrid encoder | 99 | 95.27 |

### 3.3. Discussion

Table 4 comparison indicates that the proposed framework outperforms state-of-the-art models, as reported on Figshare recently. The main novelty of this work is developing a double hybrid encoder for segmentation, followed by a lightweight EfficientNetV2-S classifier. The traditional approaches using U-Net and U-Net++ models often struggle to encode high-level context and, at the same time, fine structural details. In contrast, the double hybrid encoder can utilize complementary encoding pathways simultaneously, leading to more accurate delineation of tumor boundaries. In the classification task, EfficientNetV2-S replaced deep backbones such as ResNet50V2 and Dense169 to be able to yield state-of-the-art accuracy (99% F1-score), at a lower computational cost, and trained faster, which is paramount to have real-world clinical applications. This dual contribution—better segmentation methods and more efficient, highly accurate classification—shows the proposed models' novelty and practical significance within a neuro-oncological decision support context.

## 4. CONCLUSION

This research introduced a deep learning system for brain tumor monitoring that pairs a double hybrid encoder for segmentation with a fine-tuned EfficientNetV2-S classifier. Overall, the system performed very well with a Dice score of 95.27% and an F1-score of 99%, outperforming both models based on traditional encoders and deeper classification networks. These findings indicate that the proposed system is an accurate and efficient method to assist in the neuro-oncological diagnostic and treatment process. Conversely, this study has limitations, including the fact that the Figshare dataset focuses on T1-weighted images. Future studies should validate this framework across larger multimodal MRI inputs and enhance it with immersive imaging inputs to ensure usability on a larger clinical applicability level. These efforts will improve the generalizability, interpretability, and potential clinical utility of the proposed system.

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## AUTHOR CONTRIBUTIONS STATEMENT

This journal uses the Contributor Roles Taxonomy (CRediT) to recognize individual author contributions, reduce authorship disputes, and facilitate collaboration.

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| Lamya Gaber | ✓ | ✓ | | | ✓ | | ✓ | | ✓ | | | | | |
| Mohamed Mourad Mabrook | ✓ | | | ✓ | | ✓ | | | ✓ | ✓ | | ✓ | | |

C : **C**onceptualization
M : **M**ethodology
So : **So**ftware
Va : **Va**lidation
Fo : **Fo**rmal analysis
I : **I**nvestigation
R : **R**esources
D : **D**ata Curation
O : Writing - **O**riginal Draft
E : Writing - Review & **E**diting
Vi : **Vi**sualization
Su : **Su**pervision
P : **P**roject administration
Fu : **Fu**nding acquisition

## CONFLICT OF INTEREST STATEMENT

Authors state no conflict of interest.

## INFORMED CONSENT

Informed consent was not required for this study, as all data were obtained from a publicly accessible dataset (Figshare) containing anonymized and de-identified MRI images.

## ETHICAL APPROVAL

Ethical approval was not required for this study, since the analysis was performed on a publicly available dataset (Figshare) that contains anonymized and de-identified MRI images.

## DATA AVAILABILITY

The data supporting the findings of this study are openly available on Figshare, comprising 3,064 MRI images from 233 patients. The dataset can be accessed via the following link: [https://doi.org/10.6084/m9.figshare.1512427.v5].

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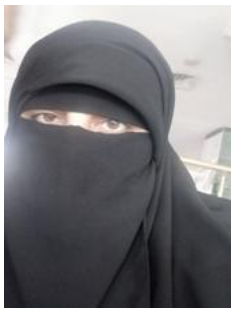

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