Deep Feature Extraction with Cubic-SVM for Classification of Brain Tumor

Extração de características profundas com Cubic-SVM para classificação de Tumor Cerebral

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ABSTRACT
Brain tumors (BT) are fatal and debilitating conditions that shorten the typical lifespan of patients. Patients with BTs who receive inadequate treatment and an incorrect diagnosis have a lower chance of survival. Magnetic resonance imaging (MRI) is often employed to assess the tumor. However, because of the massive quantity of data provided by MRI, early BT detection is a complex and time-consuming procedure in biomedical imaging. As a consequence, an automated and efficient strategy is required. The detection of brain tumors or malignancies has been done using a variety of conventional machine learning (ML) approaches. The manually collected properties, however, provide the main problem with these models. The constraints previously stated are addressed by the fusion deep learning model for binary classification of BTs that is presented in this study. The recommended method combines two different CNN (Efficientnetb0, VGG-19) models that automatically extract features and make use of the feature’s classification using a Cubic SVM classifier model. Additionally, the recommended approach displayed outstanding performance in various classification measures,
including Accuracy (99.78%), Precision (99.78%), Recall (99.78%), and F1-Score (99.78%), on the same Kaggle (Br35H) dataset. The proposed strategy performs better than current approaches for classifying BTs from MRI images.

**Keywords:** brain tumors, deep learning, Efficientnetb0, VGG-19, Cubic-SVM.

**RESUMO**
Tumores cerebrais (BT) são condições fatais e debilitantes que encurtam o tempo de vida típico dos pacientes. Pacientes com tuberculose que recebem tratamento inadequado e diagnóstico incorreto têm menor chance de sobreviver. Ressonância magnética (RM) é frequentemente utilizada para avaliar o tumor. No entanto, devido à enorme quantidade de dados fornecidos pela RM, a detecção precoce da BT é um procedimento complexo e demorado em imagens biomédicas. Consequentemente, é necessária uma estratégia automatizada e eficiente. A detecção de tumores cerebrais ou malignidades tem sido feita usando uma variedade de abordagens convencionais de aprendizagem automática (ML). As propriedades coletadas manualmente, no entanto, fornecem o principal problema com esses modelos. As restrições anteriormente declaradas são abordadas pelo modelo de aprendizagem profunda de fusão para classificação binária de BTs que é apresentado neste estudo. O método recomendado combina dois modelos diferentes de CNN (Efficientnetb0, VGG-19) que extraem automaticamente recursos e utilizam a classificação do recurso usando um modelo de classificador SVM Cúbico. Além disso, a abordagem recomendada apresentou um desempenho notável em várias medidas de classificação, incluindo Precisão (99,78%), Precisão (99,78%), Recall (99,78%) e Pontuação F1 (99,78%), no mesmo conjunto de dados Kaggle (Br35H). A estratégia proposta tem um desempenho melhor do que as abordagens atuais para classificar os BTs a partir de imagens de RM.

**Palavras-chave:** tumores cerebrais, aprendizagem profunda, rede eficiente B 0k, VGG-19, cúbico-SVM.

**1 INTRODUCTION**
A brain tumor is defined as an abnormal mass growth of brain tissues in which the cell growth control mechanism is unable to control intractably multiplying cells [1], [2]. The brain tumor in children and adults increases the death rate [3]. Thus, brain tumor detection is more important and significant for saving life of people. Similarly, early discovery results in saving life [4]. It is more worthy for detecting the tumor as the faster diagnosis aims to cure the brain tumors at early stages [5]. Image Processing is a more emerging area and covers clinical signal gathering, image formation, processing of pictures, and displaying the images for clinical diagnosis models by utilizing the features collected from images. There are several fields in medical image processing, in which some
areas use general concepts when focused on particular topics [6]. Images of the brain are produced using a magnetic resonance imaging (MRI) scanner, and any irregularities, such as tumors, may be detected in the image by specialized software. The major aim is to identify the brain tumor from MRI pictures computationally as an alternative choice for helping medical workers in early finding the diseases and also for early treatment [7].

Identifying and categorizing brain tumors in big databases of medical images for routine clinical jobs are a time-consuming and labor-intensive process [8]. Consequently, machine learning (ML) and deep learning (DL) methods have been applied to automate brain tumor segmentation, detection, and classification. DL techniques, specifically convolutional neural network (CNN) architectures, are currently utilized to analyze medical images showing various types of malignancies. Additionally, transfer learning (TL) has been employed, which includes utilizing a pre-trained model for a similar problem to solve a different but related problem [9]. This approach offers the advantage of reducing the training time needed. Both strategies have produced impressive results [10].

The SVM algorithm is widely used for classification in supervised machine learning. It constructs a decision boundary that effectively separates data points in a multi-dimensional space, ensuring new data points are assigned to the correct class. SVM identifies support vectors, which are data points that maximize the margin of classifiers. These support vectors are crucial in determining the optimal hyperplane. Additionally, kernel functions play a significant role in SVM classification [11], [12].

The goal of this research is to develop an automated and efficient method for detection brain tumor in MR images, allowing doctors to make more informed judgments. In this study, a novel model is used to detect brain tumors using pre-trained CNNs such as Efficientnetb0 [13] and VGG-19[14]. The images are then categorized using a Cubic SVM classifier model. Datasets were used in the context of brain tumor detection tasks. The Br35H : Brain Tumor detection 2020 dataset [15], is divided into two different categories, the labels "Tumor" and the labels "No Tumor".
2 RELATED WORKS

Classification of data is one of the most significant tasks in Machine learning algorithms [16]. A machine learning classifier classifies new data based on the trained classifying attribute from training dataset. The brain tumor classification of MR images can be done by feeding the image features to machine learning classification algorithms. Several pre-trained CNN models have been used in brain tumor recognition such as efficientNetB0[17]–[20], VGG-19[18], [19], [21], VGG-16[2], [22], [23], ResNet[2], [18], [19], AlexNet[2], [24], [25], Squeezenet[2], MobileNet[2], GoogleNet[26], [27].

Amran et al. [2], For the purpose of detecting BTs, they developed a system known as deeftumor networks that combines CNN and GoogleNet models. The last five layers of the GoogleNet model were swapped out for 14 deeper layers from the CNN model, which they then modified. Additionally, they maintained the fundamental CNN structure while changing ReLU AFs to leaky Re-AFs. The total number of layers increased from 22 to 33 as a result of these modifications. They achieved a remarkable classification accuracy of 99.10% by using this hybrid model.

Brain tumor classification of MRI images using CNN for feature extraction and classification by Support Vector Machine (SVM) classifiers has been tested in several works. Machhale et al. [28], For the classification of brain cancer, they employed a variety of approaches. These methods enable successful image preprocessing, image feature extraction, and subsequent classification of brain cancer. When 50 images were classified using three distinct machine learning techniques, Support Vector Machine (SVM), K-Nearest Neighbor (KNN), and Hybrid Classifier (SVM-KNN), the findings revealed that the SVM-KNN hybrid classifier had a 98% classification accuracy rate. Sarkar et al. [29], They identified the exact region of the human brain growing or harboring a tumor using a support vector machine classifier, which enabled them to distinguish between benign and malignant tumors by looking at their features. In their study, values of accuracy of 98.30%, sensitivity of 98%, and specificity of 100% were achieved. McIntyre and Tuba [30], They proposed a technique involving segmentation of brain MRI images using k-means clustering algorithm and image pre-processing. The gray level co-occurrence matrix is used to extract texture features from the region of interest,
and then these features are used to train a support vector machine for classification, accuracy rate of 95.21%. Khan et al. [31], To train a support vector machine (SVM), they use an MRI scan dataset with deep features. They use the Grab cut method in their suggested methodology to first separate the tumor region from the images. The segmented images are then used to extract deep features using a convolutional neural network (CNN). After feature extraction, the minimum Redundancy Maximum Relevance (mRMR) algorithm is used to choose the best deep features. Finally, the selected deep features are sent to the SVM in the classification module. Additionally, they employ the Black Widow Optimization Algorithm (BWOA) to optimize the CNN and SVM's hyperparameter, in their study, values of accuracy of 99.79%. Nandpuru et al. [32], They used grayscale, isotropic, and texture features to extract features from MRI images, and they used SVM with various kernel functions to divide them into the normal and abnormal categories, their model achieved an overall accuracy of 74% using Linear, 84% using Quadratic, and 76% using Polynomial Kernel Function. Mondal and Shrivastava [33], They investigated the effectiveness of the deep CNN model for brain tumor classification. They also investigated the effects of various activation functions and developed a brand-new parametric activation function for classifying brain tumors called PFpM. Its classification of brain tumors significantly improves as a result of this activation function, which increases the model's adaptability and stability. On the Figshare and Br35H datasets, they successfully applied their suggested methodology and attained astounding classification accuracy values of 99.57% and 99.00%, respectively.

3 METHODOLOGY

In this section, we describe the proposed method for splitting the Kaggle (Br35H) image dataset into two classes: the tumor class and the non-tumor class, and the training strategy used to achieve those classification results. On the other hand, using key performance indicators, we evaluate the performance of the proposed model.

Using pre-trained CNN, deep features are extracted. The fully connected layer's deep features are used by the classifier that has to be trained. From many CNN architectures deep features are derived. Then they are used by the SVM
classifier. Next, categorization is carried out, and each model's performance indicators are collected. A deep feature-based brain tumor detection model utilizing an SVM classifier is shown in Figure 1. A pre-trained model, Efficientnetb0, and VGG-19 were used in this work to extract deep features. To train the SVM classifier we use a cubic kernel function with deep features. A feature vector is created by extracting deep features from a certain layer of the CNN models. The collected characteristics are sent to the SVM classifier which divides the input images into normal and abnormal categories. The CNN network's several layers each have their own output. The image's essential features are produced by the layers and are passed on to the next layer. The size of the input image, the name of the feature layer, and the number of features in output, is shown in Table 1 for the various pre-entrained CNN models utilized. According to Table 1, a model used has a same input size (224×224), hence the image size must be changed for each model. Each input images undergoes convolution, rectified linear unit (ReLU), pooling, etc. after are applied to the pre-trained models. The aforementioned steps are repeated until the pre-trained model reaches the feature layer.

Table 1. CNN models characteristics

<table>
<thead>
<tr>
<th>CNN models</th>
<th>Efficientnetb0</th>
<th>VGG-19</th>
</tr>
</thead>
<tbody>
<tr>
<td>Input size</td>
<td>224 × 224</td>
<td>224 × 224</td>
</tr>
<tr>
<td>Feature layer</td>
<td>MatMul</td>
<td>fc8</td>
</tr>
<tr>
<td>Feature vector</td>
<td>1000</td>
<td>1000</td>
</tr>
</tbody>
</table>

Source: Authors.

Figure1, shows the suggested transfer learning model for brain tumor classification. All the pre-trained models are trained to recognize 1000 classes in ImageNet task. All the deep learning models are trained on different source datasets, which can recognize 1000 or more types of images. So, the output fully connected layer is of size 1000 neurons. The suggested approach fusion 1000 neurons of the output fully connected layer in Efficientnetb0, and in VGG-19, and replaces with 2 neurons to classify only 2 classes using Cubic SVM Classifier.
3.1 DATASET FOR A BRAIN TUMOR ON KAGGLE

Using a dataset obtained from a Kaggle (Br35H) [15], that was made available to the public, the experiments reported in this paper were carried out. 1500 MRI scans of the brain with tumors and 1500 scans without tumors made up this dataset. The dimensions of each picture were 256×256 pixels in height and breadth, making them all two-dimensional. Every picture had its cranium peeled off, and if it showed a tumor, it was labeled yes; otherwise, it was labeled no. Images with and without tumors are shown in the dataset in Figure 1 with the labels yes and no, respectively. Table 2 lists the training and testing datasets. Examples from the dataset that fall within the categories of "normal" and "malignant" are shown in Figure 2 and Figure 3.

<table>
<thead>
<tr>
<th>Tumor Class</th>
<th>Image</th>
<th>Training</th>
<th>Testing</th>
<th>Class Labels</th>
</tr>
</thead>
<tbody>
<tr>
<td>With Tumor</td>
<td>1500</td>
<td>1050</td>
<td>450</td>
<td>1 (Yes)</td>
</tr>
<tr>
<td>Without Tumor</td>
<td>1500</td>
<td>1050</td>
<td>450</td>
<td>0 (No)</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td><strong>3000</strong></td>
<td><strong>2100</strong></td>
<td><strong>900</strong></td>
<td></td>
</tr>
</tbody>
</table>

Source: Authors.
3.2 DATA SET PREPARATION

There are 3,000 images in total in the publicly available Kaggle dataset (Br35H), 1,500 of which are images of brain tumors and 1,500 of which are normal images without brain tumors. The dataset is pre-processed to make it compatible with the proposed procedures. All images must first be resized to 224 x 224 pixels using MATLAB built-in resize function according to the input image sizes used by our proposed deep learning models.

The images in the dataset were divided into two groups: a training group that represents 70% of the dataset, and a test group that represents 30% of the dataset. Furthermore, the image data was labeled as (0) to indicate normal cases, while (1) was used to represent input data for brain tumor detection in the proposed model.

<table>
<thead>
<tr>
<th>Label</th>
<th>Definition</th>
</tr>
</thead>
<tbody>
<tr>
<td>TP</td>
<td>A True Positive Test outcome is one that identifies the disease when there is a disease.</td>
</tr>
<tr>
<td>TN</td>
<td>A True Negative test outcome is one that has not identified the disease when there is no disease.</td>
</tr>
<tr>
<td>FP</td>
<td>A False Positive test outcome is one that identifies the disease when there is no disease.</td>
</tr>
<tr>
<td>FN</td>
<td>A False Negative test outcome is one that has not identified the disease when there is a disease.</td>
</tr>
</tbody>
</table>

Source: Authors.
Assessed the performance of the image-based classification based on sensitivity / recall, specificity, precision, F1-score and accuracy. Some terms are shown in Table 3 to determine these metrics and then the following mathematical expressions are defined.

**Accuracy:** Accuracy gives the total number of predictions that are correct and is given by

\[
\text{Accuracy} = \frac{TP+TN}{TP+TN+FP+FN}
\]  

(1)

**Sensitivity / Recall:** Sensitivity is the measure of the capacity to test the positive samples and is given by

\[
\text{Sensitivity / Recall} = \frac{TP}{TP+FN}
\]

(2)

**Specificity:** Specificity is the measure of capacity to test the negative samples and is given by

\[
\text{Specificity} = \frac{TN}{TN+FP}
\]

(3)

**Precision / PPV:** Precision/PPV is the proportion of predicted positives that are correct and is given by

\[
\text{Precision / PPV} = \frac{TP}{TP+FP}
\]

(4)

**F1-Score:** F-Score expresses the weighing scale between the precision/PPV and the recall and is a measure of tests accuracy. It is given by

\[
F1 - \text{Score} = 2 \times \frac{\text{PPV} \times \text{Recall}}{\text{PPV} + \text{Recall}}
\]

(5)

### 4 EXPERIMENTAL RESULTS

This section discusses the result analysis of the proposed brain MRI image classification process. This is to validate the performance of proposed algorithms
and the prediction quality based on the statistical parameters and compares the predicted result and actual data with a standard dataset. The results of the proposed work are compared with several existing methods of image classification approach for the parameters of sensitivity and accuracy-related statistical value. The results are presented in the form of a comparison table and the bar charts to express the prediction rate of the proposed ensemble model of classification process in the brain MRI image dataset. The process is implemented in the MATLAB scripting tool platform in the version of R2023a. This is to simulate and estimate the error rate to validate the results of the overall work. We will first compare the proposed method, which uses the fusion of feature extraction of Efficientnetb0 and VGG-19, with using only feature extraction of Efficientnetb0 or VGG-19.

4.1 CONFUSION MATRIX

The detection of each class is measured by a confusion matrix, a performance assessment indicator. Figure 4, displays the confusion matrix for proposed method using feature extraction of Efficientnetb0. Figure 5, displays the confusion matrix for our proposed method using feature extraction of VGG-19, and proposed model is shown in Figure 6, all models tested on the Br35H dataset. The confusion matrix of proposed method successfully detected binary tumors in this investigation and correctly identified each type of brain tumor.

![Figure 4. Confusion matrix with Efficientnetb0](Source: Authors.)
4.2 EVALUATION MATRIX

The performance of our explored model on Br35H, which is used as the balanced dataset in our work, is very excellent. Table 4 proves that our proposal in terms of fusion Efficientnetb0, and VGG-19 feature extraction using Cubic SVM Classifier gave better performance in all terms of Accuracy (99.78%), Precision (99.78%), specificity (99.78%), Recall (99.78%), and F1-Score (99.78%). For the model that was used feature extraction of Efficientnetb0, the performance was equal to the performance of our proposed model in terms of accuracy and specificity only, and for the model that was used feature extraction of VGG-19, the performance was weak with respect to all measures.
Table 4. Comparison between the proposed model and model with Efficientnetb0, VGG-19

<table>
<thead>
<tr>
<th>Br35H data</th>
<th>Proposed model</th>
<th>Efficientnetb0</th>
<th>VGG-19</th>
</tr>
</thead>
<tbody>
<tr>
<td>Accuracy</td>
<td>99.78</td>
<td>99.56</td>
<td>98.89</td>
</tr>
<tr>
<td>Sensitivity</td>
<td>99.78</td>
<td>99.34</td>
<td>99.33</td>
</tr>
<tr>
<td>Specificity</td>
<td>99.78</td>
<td>99.78</td>
<td>98.46</td>
</tr>
<tr>
<td>Precision</td>
<td>99.78</td>
<td>99.78</td>
<td>98.44</td>
</tr>
<tr>
<td>F1-Score</td>
<td>99.78</td>
<td>99.56</td>
<td>98.88</td>
</tr>
</tbody>
</table>

Source: Authors.

On the other hand, we compare our proposed method with several other basic methods from the existing literature, as shown in Table 5.

As demonstrated in Table 5, we contrasted the suggested deep tumor network with other top-notch benchmark techniques. The performance of our suggested model in binary tumor classification is astounding when compared to other benchmark techniques from the published literature.

Table 5: Presents the comparison study of suggested model with recent models

<table>
<thead>
<tr>
<th>Author (year)</th>
<th>Dataset</th>
<th>Validation Method</th>
<th>Overall Accuracy (%)</th>
<th>Average Precision (%)</th>
<th>Average Specificity (%)</th>
<th>Average Sensitivity (%)</th>
<th>Average F1-score (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mondal and Shrivastava 2022 [33]</td>
<td>Br35H</td>
<td>Hold-out (70:30)</td>
<td>99</td>
<td>99</td>
<td>99</td>
<td>99</td>
<td>98.99</td>
</tr>
<tr>
<td>Cınar et al. 2022 [35]</td>
<td>Hold-out (80:20)</td>
<td>98.33</td>
<td>98.34</td>
<td>98.33</td>
<td>98.33</td>
<td>98.33</td>
<td>98.33</td>
</tr>
<tr>
<td>Islam et al. 2023 [36]</td>
<td>Hold-out (80:20)</td>
<td>98.6</td>
<td>98.4</td>
<td>NA</td>
<td>96.6</td>
<td>97.9</td>
<td>97.9</td>
</tr>
<tr>
<td>Garg et al. 2023 [37]</td>
<td>Hold-out (90:10)</td>
<td>98.1</td>
<td>98.9</td>
<td>NA</td>
<td>98.6</td>
<td>98</td>
<td>98</td>
</tr>
<tr>
<td>Naseer et al. 2021 [38]</td>
<td>Hold-out (80:20)</td>
<td>98.66</td>
<td>97.27</td>
<td>NA</td>
<td>98.3</td>
<td>98.3</td>
<td>98.3</td>
</tr>
<tr>
<td>Kang et al. 2021 [39]</td>
<td>Hold-out (90:10)</td>
<td>98.8</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
</tr>
<tr>
<td>This work</td>
<td>Hold-out (70:30)</td>
<td>99.78</td>
<td>99.78</td>
<td>99.78</td>
<td>99.78</td>
<td>99.78</td>
<td>99.78</td>
</tr>
</tbody>
</table>

Source: Authors.

5 CONCLUSION

This research presents promising results for brain tumor detection using the combination of pre-trained models Efficientnetb0 and VGG-19 and using the Cubic SVM Classifier method. Where we used fusion of the (fully connected layer) outputs of Efficientnetb0 and VGG-19 as features, we classify them using Cubic Support Vector Machines, Proposed method achieved an excellent accuracy of 99.78% for the Kaggle (Br35H) image dataset. Finally, we believe this research can help assist people to get an earlier alert about their health state. However, more study is required to boost the accuracy of the model as well as work on using multi-classification databases. Additionally, we want to assess how well the
approach works with different kinds of data in the biomedical imaging domains, like asthma identification, lung-illness, and COVID-19.
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