Brain Tumor Classification using Machine and Transfer Learning

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Abstract: Brain tumor classification is a controversial problem in computer-aided diagnosis (CAD). Conventionally, cancer diagnosis depends mainly on its early prediction. Accordingly, the improvement of technology and the rise of machines and deep learning facilitate the tasks of tumors' detection and diagnosis while limiting human intervention. Transfer learning has been widely adopted in several applications due to its performance. In the present paper, we have combined VGG-16 and several classifiers for brain tumor classification. Indeed, after the fine-tuning step of VGG-16, we have fed the extracted features to the classifiers. The proposed approach has achieved efficient results and has outperformed several state-of-the-art studies in the topic of brain tumors in terms of precision (98.7%), recall 98.7, F1-score 98.7%.

1 INTRODUCTION

We cannot deny the fact that cancer orders as a principal cause of death, and an essential factor determining life expectancy in every nation all over the earth (Bray F), as in 2020, a brain tumor forms 1.6% of all tumors that can affect the human body, and 2.5% of fatal tumors (Sung), its constantly increasing incidence all across the world makes it a priority to the World Health Organization (WHO) in terms of screening, diagnosis, and treatment (Idlahcen Ferdaous, 2020). To be more precise, a brain tumor is an abnormal growth of tissue in the brain. Unlike other tumors, brain tumors grow by regional extension and infrequently metastasize outside the brain (DeAngelis, 2001). Consequently, the classification of brain tumors represents a challenge because of their spread in different positions. Our goal is to classify the cancer in MRI images.

Several approaches have been proposed to automatically predict the existence of a tumor in a medical images such as those based on machine learning. These approaches could be divided into two main steps: the features extraction and the classification model. Sharma et al. (Sharma, 2014) found that human life takes a crucial position in society and more precisely in the domain of medicine, it is for that the intervention, the detection, and the classification of the brain diseases appears very necessary, the resolution of this problem classification is frequently based on extracting and classifying features using a machine learning algorithm. In this regard, Javeria Amin et al. (Amin J. S., 2018) proposed a new method to detect and classify brain diseases (ischemic strokes, gliomas) at an early step, using machine learning and features extraction algorithms.

Despite the positive outcomes of these approaches, they remain limited, especially when dealing with vast databases. Another sort of approach based on Deep Learning is proving to be very effective while handling extensive data. Heba Mohsen et al. (Mohsen, 2018) presented a new approach using a DNN learning method to classify brain tumor images by using fuzzy C-means to segment the images, and also the discrete wavelet transforms (DWT) to extract the features, and principle component analysis (PCA) technique for

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reducing the dimensions, and Deep Neural Network (DNN) for classification. Milica M. Badža et al. (Badža, 2020) presented a new CNN method to detect and classify brain tumors, depending on their kind (Meningioma, Glioma, Pituitary).

To improve the studies made on the topic of brain tumors, we used a deep learning interface (API FastAI), which allows us to resize the images and speed up the training of the applied models.

Transfer learning is defined as an approach that allows using the information of a model that has already been trained to learn another target data set. Arshia Rehman et al. (Rehman, 2020) employed and explored CNN approaches (AlexNet, GoogleNet, and VGG-16) to detect and classify brain tumors, using MRI images.

In this paper, we propose an architecture based on transfer Learning using the VGG-16 model to our data set in order to get the feature extractions for the machine learning models for the purpose of having a higher prediction score.

The remainder of the paper is organized as follows: in the second section, we present the related work, followed by the material and the methods, then the experimental results, ending with a conclusion.

2 RELATED WORK

The main aim of this part is to describe previous studies related to the detection and classification of brain tumors using machine learning and deep learning models. Many researchers who used Machine Learning classifier. George, D. N. et al. (George, 2015) proposed architecture to segment brain tumors and detect regions of MRI images. In this regard, Ali and Hanbay (Ari Ali, 2018) proposed a method that included three main steps: image preprocessing, image classification with ELM-LRF, along tumor extraction using image processing techniques. Amin et al. (Amin, Sharif, Raza, & Yasmin, 2018) proposed a methodology to segment and classify the brain tumor using Deep Neural Networks (DNN) and magnetic resonance images (MRI).

Deep Learning is another powerful approach to classifying problems. H. Sultan et al. (HOSSAM H. SULTAN, 2019) suggested a deep learning approach that uses a convolutional neural network (CNNs) for the detection and classification (Meningioma, Glioma, Pituitary) kinds of brain tumors. Amin Kabir Anaraki et al. (Kabir Anaraki, 2019) presented a new approach using CNNs, and a genetic algorithm (GA) to classify brain tumors based on magnetic resonance imaging. Correspondingly, Hüseyin and Engin (Hüseyin Kultu, 2019) proposed a new approach to categorising liver and brain tumors based on the CNN efficiency in feature extraction, the capability of the discrete wavelet transform in signal processing, and the ability of memory long-term in signal classification. Parnian Afshar et al. (Afshar, Plataniotis, & Mohammadi, 2019) proposed a method to classify brain tumors into three categories: Meningioma, Pituitary, and Glioma, based on CNN usage via CapsuleNet architecture and MRI images, these are frequently used approaches for early prediction of brain disease.

Although these approaches give perfect results, another technique based on data pre-training is very effective when processing extensive data. Several methods are involved in this challenge; S. Deepak et al. (Deepak, 2019) applied a pre-trained deep network, based on GoogLeNet to classify problems (MR images brain tumors) via transfer learning, in this regard, Swati et al. (wati, et al., 2019) proposed a new method that uses the deep neural network, and trained CNN on the short data set, using a pre-trained deep CNN model, and proposed a block-based fine-tuning approach based on transfer learning.

3 MATERIAL AND METHODS

This research study has adopted three main steps method. First, image preprocessing; second, image representation; last but not least, image classification.

The structure of the proposed method is illustrated in the figure below. The acquisition of images are the first step of this method, the second step is the preprocessing of images (cropping, resize, and splitting increase) via the FastAI interface, afterwards, the classification step by transfer learning VGG-16, then, we transform the output images into arrays, in the last step in this study, various Machine Learning classification algorithms have been used to compare their performance including Random Forest, Support Vector Machine, Decision Tree, Gaussian Naive Bayes, and K-Nearest Neighbor.

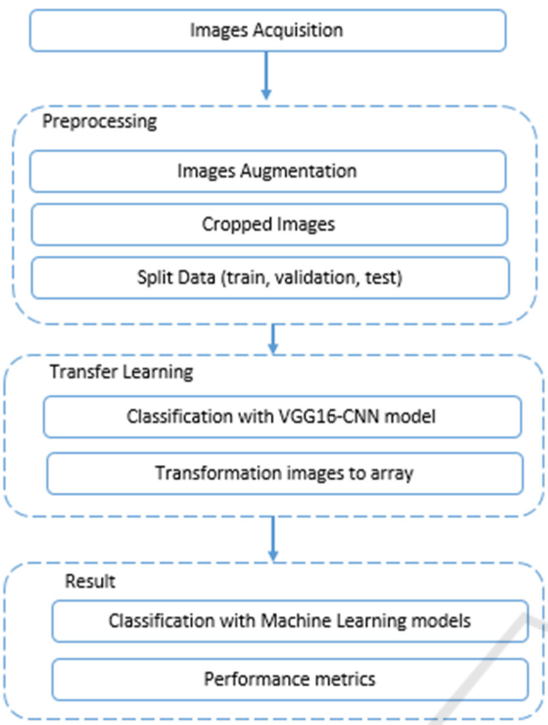


Figure 1: Diagram of Brain Tumor Classification Method.

We used a deep learning interface (API FastAI) to get a reasonable learning rate, Tensorflow, Pytorch, Keras, Pandas, Numpy, and Sklearn as libraries to build our models. During training, in order to make the model converge to the maximum state, the number of epochs was 80, and the batch size was 32 for all models. We apply RMSprop as an optimizer, binary_crossentropy as loss, and accuracy as metrics for the VGG-16 parameters model. Our experiments were run on the Kaggle notebook, which gave us 16G RAM and a GPU kernel.

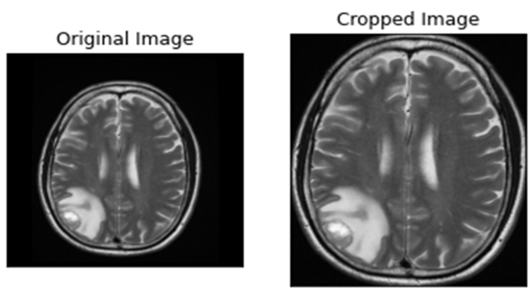


Figure 2: Sample image preprocessing (function cropped).

The last step of our method consists of classifying and detecting the tumor in the images. The output of the VGG-16 (features extraction) is fed to several machine learning models such as Random Forest, Support Vector Machine, Decision Tree Classifier, Gaussian Naive Bayes, and K-Nearest Neighbor.

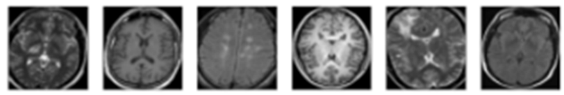


Figure 3: Sample MRI, no brain tumor.

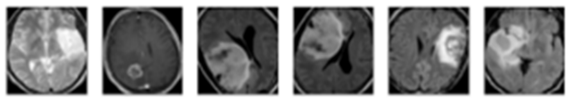


Figure 4: Sample MRI, yes brain tumor.

4 EXPERIMENTAL RESULTS

4.1 Dataset

We obtained the data on which we carried out this study (Brain MRI Images for Brain Tumor Detection) from a Kaggle competition (Rakotomamonjy, 2008). After augmenting and preprocessing the image, we split the resulting data set into three categories: data training which includes 1444 (70%) of images, data validation that contains 310 (15%) of images, and data testing that includes 309 (15%) of images, as shown in the following table(1), and then we build our VGG-16 model on our dataset. The outputs (features extraction) that we get will be the inputs of each machine learning model.

Table 1: Representation examples.

Step	Number of examples
Train	1444 (70%) of images
Validation	310 (15%) of images
Test	309 (15%) of images

As we have already stressed, Transfer learning (S. Deepak, 2019) is an approach that allows using the information of a model that has already been trained to learn another target task. Thus, in order to improve the studies made in this field of brain tumors, we have applied FastAI (Francis, 2021), which is a library that allows the processing of images, the construction of deep learning models in a simpler and faster way.

The implementation of the VGG-16 model is based primarily on the input layer of data, the different types of the layers (Conv, Pooling), and the dense layer on output. After the application on our dataset, we haven't only have gained a test accuracy of 98.7% but also, outputs which transformed into matrices to exploit them as inputs in the different models of machine learning.

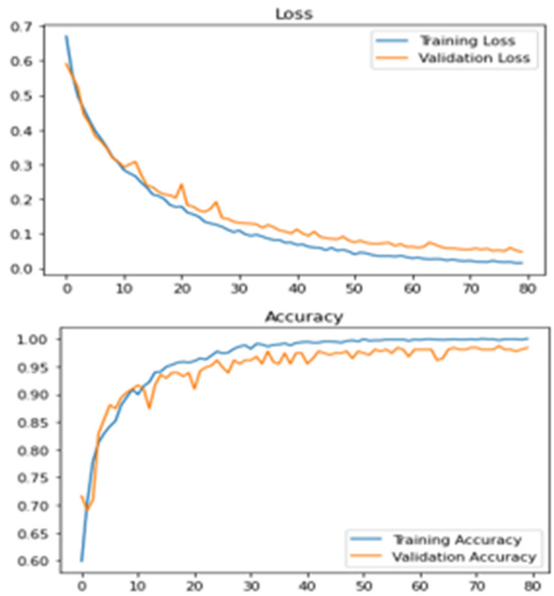


Figure 5: Loss and Accuracy of VGG-16 model.

The loss is the sum of the errors made for each example in the training or validation sets. So we assume that "the lower the loss, the better the model".

Precision is a measure of the performance of a classification model (R. Prashanth, 2016). Informally, precision indicates the percentage of accurate predictions made by the model. Following the same path, accuracy is defined as:

$$\frac{\textbf{correct prediction number}}{\textbf{total prediction number}} \tag{1}$$

For binary classification, trueness can also be calculated in terms of positives and negatives as follows:

$$\frac{\mathbf{VP + VN}}{\mathbf{VP + VN + FP + FN}} \tag{2}$$

4.2 Applied Machine Learning Models

In this paragraph, we will cite the Machine Learning algorithms used to classify brain tumors in this work.

Support vector machines (SVM) (Joachims) are supervised machine learning methods; they are linear classifiers, interested in solving discrimination and regression problems.

The Random Forest Algorithm (Breiman, 2001) is a machine learning method that applies to several decision trees formed on subsets of data.

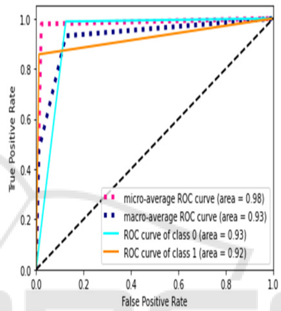
The decision tree (Quinlan, 1993) is a method that is built in the graph of a tree and gives a group of choices, the ends or the leaves of the tree represent the different possible decisions, several fields such as medicine, commerce, security use this approach

A k-nearest-neighbor (K-NN) algorithm (Peterson, 2009) is a data classification method that predicts the probability that a data point is a part of one set or the other.

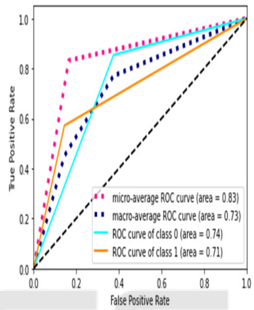
The naive Bayesian classification (Liu Ximeng, 2016) is a probabilistic classifier using Bayes' theorem.

4.3 Performances Metrics

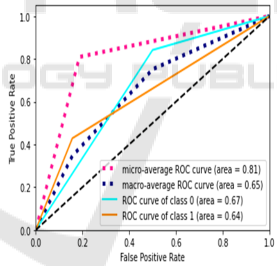
ROC curve (Receiver Operating Characteristic curve) (Hand, 2009) is a sensitivity/specificity function; it is a performance measure that allows the characteristics of a binary classifier to be evaluated.



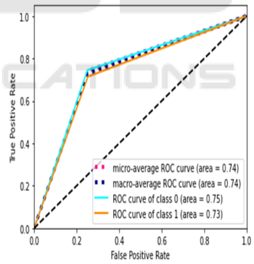
ROC curve VGG-16



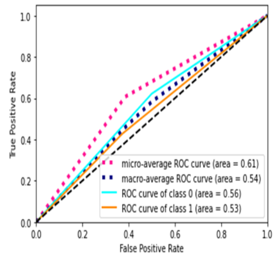
ROC curve SVM



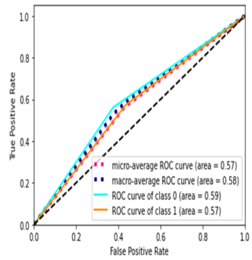
ROC curve Random Forest



ROC curve Decision Tree



ROC curve Gaussian Naive Bayes



ROC curve K-Nearest Neighbor

Figure 6: ROC curve Machine Learning models

A confusion matrix (S Visa, 2011) is a tool used to assess the performance of a classification problem. A confusion matrix is an array of a two-dimensional

Table 2: Comparison between machine learning models prediction.

Model	Accuracy	Precision	Recall	F1_score
VGG-16	0.987	0.987	0.987	0.987
SVM	0.825	0.827	0.805	0.830
Random Forest	0.887	0.887	0.887	0.887
Decision Tree	0.686	0.686	0.686	0.686
Naive Bayes	0.595	0.622	0.595	0.585
K-NN	0.796	0.824	0.796	0.6794

array: rows contain predicted values, and columns have actual values.

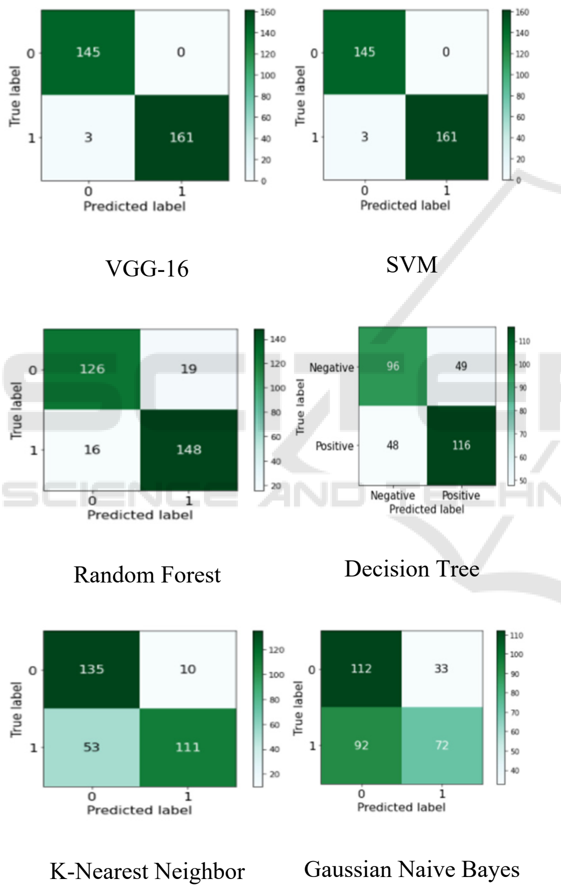


Figure 7: Confusion Matrix

In this study, we built five different machine learning models, starting with the implementation and augmentation of the dataset to have more images for the training, the evaluation, and the test of the model built. We applied the VGG-16 model, followed by getting the features extraction of this model and consider them as inputs for all the machine learning models built. In the end, we get the results of each model.

After applying the VGG-16 model on our dataset, along with considering its outputs (features extraction) as inputs of the following models, the prediction results based on our machine learning models achieved 98.7% in terms of accuracy (test). They ranked as follows (SVM: 82.5%, Random Forest: 88.7%, Decision Tree: 68.6%, Naive Bayes: 59.5%, and 55.6% K-Nearest Neighbor).

5 CONCLUSION AND FUTURE WORK

In the manuscript, we have built several machine-learning models to classify brain tumors. Firstly, we have implemented and augmented the data set in order to have more images for the training. Secondly, we have split the data set into training, validation, and testing steps. After applying the VGG-16 model, we extracted the outputs of this model (features extraction) and considered them as inputs for all the machine-learning models built. Finally, we get the results of each model, and we compared them. Our experimental findings are remarkable bearing in mind the fact that they demonstrate the capability of deep learning pre-trained models toward a promising computer-aided diagnosis in digital pathology. Eventually, this study is an initiation to other researches, in light of the fact that some cancer patterns can not be gleaned by human examination.

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