Brain Tumor Detection using Hybrid Machine Learning Models

¹Isha Dave, ² Shreyas Tuttagunta

B. Tech IT MPSTME NMIMS

Abstract- Brain tumor detection holds a critical role in swiftly diagnosing and planning treatments for improved patient outcomes. Conventional approaches to detecting brain tumors rely on radiological imaging methods and manual analysis, which can be time-consuming and prone to human error. However, in recent years, the advent of machine learning models has revolutionized this process by offering automated brain tumor detection. This promising advancement not only enhances accuracy but also boosts efficiency levels significantly.

This research paper delves into an examination of utilizing machine learning models for the purpose of brain tumor detection. The primary aim of this study is to investigate and determine the efficacy of various machine learning algorithms in accurately identifying brain tumors from medical imaging data, specifically MRI scans.

Keywords: Brain tumor detection, machine learning, deep learning, medical imaging, MRI scans, convolutional neural networks.

I. INTRODUCTION

Machine learning algorithms possess the capability to identify patterns and correlations in data, enabling them to effectively analyze medical imaging data like MRI scans. By training these models on a diverse collection of brain MRIs, they acquire the ability to distinguish between healthy brain tissue and tumor regions. Consequently, these trained models can accurately predict the presence and location of brain tumors in newly conducted MRI scans.

This research paper intends to investigate the effectiveness of various machine learning algorithms in detecting brain tumors from MRI scans. By comparing and evaluating different approaches, including deep learning models like convolutional neural networks, the aim is to determine the most precise and efficient method for tumor detection.

II. EXISTING MODELS

A variety of unsupervised learning techniques, including SVM, logistic regression, and K-means, as well as supervised learning techniques, including random forest classifier, artificial neural networks, and naive Bayes, have been employed by various researchers to categorize the grade of brain tumors.

Preprocessing, tumor identification, characteristics extraction and selection, and classification of brain tumor grade are the four general phases of the brain tumor classification task (Khan, Lali, et al., 2019).

A book for the detection of brain tumors, Fidon et al. (2017) suggested a scalable multimodal deep learning architecture with dice scores of 0.77, 0.64, and 0.56 on the BraTS 2013 data set. A CNN framework for automatic brain tumor identification and detection was introduced by Seetha and Raja (2018). Fuzzy-Cmeans generates features that are segregated from segmented areas for the segmentation and texturing of brain tumors. Finally, these features are supplied to the 97.5% accurate fused DNN and SVM classifiers. Using an improved version of AlexNet CNN, Khawaldeh et al. (2018) established a non-invasive graduation method of brain glioma tumors.

Regression was obtained for whole-brain MR images, and image labeling was performed at the image level rather than at the pixel level. The experimental findings indicate that 91.16% of the procedure delivered a respectable performance. A thorough technique for grading brain tumors was proposed by Sajjad et al. (2019). For this reason, the pre-trained VGG-19 CNN was fed the tumorous region following data augmentation.

The reported rating accuracy for the data before and after the augmentation was 87.38 and 90.67%, respectively. In order to assess brain cancers, Zyurt, Sert, Avci, and Dogantekin (2019) combined CNN with the neuromorphic, optimistic entropy of the total fuzzy expert (NS-CNN). The CNN was then used to extract features from these images. Eventually, the SVM classifier is fed with the retrieved features to classify them as benign or malignant with an average 95.62% precision.

III. RESEARCH BACKGROUND

Convolutional Neural Networks (CNNs), Vision Transformers (ViTs), Artificial Neural Networks (ANNs), and Support Vector Machines (SVMs) have gained popularity as machine learning models utilized for brain tumour detection. These models, whether employed individually or in hybrid combinations, possess distinct strengths and capabilities when analysing medical imaging data. CNNs have brought about a revolution in the field of computer vision, showcasing remarkable potential in the detection of brain tumours. Their remarkable ability to autonomously acquire knowledge from images makes them exceptionally capable at grasping intricate patterns and features within brain MRI scans. Typically, CNNs comprise convolutional layers that extract essential features, succeeded by fully connected layers responsible for accurate classification. Regarding the detection of brain tumours, CNNs excel in learning how to discern between tumour affected areas and healthy regions with an impressively high level of accuracy.

Vision Transformers (ViTs) have emerged as a notable approach in image analysis. In contrast to traditional CNNs ViTs leverage self-attention mechanisms to grasp the global connections among image patches. Consequently, they excel in understanding the entire image context. ViTs have demonstrated promising outcomes across various computer vision tasks and exhibit potential in brain tumour detection by capturing both distant associations and subtle image characteristics.

Artificial Neural Networks (ANNs) on the other hand, serve as versatile models that can be utilised for a wide array of objectives, including brain tumour detection. ANNs comprise interconnected nodes (neurons) organized in layers enabling them to comprehend complex relationships within data. Through training on labelled brain MRI scans ANNs become proficient at accurately classifying tumour and non-tumour regions. The versatility of ANNs in terms of architecture allows them to be tailored according to specific requirements.

Support Vector Machines (SVMs) are robust models frequently utilized in classification tasks, demonstrating their powerful capabilities. The fundamental goal of SVMs is to identify an optimal hyperplane that effectively separates data points belonging to distinct classes while maximizing the margin. In the context of brain tumour detection, SVMs have been applied by extracting pertinent features from brain MRI scans and mapping them into a higher-dimensional space. One noteworthy advantage of SVMs resides in their capacity to manage high-dimensional data, resulting in interpretable outcomes.

Moreover, researchers have explored the potential of developing hybrid models for brain tumour detection - amalgamations combining various machine learning techniques. Particularly, incorporating Convolutional Neural Networks (CNNs) or Vision Transformers (ViTs) with SVMs proves advantageous as it leverages the strengths possessed by each model component. By employing CNNs or ViTs, relevant features can be efficiently extracted from brain MRI scans; subsequently, the SVM component performs the crucial task of final classification. Through integrating these hybrid models, accuracy rates may potentially increase as they unite both deep learning models' discriminative power and SVM's interpretability aspect.

In this research paper, we will delve into the exploration of different machine learning models such as CNNs, ViTs, ANNs, and SVMs. Additionally, we will investigate their hybrid combinations to address the perplexity involved in brain tumour detection. Our main goal is to scrutinize their performance, accuracy, and efficiency when it comes to accurately identifying brain tumours from MRI scans. The outcome of our findings will play a pivotal role in grasping both the strengths and limitations exhibited by each model. Furthermore, it will aid in determining which approach proves most effective for automated brain tumour detection.

IV. ETHICAL APPROVAL

No experiments are conducted on animals and humans. Only publicly available benchmark data sets are used for experiments.

V. PROPOSED MODEL

V.I. DATA SET DETAILS

The dataset we have used [1], consists of 3,762 unique images of the brain in the black and white format with a comma-separated values (csv) file which divides the images into five first-order features and eight texture features. First-order features:

- a. Mean: Measure of central te-ndency, represe-nts the average value- obtained from a set of numbers.
- b. Variance: Variance- is a statistical measure that allows us to understand the- spread or dispersion of a dataset. By quantifying the- average squared de-viation from the mean.
- c. Standard Deviation: It is the square root of the variance and provides a measure of how much the individual data points deviate from the mean.
- d. Skewness: Skewness gauges a probability distribution's asymmetry. It reflects whether the dataset deviates from a normal distribution more to the left (negative skewness) or more to the right (positive skewness). A distribution that is completely symmetrical has a skewness value of 0.
- e. Kurtosis: This statistic gauges how a probability distribution's tails are shaped. It measures how much a distribution deviates from a normal distribution in terms of heavy tails or abrupt peaks. Negative kurtosis denotes lighter tails, and positive kurtosis denotes heavier tails.

Texture Features:

- a. Contrast: When discussing image processing, contrast is used to describe the difference in brightness between an image's brightest and darkest areas. It displays the degree of pixel intensity fluctuation.
- b. Energy: An image's total squared pixel intensities are represented by the statistical concept of energy. It gives details on the overall power or size of the image.
- c. Angular second moment: The angular second moment computes the sum of squared components in the gray-level co-occurrence matrix, also known as uniformity or energy entropy. It displays how evenly pixel intensity pairings are distributed throughout a picture.
- d. Entropy: Entropy is a measurement of the randomness or uncertainty in a picture. It measures the complexity or information richness of the picture in the context of image processing. Greater complexity is indicated by higher entropy levels.
- e. Homogeneity: Homogeneity assesses how similar adjacent pixel intensities are to one another. It measures how closely spaced apart the pixel intensities are in a certain neighbourhood.
- f. Dissimilarity: Dissimilarity evaluates the contrast or difference between adjacent pixel intensities. It measures the pixel value fluctuation within a certain neighbourhood.
- g. Correlation: The statistical link between two variables is measured through correlation. It measures the linear relationship between pixel intensities at various spatial places in the context of image processing.
- h. Coarseness: The term "coarseness" refers to how rough or grainy a picture texture is. It measures how quickly the pixel intensity levels inside a picture change.

V.II. PRE-PROCESS STAGE

The initial step is the loading of brain tumor images utilizing the PIL library's Image.open() function. Afterwards, each image undergoes resizing to a consistent dimension of 224x224 pixels through the implementation of the img.resize() method. This particular action guarantees that all images possess identical dimensions, which proves essential for their input into the machine learning model.

Next up is normalization. Once the images are loaded and resized, their pixel values experience normalization via the line X = np.array(X) / 255.0. To achieve this, the images are converted into NumPy arrays denoted as X and subsequently divided by 255.0. Through division by 255.0, scaling of pixel values occurs from an original range spanning from 0 to 255 down to a normalized range spanning from 0 to 1 instead. The purpose behind this normalization process stands as ensuring that input data consistently falls within an acceptable range while hindering one specific feature or color channel from overpowering the entire model training procedure

V.III. WORKING

a. CNN and ViT

Once the data has been preprocessed, it is divided into two sets: one for training and one for testing. To enhance the training data and improve the model's ability to generalize, we utilize data augmentation techniques via the ImageDataGenerator() class from Keras. By configuring various augmentation parameters such as rotation range, shift range, shear range, zoom range, horizontal flip, and fill mode, this class generates augmented images on-the-fly during model training. This introduction of variability helps reduce overfitting.

For feature extraction, we make use of a pre-trained EfficientNetV2S model. In order to preserve the learned representations within this model, we freeze its pre-trained layers so that they remain non-trainable. We then add new layers on top of the EfficientNetV2S model which include a global average pooling layer, a dense layer with ReLU activation function, a dropout layer for regularization purposes, and finally a dense layer with sigmoid activation function for binary classification.

The utilization of the model incorporates fitting it with an appropriate optimizer, loss function, and evaluation metrics. Specifically, in this case, the Adam optimizer is employed along with binary cross-entropy loss as well as accuracy metric. The training data serves as the basis for augmenting and subsequently training the model with the assistance of the fit() function.

b. CNN and ANN

Using Keras' Sequential API, the model can be defined, enabling the creation of a stack of layers in a linear order.

Performing feature extraction, the input image undergoes convolving filters implementation and ReLU activation is applied to introduce non-linearity. The convolving filters have a kernel size of (3,3) and there are 32 filters in the first convolutional layer. In the model architecture, max pooling layers follow the convolutional layers.

Reducing the spatial dimensions and extracting dominant features, a max pooling layer is added next. It has a pool size of (2,2) and downsamples the feature maps from the previous convolutional layer.

The model can learn more complex and abstract features from the input data through the process, repeated with another max pooling layer, this time with 64 filters, and a convolutional layer.

The feature maps are flattened following the convolutional and pooling layers, reshaping the multi-dimensional output into a single vector. This allows for input into the dense layers.

To introduce additional non-linearity to the model, a dense layer with 128 units and ReLU activation is added next. This layer fully connects all the neurons from the previous layer.

The presence or absence of a brain tumor can be determined by the output of the final layer, which consists of a single neuron. A sigmoid activation function is applied to this layer to ensure that the output falls within the range of 0 to 1, effectively representing the probability of a tumor.

The model's performance is evaluated by specifying the optimization algorithm, the loss function to minimize, and the metric. It is compiled using the Adam optimizer with a default learning rate, binary cross-entropy loss function, and accuracy metric, setting up the model for training in this configuration.

c. CNN and SVM

Using Keras Sequential API, we have defined a CNN model which consists of three sets of convolutional and max pooling layers which are followed by a flatten layer. The convolutional layers are used to apply filters to extract features from the input images and the max pooling layers are utilized to downsample the feature maps which helps in capturing the most important information. The flatten layer will reshape the output obtained from the previous layers into a one dimensional vector, and prepare it for the later classification layers.

The model is then compiled using the Adam optimizer, binary cross-entropy loss function, and accuracy metric.

After training the CNN model, it is used to extract features from the training and testing data and the resulting features are stored accordingly.

Next we define the SVM model with a linear kernel. It is then trained on the extracted features obtained from the CNN model. Finally the trained SVM model is then utilized to make predictions.

VI. RESULTS

After rigorous observation and examination, as shown in the table mentioned below, we have discerned that the combination of a Convolutional Neural Network (CNN) and a Support Vector Machine (SVM) in the hybrid model surpasses all other models in terms of accuracy. This makes it the clear choice for the task at hand.

Without a noticeable gap in precision, the joint effort of CNN and Artificial Neural Network (ANN) exhibits the least accurate results when compared to the other models.

Contrarily, an unexpected phenomenon arose when the dimensions of the test size grew bigger: the collaboration between CNN and SVM, along with CNN and Vision Transformer (ViT), exhibited a noteworthy improvement in accuracy. Conversely, the combination of CNN and ANN experienced a drastic decline, which intensified significantly.

The accuracy dynamics of the different models were affected by the expansion of the test size, highlighting the dominance of the CNN-SVM hybrid model and the subpar performance of the CNN-ANN alliance.

	Accuracy (TP+TN/T otal)	True Positive	True Negative	Total
CNN + SVM	88.66%	91	42	1050
CNN + ANN	79.33%	96	23	1050
CNN + ViT	81.99%	92	31	1050

[2][Table 1 - Accuracies between all the models]

REFERENCES:

- 1. Dataset: Brain Tumor Extracted features for brain tumor by Jakesh Bohaju (Kaggle). DOI 10.34740/kaggle/dsv/1370629
- 2. The table with the accuracies, true positive, true negative and total is a reflection of the code we executed using the dataset, divided into training and testing.
- Khan, M. A., Lali, I. U., Rehman, A., Ishaq, M., Sharif, M., Saba, T., ... Akram, T. (2019). Brain tumor detection and classification: A framework of marker-based watershed algorithm and multilevel priority features selection. Microscopy Research and Technique, 82(6), 909–922.
- 4. Seetha, J., & Raja, S. S. (2018). Brain tumor classification using convolutional neural networks. Biomedical Pharmacology Journal, 11, 1457–1461.