Hybrid Machine Learning Model For Brain Tumor Classification

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Hybrid Machine Learning Model For Brain Tumor Classification

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Abstract

A brain tumor is often a substantial public health concern. In order to acquire a diagnosis and to assess the most appropriate medical strategy, the data that is produced from brain tumors must be first classified according to their important features. In the realm of medicine, the process of brain image segmentation is essential for the planning of surgical and personalized treatment. In this study, a computer vision technique is described that uses a hybrid machine learning model to achieve excellent accuracy in the detection of brain tumors. In this research article, to provide an image recognition approach for the detection and identification of brain cancers in MRI images, a hybrid model was created. Pre-trained Squeeze-Net model with SVM and with fine-tuning technique hybrid model was used for brain tumor classification. The proposed model was found good in classifying the brain tumor MRI images which were verified using two brain tumor datasets which were generating an accuracy of around 93%. In addition to its use in medicine, the method has the potential to be integrated into automated treatment technologies as well as complicated applications in surgical procedures.

1 Introduction

The field of medical image processing is one that is now seeing significant expansion and increasing concentration. Techniques of medical image analysis are used in the diagnosing and treatment of ailments. A brain tumor, which is an abnormal development of brain cells inside the brain, is an example of this kind of basic ailment that has the potential to be deadly. Because of the intricate nature of the brain's structure and in order to improve the study related to Magnetic Resonance Imaging (MRI) this research aims to increase both efficiencies and reduce the overall complexity of the image segmentation process. During the course of this research project, the images from the brain tumor dataset are analyzed.

MRI procedure is a method for identifying any issues that manifest in the brain. MRI is famous for the fact that it exposes patients to radiation that does not cause ionization during the sweep. In addition to being the only one of its kind to target delicate tissue, it also has the ability to get a variety of images by making use of a variety of imaging limits or by using professionals who can boost contrast. The MRI not only provides a lot of information about our brain, but also it pinpoints issues in our brainstem and cerebellum. Axial, sagittal, and coronal orientations are the three different ways that brain MRI data may be represented. In this research, MRI images of the brain are analyzed for the presence of tumors.

The purpose of this study is to offer a strategy based on machine learning for segmenting brain images and identifying tumors. Artificial intelligence (AI) is centered on the field of machine learning (ML). Artificial intelligence, for the most part, makes use of acceptance and mix, which enables computers to learn new knowledge by mimicking the behavior of the human brain. It does this in order to continually improve the performance of the computer by rebuilding previously learned information. A number of other industries, such as medical diagnosis, agriculture, and computer vision, make extensive use of AI.

1.1 Background Motivation And Scope

Authors in (Vankdothu and Hameed; 2022) state that the tumor developing in the brain can be either malignant (cancerous) or benign (non-cancerous). Dangerous (malignant) cerebrum growths generally develop more quickly than innocuous (benign) tumors, and they quickly permeate the surrounding tissues. Malignant growths are referred to as cancers. As a tumor, whether benign or malignant, increases in size, it may cause the pressure within the skull to increase. The cerebellum might be pushed downwards, putting the patient's life in danger, if the tumor continues to grow and may cause an increase in pressure inside the brain.

In the realm of medicine, the process of brain image segmentation is essential for the planning of surgical and personalized treatment. In this study, a computer vision technique is described that uses a hybrid machine learning model to achieve excellent accuracy in the detection of brain tumors. In this study, brain tumor images are classified into glioma tumor, no tumor, meningioma tumor, and pituitary tumor. To achieve this previous works of the last five years in this field are being analyzed and further study has been done in this paper.

The proposed model has the potential to be integrated into automated treatment technologies or surgical procedures for brain tumor classification. Some ways this could be done include :

- Image-guided surgery: This model can be used to classify brain tumors in real time during a surgical procedure. This can help surgeons navigate around important structures and avoid damage to healthy tissue.

- Automated biopsy: This model can be used to classify brain tumors in real-time during a biopsy procedure. This can help to ensure that the right tissue is being biopsied, which can reduce the need for multiple biopsy procedures.

- Treatment planning: This model can be used to classify brain tumors and predict their aggressiveness, which can help to inform treatment planning.

- Radiotherapy planning: This model can be used to assist in the segmentation and quantification of tumors, which is important in order to plan conformal radiotherapy and thus minimize the damage of surrounding healthy tissue.

1.2 Objective

The objective of this paper is to provide an image recognition approach for the detection and classification of brain cancers in MRI images. The area of medical image analysis is no exception; Deep Learning (DL) has recently been the cutting edge in this and many other disciplines. Unlike traditional methods, deep learning is able to analyze enormous amounts of unstructured data by splitting it up into numerous layers, each of which may extract features before passing them on to the next. The deep learning method is defined by its primary feature, the automated extraction of features that describe data representations. In the field of medical imaging, Convolutional Neural Networks (CNNs) have emerged as the dominant form of deep learning. Automatic feature extraction of structured data representations from medical pictures is made possible by the CNN model's efficient processing power.

In this study, a new method based on the hybrid SqueezeNet-SVM method is used to classify brain tumor MRI scans. This study's contribution can be summed up in the following points:

- It makes use of a hybrid machine learning model to detect brain tumors early and allow for a quicker start to therapy and prevention of the tumor tissues from spreading.
- It demonstrates that compared to conventional techniques, adopting a hybrid machine learning technique, which combines Squeeze-Net with SVM, produces more precise and superior results.
- The proposed model is validated using two brain tumor MRI datasets.
- The results of the implementation are compared with the models that are presented in the related work section.
- This model will help radiologists avoid making mistakes when they use MRI to look for tumors.

1.3 Research Question

A) Will Squeeze-Net with the SVM and fine-tuning technique be suitable for brain tumor classification ?
B) Is Grey Level Co-occurrence Matrix(GLCM) feature extraction technique with SVM classifier suitable for brain tumor classification ?
C) How will the proposed model perform for other brain tumor datasets?

1.4 Structure of the Report

This report has 7 sections where the first section discusses the introduction of the paper followed by Section 2 which discusses the Related work followed by Section 3 which deals with methodology and details of the suggested strategy is explained followed by Section 4 which deals with the Design Specification of the model used followed by Section 5 which contains the implementation of the proposed method followed by Section 6 which contains the details of experiments conducted and its results followed by section 7 which contains Conclusion and future work

2 Related Work

2.1 Brain Tumor Classification Using Supervised Machine Learning Techniques

In this section, various supervised machine learning algorithms have been discussed which when implemented has proved to be effective in classifying brain tumor. Experts from (Kibriya et al.; 2022) have stated that since 2016 out of 200 Deep learning algorithms based research in brain tumor classification, CNN is implemented 190 times by researchers which has achieved the ground-breaking outcome.

Researchers in (Kibriya et al.; 2022) have also suggested an approach that extracts several low-level and high-level features from various architectures such as ResNet18, GooLeNet, and AlexNet. Then, in order to create a single vector, these features are combined using a deep feature fusion. This novel feature vector is then used in SVM and KNN-classifier to predict the result. The suggested technique has a 99.7% accuracy rate, a recall value of 1.0, a precision score of 0.99, and an f1-score of 0.99 after being trained and assessed on 15,320 Magnetic Resonance Images (MRIs). In comparison to independent CNN feature vectors, the novel feature vector performed better. Additionally, the feature fusion approach helps to overcome the shortcomings of a single CNN model, leading to improved performance, especially for bigger datasets. Other than CNN there are other supervised machine learning techniques that have proved to be effective in brain tumor classification, some of which are implemented in (Anand et al.; 2022) paper. This technique uses MRI scans and machine learning to segment and classifies brain tumors. The geometric mean filter removes noise during image pre-processing. Fuzzy c-means algorithms segment images which help extract the areas to focus. GLCM is used to reduce dimensions. After GLCM extracts image characteristics, the images are categorized using machine learning algorithms including SVM, RBF, ANN, and AdaBoost. SVMs using RBF kernels perform better when analyzing MRIs for brain tumors. Traditional classification methods had low training and testing rates and required many contrast-enhanced brain MRI images to produce good results. These traditional classification methods are difficult to implement due to overfitting during training and testing. To Reduce overfitting Extreme Machine Learning(EML) and co-active adaptive neuro-fuzzy inference system(CANFIS) classification methods are suggested in (Jeevanantham and MohanBabu; 2021) this study used a model for brain tumor classification which needs low contrast and fewer pictures. This research suggests using an index filter to detect and remove noise from brain MRIs to improve accuracy. Brain pictures in spatial domain format after noise removal are inappropriate for feature extraction. So, all spatial pixels must be multi-orientation. In this work, the spatial picture is changed using Gabor. Gabor-modified images are utilized to compute GLCM and LDP features. EML identifies tumor images, whereas CANFIS diagnoses tumor sections. BRATS 2016 brain tumor dataset is used in this study to classify tumors. The recommended tumor diagnosis approach has a 99.4% classification rate for moderate and severe cases of brain tumors. (Rasool et al.; 2022) This article describes a CNN-SVM-based deep-learning classification method. This approach uses Google-Net and SVM to detect and categorize MRI brain tumor types. The new hybrid CNN architecture classifies MRI brain pictures as meningioma, glioma, pituitary tumor, or not a tumor. Hybrid CNN has the greatest accuracy and speed among all deep-learning approaches. According to the results, the recommended strategy might be used to highlight dubious brain locations. This method immediately identifies tumors. This study suggests that in the future CNN models, such as Squeeze-Net combined with SVM and fine-tuning, may more accurately categorize brain tumor images.

2.2 Brain Tumor Classification using Unsupervised Machine Learning techniques

In this section, some of the unsupervised machine-learning techniques are discussed for brain tumor classification. Fuzzy c-means clustering, often known as FCM, is one of the best-known methods for clustering that has been developed to automatically rearrange the many features of big datasets and provide exact results. One such implementation of FCM is discussed by experts in (Simaiya et al.; 2021) research paper. They have implemented a hybrid model known as the Hierarchical K-means clustering with Fuzzy C and Super Rule tree (HKMFSRT-Model). The proposed HKMFSRT-Model seems to be a combination of the Super-Rule-Tree, the k-means clustering method, the patch-based system for image acquisition, and the object counting method. A set frame rate that has been specified in advance is required for a number of ways to recognize the patterns. The suggested technique develops a plus-Rule-Tree using a super-rule architecture to address the problem of misplaced patterns. The proposed approach has an accuracy result of 88.9%, whereas the current k-Means clustering method has an accuracy result of 85.4%. Another unsupervised machine learning technique in which Fuzzy C-means is used with machine learning techniques like SVM and the required optimization technique to improve the performance is implemented in (Vankdothu and Hameed; 2022). In this study, brain tumor database images are evaluated, and an adaptive median filter preprocessing approach is used to increase image clarity. Preprocessing removes noise and high-frequency artifacts. The median filter is a prominent nonlinear digital noise-reduction filter. The picture is categorized as normal or abnormal using the Adaptive Neuro-Fuzzy Inference System (ANFIS) and Support Vector Machine (SVM) classifiers. After classification, the Fuzzy C-Means (FCM) clustering method and associated optimization techniques are employed to monitor and segment aberrant images. The proposed technique combines a Genetic Algorithm (GA) with Grey Wolf Optimization (GWO) and Social Spider Optimization (SSO) to enhance FCM centroid accuracy. The suggested work has the most extreme tumor picture segmentation evaluation method. The hybrid strategy (SSO-GA) yields 99.24% accuracy, compared to other standalone algorithms. This work uses MATLAB 2014 to segment and classifies brain tumors. Researchers in (Preetika et al.; 2021) used FCM, K-Means, and K-nearest Neighbor to categorize brain tumors. In this study brain magnetic resonance imaging was utilized to construct a machine learning-based program that is used for segmentation and to determine if a tumor is benign or malignant. A cycle known as "skull stripping" is most often used in this paper's contrast enhancement process, which involves twofold thresholding and is completed using morphological tasks to improve the MRI image. The accurate delineation of the tumor district is completed in less computation time using the inference of the image highlights using the GLCM. This is accomplished by carefully planning how to prepare these highlights. K-means, KNN, and FCM features derived from the GLCM may thus be used in the suggested framework to achieve greater accuracy and efficiency. This is completed using the triple approach K-Means, FCM, and KNN to calculate the accuracy and error rate for the brain MRI image.

2.3 Feature Selection in Brain Tumor Classification

In this section, some of the feature selection techniques have been reviewed with respect to brain tumor classification. Researchers in (Vidyarthi et al.; 2022) study combines three well-known classifiers, K-Nearest Neighbor (KNN), Multi-Class Support Vector Machine (M-SVM), and Neural Network, with three feature selection algorithms: proposed Cumulative Variance Method (CVM), Independent Component Analysis (ICA), and Genetic Algorithm (GA). The trial outcomes of each feature selection technique are compared. The experimental findings demonstrate that, in comparison to other feature selection algorithms like ICA and GA, the CVM feature selection algorithm performs better in terms of accuracy outcomes for each class of malignant brain tumor prediction. In terms of accuracy results, the feature selection method is determined to be in the following order: CVM followed by GA followed by ICA. Additionally, it has also been noted that the classier's performance level varies. The greatest average accuracy attained with Neural Network(NN) is 95.86% using CVM feature selection technique for malignant tumor class label prediction. The classification order in terms of accuracy is NN followed by mSVM followed by KNN.

(Vijithananda et al.; 2022) Each patient's MRI are used to extract information based on their demographics, mean pixel values, skewness, kurtosis, properties of the Grey Level Co-occurrence Matrix (GLCM), variance, energy, entropy, contrast, homogeneity, correlation, prominence, and shade. Extracted features are checked if it is valid or not using an ANOVA f-test. The output of several Machine Learning classification methods is then evaluated using these features as input. The two features with the lowest ANOVA f-test scores were skewness (3.34) and GLCM (3.45), according to the findings of the feature selection procedure. Therefore, in order to continue the experiment, both qualities skewness and GLCM are eliminated. This research comes to the conclusion that the features listed above, with the exception of skewness and GLCM, are useful in identifying and distinguishing benign from malignant brain tumors.

Bayesian inference technique now attracts interest in uncovering underlying dynamics and correlations between characteristics via analysis of static features. Researchers in (Hussain et al.; 2022) have analyzed Meningioma and pituitary MRIs to calculate the GLCM features, which are subsequently sorted using entropy ranking approaches. The top-ranked Energy feature collected from brain MRIs is selected as the target variable for further empirical research of dynamic profiling and optimization. The Bayesian inference technique can be employed as a biomarker to understand a thorough examination of extracted data and offer a calculated future for further research. In the future, more Bayesian inference techniques can be implemented with more clinical information and bigger datasets.

(Ahmadi et al.; 2021) In this study, researchers have introduced a unique neural network-based classifier that uses wavelet transformation and fuzzy logic. A layer in a classifier is used to forecast the numerical characteristic that corresponds to labels or classes. A fractal model with four Gaussian functions is employed for feature extraction. Classification is carried out on 2000 MRI pictures. Regarding the outcomes, the accuracy rates of the Decision Tree (DT), k-nearest neighbors (KNN), Latent Dirichlet Allocation (LDA), Naive Bayes (NB), Multi-layer perceptron (MLP), and SVM's are 93.5%, 87.6%, 61.5%, 57.5%, 68.5%, and 43.6% correspondingly. The findings show that the given FWNNet has a 100% accuracy rate by using the fractal feature extraction technique with MRI-based brain tumor diagnosis.

2.4 Optimization techniques in brain tumour classification

One of the most popular optimization techniques for brain tumor classification is the genetic algorithm which is implemented by researchers in (Mathiyalagan and Devaraj; 2021). Researchers in this paper have implemented a machine learning classification methodology to establish a computer-aided, completely automated method for identifying and categorizing glioma brain magnetic resonance imaging (MRI). The noise-removed image's edges are then recognized using fuzzy logic, and contrast adaptive local histogram equalization is used to enhance the edge pixels. The Ridgelet filter removes noise from the original brain MRI picture. The characteristics are computed from the Gabor-transformed augmented brain image. Adaptive neuro-fuzzy inference system (ANFIS) classifies computed characteristics into glioma and non-glioma brain pictures. The genetic algorithm improves calculated characteristics. Finally, the fuzzy C means technique is used to segment the tumor patches on the glioma brain picture. In (Arif et al.; 2022) segmentation using Genetic Algorithm is done in four phases. The first phase is to select the genotype by using the fitness function, the second phase is to select the individual, the third phase is mutation and crossover of individuals selected fourth phase is the evaluation of termination condition. This study also introduces a powerful deep-learning model for the identification and classification of brain tumours. They have implemented the U-Net model to identify and classify brain tumour images. A genetic Algorithm is employed as a segmentation approach to identify tumour areas, and Particle swarm optimization(PSO) is used to pick features, which improved the classification stage. According to the assessment of the experiment, this model performs better than other models with an accuracy of 0.97, sensitivity of 0.98, and specificity of 0.98.

2.5 Conclusion

The following things may be summarized from the related works that were discussed earlier:
a) It can be inferred from (Kibriya et al.; 2022) paper that the performance of novel feature vectors resulting from the fusion of many architectural styles is superior to that of an individual CNN feature vector.
b) It can be inferred from (Anand et al.; 2022) paper that the problem of overfitting was seen in the conventional classification methods.
c) From article (Preetika et al.; 2021) it can be seen that the accuracy of the tumor area segmentation in the MRI images is not suitable for any subsequent procedures for the diagnosis of tumors.

3 Methodology

The project will make use of the KDD approach, which stands for "knowledge discovery in databases." There will be a step-by-step progression through all six phases that are outlined in the design of the project as shown in Figure 1. Different phases in the design of the project for dataset 1 and dataset 2 is shown in Figure 2 and Figure 3 respectively. In this study a hybrid model is proposed which is Squeeze-Net with SVM for brain tumor image classification.
SqueezeNet is a small convolutional neural network (CNN) architecture that was designed

to be efficient in terms of memory and computational requirements while still maintaining good accuracy on image classification tasks. Researchers in (Wang et al.; 2019) have pointed out that one of the key techniques used in SqueezeNet to achieve this is the use of ”fire” modules, which are small, densely connected layers that are interleaved throughout the network. The operations of the fire module is discussed in section 4 of this report.
One of the key elements in the fire module is the expansion layer which is responsible for increasing the number of feature maps, this is done by applying 3x3 filters with a stride of 1, this operation can increase the computational and memory requirements. To mitigate this problem, zero-filling for the 3x3 filters in the expansion layer is proposed in this study.

The zero-filling technique consists of setting some of the coefficients of the 3x3 filters to zero, which reduces the number of parameters and computations in the expansion layer without significantly affecting the accuracy of the model. Specifically, setting the central element of the 3x3 filters to zero, reduces the number of parameters in the expansion layer by a factor of 9. This reduction in parameters and computations is one of the key ways that SqueezeNet is able to achieve its high level of efficiency.

The robustness of this hybrid model to variations in the data depends on several factors, including the specific architecture of the network, the quality, and diversity of the training data, and the specific task the network is being used for.

In summary, zero-filling the 3x3 filters in the expansion layer of SqueezeNet allows for a reduction in the number of parameters and computations, which makes the model more efficient in terms of memory and computational requirements. This technique has a small impact on the model’s accuracy, but overall the model can still perform well on image classification tasks. Squeeze-Net with SVM can be robust to variations in data depending on the specific task, the architecture, and the training data, yet in certain cases, they may need fine-tuning or to use other techniques to improve generalization. So in this study fine-tuning technique is also proposed to improve robustness.

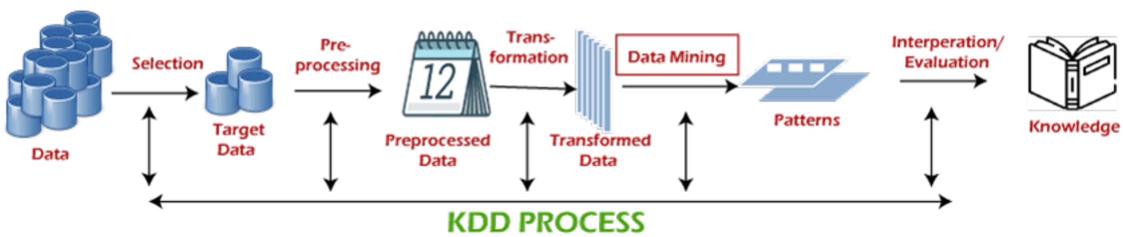

Figure 1: KDD

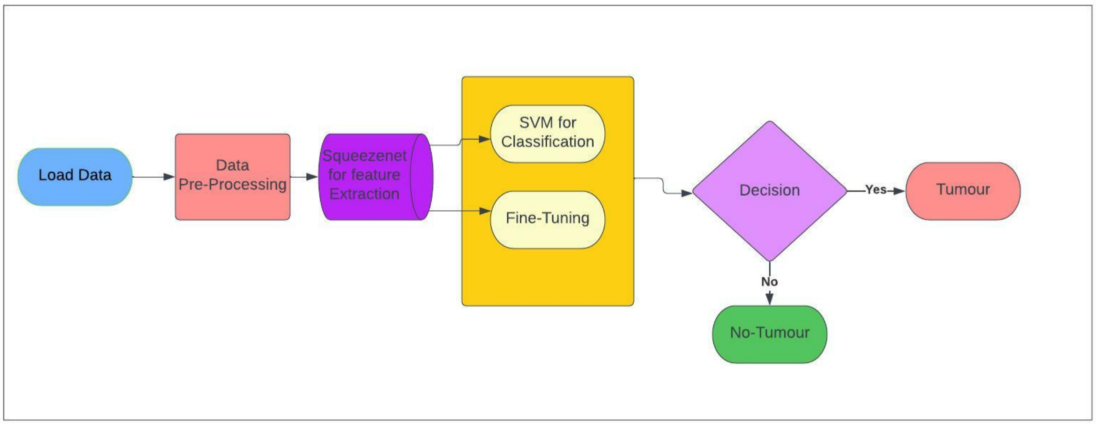

Figure 2: Block Diagram with Dataset 1

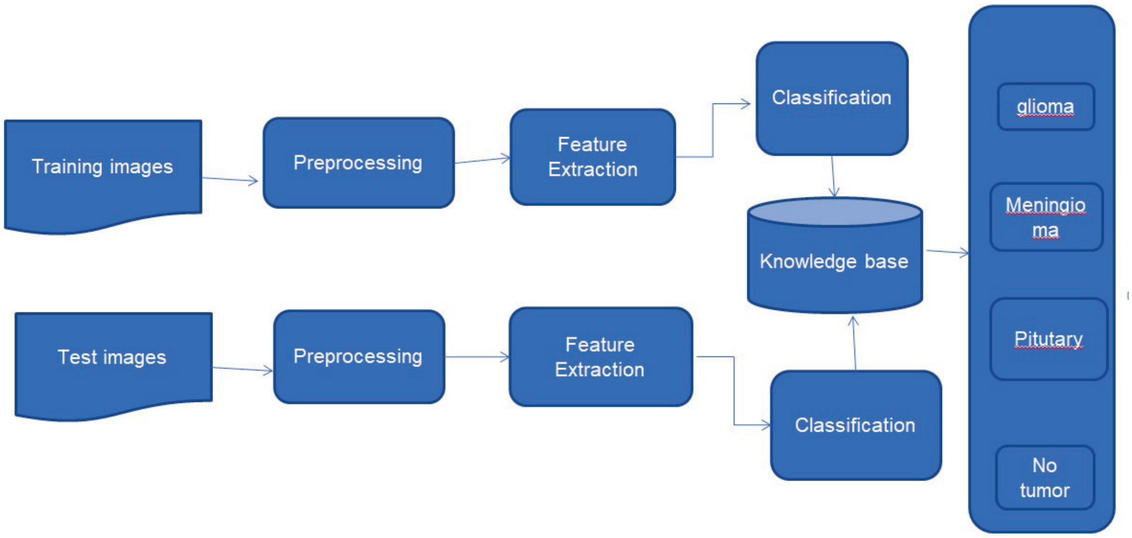

Figure 3: Block Diagram with Dataset 2

3.1 Data Acquisition

Dataset 1 - This dataset is taken from Kaggle [1]. It consists of 253 pictures of people's brains out of which 155 pictures of people's brains that are affected by tumors, and 98 pictures of people whose brains are normal and do not have tumors and the aim is to detect if the image has tumor or not using deep learning model.

Dataset 2 -

The dataset [2] was first published on the internet in the year 2017 by Jun Cheng, then Sartaj Bhuvaji revised it in the year 2020 . Kaggle.com provided the source for the 3064 T1-weighted contrast-enhanced MRI scans that are included in the image collection. Meningiomas have 708 photos; gliomas have 1426 images and pituitary tumors have 930

[1] Dataset 1: `https://www.kaggle.com/datasets/navoneel/brain-mri-images-for-brain-tumor-detection`

[2] Dataset 2: https://www.kaggle.com/datasets/sartajbhuvaji/brain-tumor-classification-mri

images. All the images were taken in three planes from 233 patients: sagittal (1025), axial (994), and coronal (1025). (1045 images). Randomly, 80% of the data was given for training and 20% for testing. Folders have four subfolders each. These folders include tumor MRIs. Meningioma, glioma, pituitary, and not-tumor are presented in this sagittal, axial, and coronal figure.

3.2 PRE-PROCESSING

The MR picture that was entered is pre-processed so that any noise that may have been produced during image production is eliminated. The elimination of noise enables us to get rid of undesired signals, the processing of which may otherwise result in mistakes. A median filter is used for noise reduction since it maintains edges while simultaneously eliminating noise. In the next step, the picture that has been filtered is transformed into an 8-bit grey level in order to decrease the bands in the image. The original three-band color picture is transformed into a comparable intensity image with a value that may fall anywhere between 0 and 255. Following preprocessing, the original picture is transformed into a noise-free, intense image that is 256 $\times$ 256 pixels in size. This image is then used as input for the subsequent phase.Following the transformation of the picture into its greyscale equivalent, the image is preprocessed before being sharpened. The input grey picture is sharpened so that the soft tissues may be seen more clearly in the MR scan. This is done since the soft tissues are a worry. An picture may be made to seem sharper by making use of high-pass filters. These filters allow high-frequency components to get through while removing low-frequency components. As a consequence of this, the picture that is produced after going through a high pass filter results in a sharper image in which both soft tissues and edges can be seen. The MR images are sharpened with the use of a high pass Gaussian filter in this particular piece of research.

3.3 FEATURE EXTRACTION

This chapter gives in-depth information on the many types of characteristics that are used by machine learning in order to make a prediction about the severity of the cancer. This varied feature vector contains features such as those based on intensity, those based on frequency, those based on texture, those based on shape, those based on contour, and those based on moments. The produced feature set ultimately leads to the advantage of being able to process a single picture in a range of its representation forms, which was not possible before. Both the frequency domain and the spatial domain have significance over one another as image representation forms due to the fact that digital computers may process and represent images in either of these two domains: the frequency domain or the spatial domain.In this paper GLCM and Squeeze-Net model is used for feature extraction.

3.3.1 GLCM

the Grey Level Co-Concurrent Matrix (GLCM) technique is used To extract features from images.To differentiate one grayscale picture from another, feature extraction uses texture analysis, which seeks to identify a grayscale image's features. In this work, the picture is retrieved based on four characteristics: contrast, energy, correlation and entropy factors. Each attribute is a crucial element since it provides significant information to a image.

3.4 Modelling

The fundamental objective of this paper is to provide a new hybrid deep-learning model technique. This strategy look at distinct types of hybridization which combine SqueezeNet with the support vector machine and with fine-tuning for two different brain tumor dataset. The block diagram of the suggested research technique is shown in Figure 2 and Figure 3 for dataset 1 and dataset 2 respectively.The SVM classification function does its task by first distinguishing between the different groups and then locating an appropriate hyperplane on which to base a solution to the learning issue. The SVM method is comprised of three components: basic ideas for linearly separable groups, an extension to the non-linearly separable situation that makes use of kernel functions, and an evaluation phase. The radial basis function (RBF) kernel is one of the kernel functions. It is often employed in situations in which there is no previous knowledge of the outcomes. This kernel function gives a piecewise linear solution in situations in which discontinuities are appropriate. The suggested method is broken down and discussed in further depth in the following subsections.

3.5 FINE-TUNING

A pre-trained model may be fine-tuned to complete a classification assignment by restoring it to its original condition or making tiny alterations. We can utilize what the model has previously learnt if we implement an artificial neural network that has already been created and trained.

3.6 Evaluation

The suggested methods are evaluated by an empirical process that makes use of classification accuracy (Acc), recall (Rec), precision (Pre), F1-score and Confusion Matrix, all of which are stated using Equations (1)–(4) and in Table 1 where True Negative(TN), True Positive(TP), False Positive(FP) and False Negative(FN) are used to calculate the metrics.The percentage of real outcomes in relation to the total cases investigated is the accuracy. Paper (Hossin and Sulaiman; 2015) defines Precision, recall, and F1 score. The ratio of True Positives to all the positives predicted by the model is known as precision. Low precision means if the precision decreases as the model predicts more False Positives. The proportion of True Positives to all the Positives in your Dataset is known as Recall (Sensitivity). Low recall means the recollection decreases as the model predicts more False Negatives. Precision and memory issues are balanced by F1 score. Low false positives and low false negatives are indicators of a high F1 score.

$$\mathrm{Acc} = ((\mathrm{TN} + \mathrm{TP})/(\mathrm{TP} + \mathrm{TN} + \mathrm{FP} + \mathrm{FN})) \times 100 \tag{1}$$

$$\text{Rec.} = \mathrm{TP}/(\mathrm{TP} + \mathrm{FN}) \tag{2}$$

$$\text{Pre.} = \mathrm{TN}/(\mathrm{TN} + \mathrm{FP}) \tag{3}$$

$$\text{F1-Score} = (2 \times (\text{ Pre. } \times \text{ Rec. }))/(\text{ Pre. } + \text{ Rec. }) \tag{4}$$

Table 1: Evaluation Metric Details.

Metric	Description
Precision (Pre.)	ratio of true Negative samples to total Negative sample
Recall (Rec)	ratio of true Positive samples to total Positive samples
Accuracy (Acc.)	% of the overall percentage of accurate detection
F1-Score	The harmonic mean of Precision and Recall

4 Design Specification

The primary purpose of SqueezeNet is to achieve competitive accuracy while using a limited number of parameters. According to authors,(Wang et al.; 2019) There are three primary approaches used in order to accomplish this objective. To begin, the 3 x 3 filter was changed to a 1 x 1 filter since it has fewer parameters than the previous filter. Second, we cut the number of input channels down to the 3 x 3 filters and simplified the process. In the last step, we made the convolution layer with a significant activation by using subsampled operations in the latter stages of the network. The concept of the Inception module was used by SqueezeNet when designing the Fire module, which consists of a squeeze layer and an expansion layer. Compressing the input elements using a 1 x 1 convolution kernel was done by the squeeze layer. This was done so that the number of channels for the input elements may be reduced. Concatenating and multi-scale learning were accomplished by the employment of the 1 x 1 and 3 x 3 convolution kernels in the expansion layer.

Figure 4 shows the dimensions of the feature maps submitted into the system. First, input feature maps are compressed using a squeeze layer, resulting in output feature maps with dimensions h x w x s1. The number of feature maps is the same, but the number of channels is s1. The squeeze layer's output feature maps are sent to the expand layer's 1x1 and 3x3 convolution kernels. Concatenate the convolution's output. The total number of channels equals (e1x1 + e3x3), where e is the expansion layer. To guarantee that the 1 x 1 and 3 x 3 filters of the extension module have the same height and width, the input 3 x 3 filters are zero-filled with 1 pixel. This is done so both filter outputs have the same height and breadth. ReLU activates a squeezing layer and an expansion layer. SqueezeNet lacks a full-connection layer at this time.

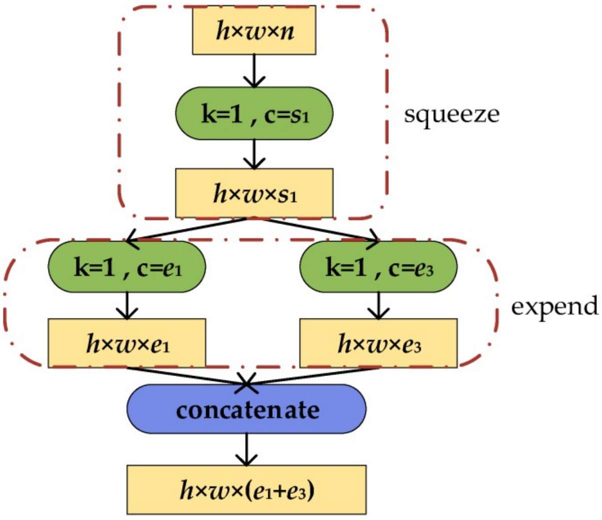

Figure 4: Operation process of Fire module

5 Implementation

5.1 Softwares and Technologies Used

In order to create the outputs and the results, the following specifications for the softwares and libraries are employed :

- **Programming Language -** Python
- **IDE -** Goggle Colab
- **Python Libraries/Modules:**
  Pre-processing- Numpy, Pandas
  Feature Engineering - skimage, matplotlib, scipy
  Modelling and Evaluation - Sklearn, tensorflow, keras, tqdm

5.2 Pre-Processing

5.2.1 Gaussian Filtering

The use of a Gaussian filter allows for the removal of speckle noise that may be present in MRI or ultrasound pictures of the brain. Using this method, the average value of the pixels that are nearby to the noisy pixel that is already present in the picture is used to replace the noisy pixel which can be seen in figure Figure 5. This method is based on the Gaussian distribution.

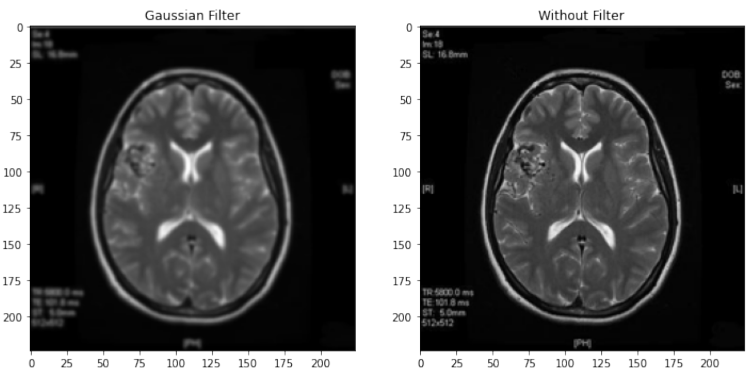

Figure 5: Gaussian Filter

5.2.2 Sobel Filtering

This filtering technique helps in enhancing the edges of the pictures which can be seen in figure Figure 6.

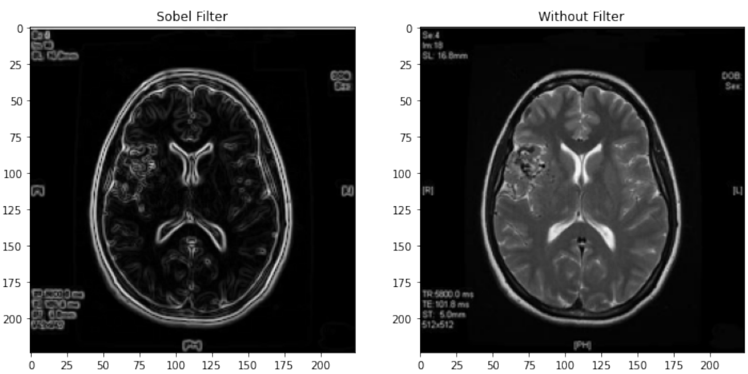

Figure 6: Sobel Filter

5.2.3 Laplace Filtering

An edge detector is what's known as a Laplacian filter, and it's what's used to calculate an image's second derivatives by detecting the rate at which the image's first derivatives changes as seen in figure Figure 7.

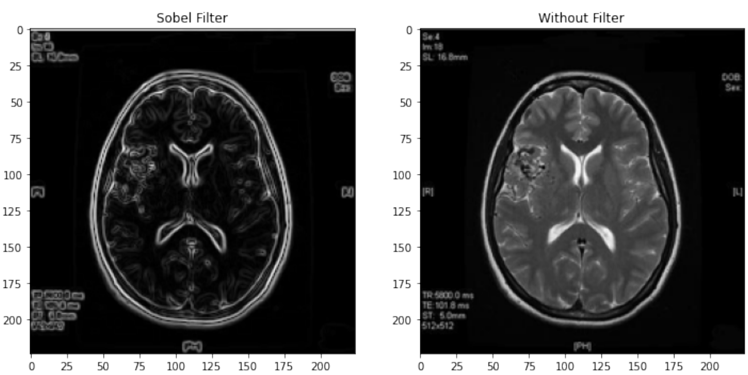

Figure 7: Sobel Filter

5.2.4 Gabor Filtering

A linear filter known as a Gabor filter has a Gaussian kernel at its center and is modulated by a sinusoidal plane wave.Computer vision and image processing often make use of something called a Gabor filter bank. They are particularly useful for edge recognition as well as the categorization of textures as seen in figure Figure 8.

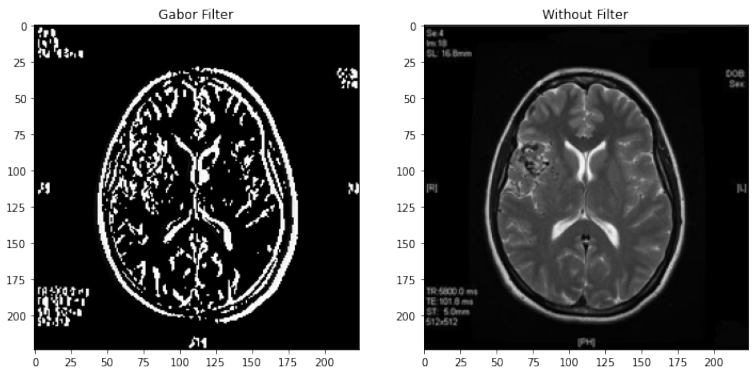

Figure 8: Gabor Filter

5.2.5 Hessian Filtering

This filter is able to identify continuous edges which can be seen in figure Figure 9.

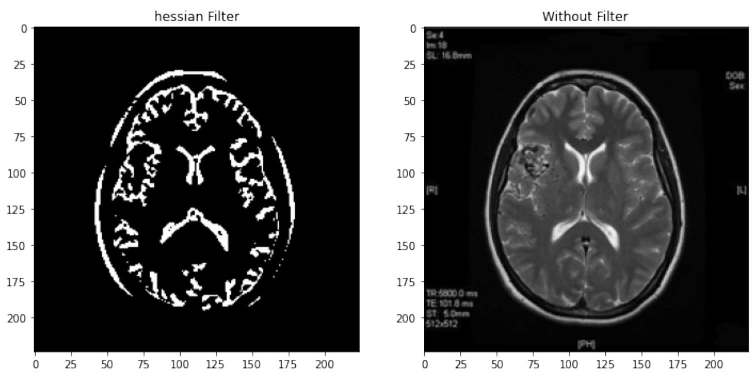

Figure 9: Hessian Filter

5.2.6 Prewitt Filtering

In image processing, the Prewitt operator is used, notably inside edge detection methods. In technical terms, it is known as a discrete differentiation operator and it computes an estimate of the gradient of the picture intensity function as seen in figure Figure 10.

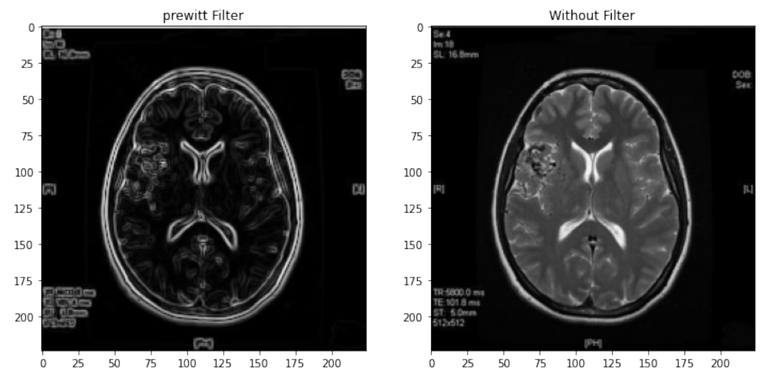

Figure 10: Prewitt Filter

5.3 Feature Engineering

In this paper pre trained Squeeze-Net is used for feature extraction.SqueezeNet eliminated the conventional 3 x 3 convolution kernels and replaced them with a large number of 1 x 1 convolution kernels. This resulted in a relative decrease in the amount of retrieved features.The fact that there were more convolution kernels of size 1 x 1 than 3 x 3 meant that the number of parameters in a network could be reduced, resulting in a more compact model.

5.4 Model Training

In this research hybrid machine learning model is used which is Squeeze-Net with SVN with fine-tuning to classify brain tumors. Pre-trained Squeeze-Net model is used to identify the features then the features are passed to SVM classifier for the classification of images and then the model is fine-tuned using GridSearchCV and 5 fold cross-validation to identify best hyperparameters and improve recall score.

6 Evaluation

6.1 Experiment 1

6.1.1 Algorithm

Inputs: Model is trained with the testing images from Dataset 1 which contains two classes of images one with tumors and the other which doesn't have tumor
Outputs: Accuracy is calculated after testing the model with the testing set of images from Dataset 1
Step 1: Convert the image to grayscale and blur it slightly. crop the image from the original image using the four extreme points which are left, right, top, and bottom then resize the image which is each image should be of size (256,256,3)
Step 2: Spit the data into testing and training set which is 80 percent of data as a training set and the rest 20 percent as a testing set.
Step 3: Load pre-trained Squeeze-Net model of CNN.
Step 4: Make all the layers of the Squeeze-Net model nontrainable as the Squeezenet model is not used for training the model it is only used for feature extraction. Then

Extract features using the Squeeze-Net model.
Step 5: Pass all the features extracted from the Squeeze-Net model to SVM classifier.
Step 6: Fine Tune the model using GridSearchCV and also cross-validate it using 5 fold cross validation
Step 7: The output Layer yields one of two classes: yes and no. Yes for the presence of tumor and No for the absence of tumor

Return accuracy

6.1.2 Result

The model is good in identifying the images which does not have tumor which can be seen from Figure 11. The accuracy obtained using this model is 89% and the Precision, Recall and F1 Score obtained is 87.5%, 98% and 92% respectively which can be seen from Figure 12.

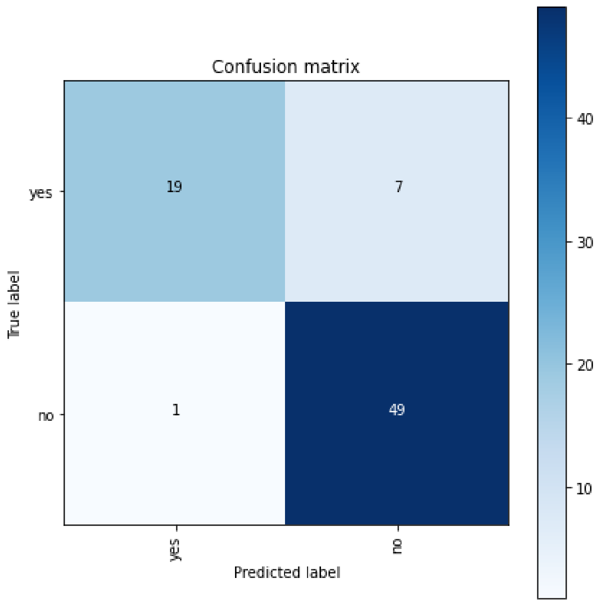

Figure 11: Confusion Matrix Of Experiment 1

```
# accuracy: (tp + tn) / (p + n)
accuracy_svm = accuracy_score(y_test, y_pred)
print('Accuracy: %f' % accuracy_svm)
# precision tp / (tp + fp)
precision_svm = precision_score(y_test, y_pred)
print('Precision: %f' % precision_svm)
# recall: tp / (tp + fn)
recall_svm = recall_score(y_test, y_pred)
print('Recall: %f' % recall_svm)
# f1: 2 tp / (2 tp + fp + fn)
f1_svm = f1_score(y_test, y_pred)
print('F1 score: %f' % f1_svm)
```

```
Accuracy: 0.894737
Precision: 0.875000
Recall: 0.980000
F1 score: 0.924528
```

Figure 12: Result Of Experiment 1

6.2 Experiment 2

6.2.1 Algorithm

Inputs: Model is trained with the testing images from Dataset 1 which contains two classes of images one with tumors and the other which doesn't have tumor.
Outputs: Accuracy is calculated after testing the model with the testing set of images from dataset 1
Step 1: Convert the image to grayscale and blur it slightly.crop the image from the original image using the four extreme points which is left, right, top, bottom then resize the image which is each image should be of size (256,256,3)
Step 2: create GLCM using graycomatrix and derive statistical features like contrast, homogeneity, correlation and energy using graycoprops and store it into a pandas data frame. **Step 3:** Spit the data into testing and training set which is 80 percent of data as training set and the rest 20 percent as testing set.
Step 4: Pass all the features extracted from GLCM to SVM classifier.
Step 6: Fine Tune the model using GridSearchCV and also cross-validate it using 5 fold cross validation
Step 7: The output Layer yields one of two classes: yes and no. Yes for the presence of tumor and No for the absence of tumor
Return accuracy

6.2.2 Result

The model is good in identifying the images which does not have tumor which can be seen from Figure 13. The accuracy obtained using this model is 51% and the Precision, Recall and F1 Score obtained is 67.7%, 56.7% and 61.7% respectively which can be seen from Figure 14.

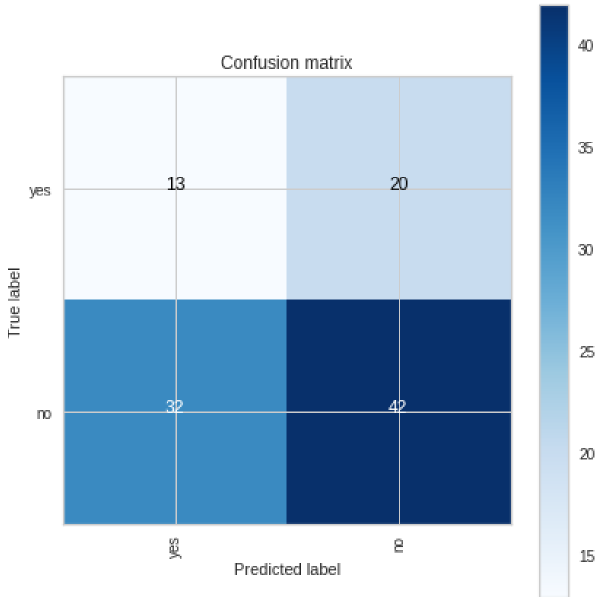

Figure 13: Confusion Matrix Of Experiment 2

```
# accuracy: (tp + tn) / (p + n)
accuracy_svm = accuracy_score(y_test, y_pred)
print('Accuracy: %f' % accuracy_svm)
# precision tp / (tp + fp)
precision_svm = precision_score(y_test, y_pred)
print('Precision: %f' % precision_svm)
# recall: tp / (tp + fn)
recall_svm = recall_score(y_test, y_pred)
print('Recall: %f' % recall_svm)
# f1: 2 tp / (2 tp + fp + fn)
f1_svm = f1_score(y_test, y_pred)
print('F1 score: %f' % f1_svm)
```

```
Accuracy: 0.514019
Precision: 0.677419
Recall: 0.567568
F1 score: 0.617647
```

Figure 14: Result Of Experiment 2

6.3 Experiment 3

6.3.1 Algorithm

Inputs: Model is trained with the testing images from Dataset 2 which contains five classes which are Not-Tumour, Glioma-Tumour, Meningioma-Tumour, and Pituitary-Tumour.
Outputs: Accuracy is calculated after testing the model with the testing set of images from dataset 2
Step 1: Convert the image to grayscale and blur it slightly.crop the image from the original image using the four extreme points which is left, right, top, bottom then resize the image which is each image should be of size (256,256,3)

Step 2: Spit the data into testing and training set which is 80 percent of data as training set and the rest 20 percent as testing set.
Step 3: Load pre-trained Squeeze-Net model of CNN.
Step 4: Make all the layers of the Squeeze-Net model as nontrainable as the Squeezenet model is not used for training the model it is only used for feature extraction. Then Extract features using the Squeeze-Net model.
Step 5: Pass all the features extracted from the Squeeze-Net model to SVM classifier.
Step 6: Fine Tune the model using GridSearchCV and also cross-validate it using 5 fold cross validation
Step 7: The output Layer yields one of four classes:
1 Not-Tumour
2 Glioma-Tumour
3 Meningioma-Tumour
4 Pituitary-Tumour
Return accuracy

6.3.2 Result

The model is good in identifying the images with glioma tumor,no_tumor and pituitary_tumor which can be seen from Figure 15. The accuracy obtained using this model is 94% and the Precision, Recall and F1 Score obtained for gliopma_tumor, meningloma_tumor,no_tumor and pituitary_tumor can be seen from Figure 16.

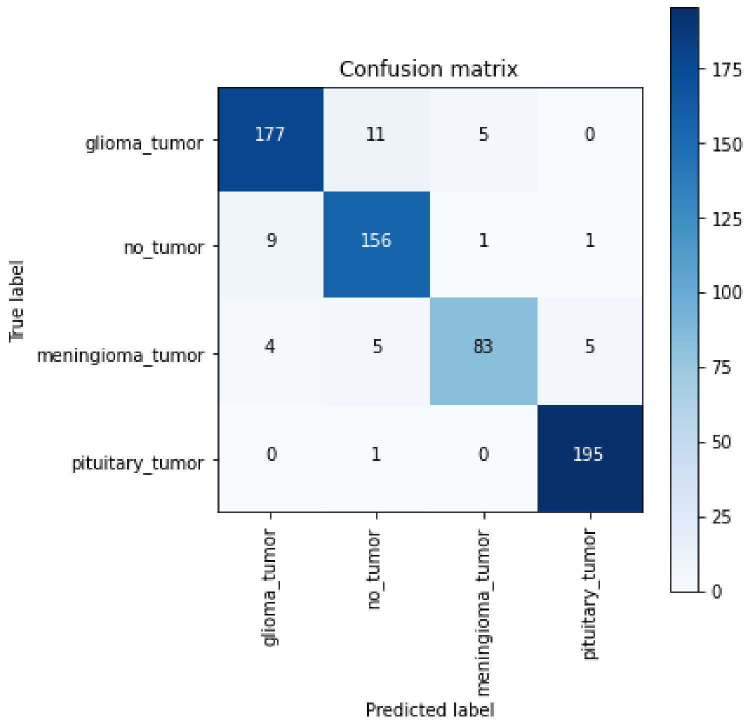

Figure 15: Confusion Matrix Of Experiment 3

```
# Classification Summary
print(classification_report(y_test, y_pred))
```

```
                  precision    recall  f1-score   support

    glioma_tumor       0.93      0.92      0.92       193
meningioma_tumor       0.90      0.93      0.92       167
        no_tumor       0.93      0.86      0.89        97
 pituitary_tumor       0.97      0.99      0.98       196

        accuracy                           0.94       653
       macro avg       0.93      0.93      0.93       653
    weighted avg       0.94      0.94      0.94       653
```

Figure 16: Result Of Experiment 3

6.4 Discussion

Authors in paper (Rasool et al.; 2022) suggested using Squeeze-Net and SVM with fine-tuning technique and as done in experiment 3 using the same dataset used in paper (Rasool et al.; 2022), the accuracy is coming around 93% and the result is also verified using another brain tumor classification dataset as done in Experiment 1 where accuracy is coming around 89% while the accuracy which the researchers of (Rasool et al.; 2022) are getting using Google-Net and SVM hybrid model is around 98%. The accuracy of the classification performed on the dataset dropped by a substantial amount. The reason for this is that SqueezeNet substituted the conventional 3 x 3 convolution kernels with a high number of 1 x 1 convolution kernels, which resulted in a relative loss of more extracted features. But after looking at the confusion matrix Google-Net and SVM hybrid model is better at classifying glioma and meningioma tumors while the Squeeze-Net and SVM model is better in classifying no_tumor and pituitary tumor so it can be said that the model Squeeze-Net and SVM using fine-tuning is equally good in classifying brain tumor images. The zero-filling technique consists of setting some of the coefficients of the 3x3 filters to zero, which reduces the number of parameters and computations in the expansion layer without significantly affecting the accuracy of the model. Specifically, setting the central element of the 3x3 filters to zero reduces the number of parameters in the expansion layer by a factor of 9. This reduction in parameters and computations is one of the key ways that SqueezeNet is able to achieve its high level of efficiency.

In this study for both the datasets the accuracy we are getting for each type of brain tumor is nearly the same which shows that the performance of the model is not getting affected by the factor of whether the dataset is balanced or not so it is not implemented for both the dataset during the research. Also as in many other papers, authors have been using GLCM as a feature extraction technique so an attempt has been in this paper to check its effectiveness which can be seen in experiment 2 but using the GLCM feature extraction technique with SVM classifier has not proven to be a good approach in classifying brain tumors which is giving only 51% accuracy.

7 Conclusion and Future Work

In this paper, the hybrid machine learning model is efficient in classifying brain tumor MRI images with 93% accuracy. According to the findings, the strategy that is suggested is the one that may provide the most desirable outcomes. This is due to the fact that the hybrid model that has been presented combines the benefits of Squeeze-automated Net's feature extraction capabilities with the classification prowess of SVM classifiers. Using the suggested approach, an inexperienced radiologist is just as capable of classifying the kind of brain tumor as an experienced one. As a result, the work that is being suggested has the potential to save thousands of lives.

The next stage would be to apply this model to a dataset that is much more extensive. If the data set were much bigger, the model could be trained using a greater number of examples, which would improve its ability to generalize. Another step that may be taken would be to take into account the various kinds of tumors, as well as their phases, to place an emphasis on early diagnosis.

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