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Brain Tumour Detection and Classification using Deep Convolutional Neural Network (DCNN)

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of brain cells. Manual method of classifying is time consuming and can be done at selective diagnostic centers only. Brain tumour classification is crucial task to do since treatment is based on different location and size of it. Magnetic
 Resonance Imaging (MRI) is most suitable way to do so. Hence there is a need to build such system which will automatically classify the brain tumour type based on input MR images only. The objective of the proposed system isto classify the brain tumour images into three sub-types: Meningioma, Glioma and Pituitary using convolutional neural network (CNN) and Support vector machine (SVM). Images from the dataset are downsized to reduce computation and some salt noise is added to make model robust and increase the dataset. The performance comparison is done on Google Colab and tensorflow platform in python language. Keywords : Brain Tumour, MRI, Classification, Support Vector Machine, Convolution Neural Network.

I. INTRODUCTION

Tumour is the undesired mass in the body. Brain tumour is the significant growth of brain cells. Manual method of classifying is time consuming and can be done at selective diagnostic centers only. Brain tumour classification is crucial task to do since treatment is based on different location and size of it. Magnetic Resonance Imaging (MRI) is most suitable way to do so. Hence there is a need to build such system which will automatically classify the brain tumour type based on input MR images only. The objective of the proposed system isto classify the brain tumour images into three sub-types: Meningioma, Glioma and Pituitary using convolutional neural network (CNN) and Support vector machine (SVM). Images from the dataset are downsized to reduce computation and some salt noise is added to make model robust and increase the dataset. The performance comparison is done on Google Colab and tensorflow platform in python language.

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In order to speed up the diagnosis and to serve as second decision for neurologists, this method is proposed. Since bio-medical images are difficult to analyze therefore CNN and SVM are chosen due to their classification based on depth of feature extraction. CNN does the extraction using convolution layers and as the depth increases level of feature goes higher. Whereas in SVM, features are extracted depends on type of texture or pattern in the image and classes which have similar features, can be classified easily.

Manual method of classifying is time consuming and can be done at selective diagnostic centers only. Brain tumour classification is crucial task to do since treatment is based on different location and size of it. Magnetic Resonance Imaging (MRI) is most suitable way to do so. Hence there is a need to build such system which will automatically classify the brain tumour type based on input MR images only. The objective of the proposed system isto classify the brain tumour images into three sub-types: Meningioma, Glioma and Pituitary using convolutional neural network (CNN) and Support vector machine (SVM).

The purpose of this project is to classify the brain tumor images into three sub-types: Meningioma, Glioma and Pituitary using convolutional neural network (CNN) and Support vector machine (SVM). Images from the dataset are downsized to reduce computation and some salt noise is added to make model robust and increase the dataset

II. RELATED WORK

The diagnosis and segmentation of brain tumors MR images troublesome using is а and significant undertaking in the clinical field. Early identification and limitation of cerebrum growths saves lives and gives clinicians the choices to pick powerful treatment choices sooner rather than later [1]. The growths are forerunners to disease, and endurance earlv rates are low. Hence.

identification and characterization of growths can save many lives [2]. To additionally use the 3D data implanted in such datasets, this paper proposes a multi-view dynamic combination structure (from now on alluded to as MVFusFra) to work on the presentation of mind growth division the proposed structure has three primary parts [3].

Recently, a system based on computer-assisted diagnosis has shown guarantee as an assistant to Magnetic Resonance Imaging (MRI) finding of mind growths. In current utilizations of pre-prepared models, highlights are typically separated from the lower layer, which is unique in relation to normal and clinical pictures [4]. A half breed include extraction strategy utilizing a Regularized Intensive Learning Machine (RILM) to foster a precise cerebrum cancer classifier [5].

A Cerebrum Cancer Division Calculation for Lost Mode. Because of the solid relationship between's different techniques, association models have been proposed to explicitly address the basic multi-source cooperation [6]. Existing examination on mind cancer division involves U-Net for cerebrum division, which growth has the issue of unfortunate decrease highlight extraction, bringing about loss of up testing data [7].In any case, MRI is generally utilized because of its better picture quality and absence of dependence on ionizing radiation. Deep Learning (DL) is a subfield of AI that has as of late shown Deep execution, especially in characterization and division issues [8]. Growths are uncommon and come in many structures, they are hard to recognize. by Magnetic These growths can be recognized Resonance Imaging (MRI), which assumes а significant part in cancer confinement, manual detection is time-consuming, troublesome and can be off base [9]. Although a few biomedical imaging techniques have been utilized to restrict growths, they miss the mark on Data pre processing Data segmentation Feature extraction Feature Selection



picture

handling

and

computer

vision

Sigmoid function Classification Risk level spatial to accurately delineate the boundary between brain tumors and normal brain tissue. Automated segmentation methods for brain tumors often use manually generated features. Likewise, traditional methods convolutional deep learning brain organizations, require a lot of marked information for preparing, which is frequently hard to get in the clinical field [11]. Various imaging modalities are utilized to analyse mind growths. MRI has been utilized for such undertakings in light of its unmatched picture quality [12]. How much applied electric field has been corresponded with antitumor reactions [13].However, peritumoraledema causes an electrical barrier around the tumor, thereby the intratumoral electric field [14]. The reducing U-Net framework is popular because it integrates feature information with high-level low-level feature information by using skip links [15], which greatly improves the accuracy of segmentation. A number of deep learning techniques based on transfer learning are analysed to detect brain tumors using several traditional classifiers. The findings depend on a named dataset of ordinary and unusual brain images [16]. Image segmentation is one of many fields that has seen new executions being created totake care of issues [17]. It is still difficult to pick different CNN designs, as every engineering displays different execution on the equivalent dataset. Given the intricacy of mind cancer and Alzheimer's sickness information, the goal of this study was to assess the reliance of CNNs on cerebrum X-ray in various prescient models. A mind Convolutional network-based convolutional neural network (CNBCN) with upgraded initiation capability for attractive reverberation imaging characterization of cerebrum growths. The organization structure is produced by а haphazardly created chart calculation [19] as opposed to being planned and upgraded physically. With the improvement of profound learning, CNN (Convolutional Neural Network) has accomplished superb execution in

[20].Convolutional Neural Networks (CNNs) for mind growth division are normally evolved utilizing entire attractive reverberation imaging (Xray) arrangements for preparing and derivation. Consequently, these calculations are not prepared for practical clinical situations, where some MRI sequences utilized for preparing might be lost during surmising [21]. To resolve the normal issues of inadequately huge cerebrum cancer datasets and fragmented picture designs, the expansion of mind MR pictures utilizing a pairwise Generative Adversary Network (GAN) model recommends growing the preparation dataset [22].An automated system incorporating a biochip, driver unit, and hardware tests the electrical opposition of human mind tissue to separate ordinary from cancer. Focusing on the low exactness of ordinary cerebrum growth recognition, this paper presents a technique consolidating multimodal data combination and convolutional brain network [24]. Proposes a strategy for mind growth identification. Finding precise pictures of mind growths from magnetic resonance imaging (MRI) chronicles can be an overwhelming errand for radiologists. Most web indexes recover pictures in view of customary literary techniques [25].Magnetic resonance imaging(MRI) is regularly used to recognize cerebrum cancers, however accomplishing high exactness and productivity stays significant test for most recently proposed а mechanized clinical findings [26]. Manual division is reliant upon clinical experience and is troublesome and tedious [27]. Contrasted with generally utilized perform multiple tasks models that a variational auto-encoder (VAE) incorporate decoder for recreating the information, multimodel highlights result from the utilization of picture combination as an extra formalism for include learning. Assists with accomplishing better mix. It very well may be valuable for multimodal picture division issues [28]. Given the difficulties of cancer biopsy, three-layered (3D) Magnetic resonance



imaging (MRI) is generally used to concentrate on cerebrum growths utilizing profound learning [29]. Clinical Picture Examination, however Organization Profundity Cutoff points Execution. Likewise significant is the way to accelerate data scattering and completely use all utilize all hierarchical features in the network [30].

2.1 Limitation of the research

- Most previous classifiers categorize tumour areas into benign and malignant.
- The classification rate of these methods is insufficient for tumour diagnosis
- The precision of tumour segmentation by conventional methods is low.
- Conventional methods only detect the inner regions of the tumour.
- The effect of brain tumors on stroke has not been analysed using conventional methods.

III. PROPOSED SYSTEM

The proposed system is to classify the brain tumour images into three sub-types: Meningioma, Glioma and Pituitary using convolutional neural network (CNN) and Support vector machine (SVM). Images from the dataset are downsized to reduce computation and some salt noise is added to make model robust and increase the dataset. The performance comparison is done on Google Colab and tensorflow platform in python language.



Fig 1: Brain tumour image classification system

Figure 1 shows the block diagram of the proposed system in which raw images are labeled and preprocessed to enhance the performance and robustness of the model. Then dataset split into training (60%), validation (20%) and test (20%) sets. Certain hyperparameters are tuned to make model more efficient and finally model is trained and tested. Performance computation is analyzed on the basis of precision, recall and accuracy.

3.1 CNN APPROACH

Convolutional Neural Network (ConvNet or CNN) well known neural network for specially image recognition and classification. CNN is highly excellent in extracting complex features for classifications. CNN consist of neurons where weight and bias can be learned. Each neuron receives some input; weighted sum is taken then given to the activation function. CNN uses successive convolution layer and non linear ReLU function to extract valuable feature with specific dimension [7] [8] [11]. Maxpooling layer is used to downsize the feature map. In Fully connected layer, each neuron is connected to every other neuron of previous dense layer. Back- propagation and gradient descent are used while training the network. Softmax function is probability distribution to limit all class output value between 0 and 1. CNN provides feature maps which helps neural network to learn small features of the image depending on the depth of hidden layers. Proposed architecture is as shown in Figure 2.



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Fig 2 : CNN Architecture

3.2 SVM Approach

Support vector classifier is a supervised learning algorithm that works on the feature matrix taken from the input images, recognize the patterns and finally find the maximum separated hyper plane three types of tumour. By combining the binary classification decision function; this classifier classifies three different types of tumor in brain. For multiclass classification support vector machine models are of two types namely: One versus One decomposition and one versus All decomposition [9]. Here, One versus All decomposition is used to classify the brain tumor of type Meningioma, Glioma, and Pituitary. By using One versus All decomposition, multiclass problem is being transformed into a series of binary subtasks and that is being trained by binary support vector machine (SVM). Linear SVM differ from polynomial SVM by a hyper









```
from PIL import Image
#import pandas as pd
import numpy as np
import os
import tensorflow as tf
import keras
import warnings
warnings.filterwarnings("ignore")

from google.colab import drive
drive.mount('/content/drive')

Mounted at /content/drive
```





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```
import keras
```

I

```
def cnn model(path loc):
   import tensorflow as tf
    import keras
    from keras.models import Sequential
   from keras.layers import Convolution2D
    from keras.layers import MaxPool2D
    from keras.layers import Flatten
   from keras.layers import Dense
   # Initializing CNN
   classifier = Sequential()
    # Step 1 : convolution
    classifier.add(Convolution2D(32,3,3,input_shape=(64,64,3),activation='relu')
    # Step 2 : Pooling
   classifier.add(MaxPool2D(pool size=(2,2)))
   # Adding second convolution layer.
   classifier.add(Convolution2D(64,3,3,activation='relu'))
   classifier.add(MaxPool2D(pool_size=(2,2)))
    # step 3 : flattening
   classifier.add(Flatten())
    # step 4 : Full connection
   classifier.add(Dense(output_dim= 128,activation='relu'))
```

Fig 5. Results screenshot

classifier.compile(optimizer='adam',metrics=['accuracy'],loss='categorical_crossentropy')

```
# fitting CNN to the images
from keras.preprocessing.image import ImageDataGenerator
train_datagen = ImageDataGenerator(rescale = 1./255, # image agumentation
                                shear_range = 0.2,
                                zoom_range = 0.2,
horizontal_flip = True)
test_datagen = ImageDataGenerator(rescale=1./255) # test data don't need much image agumentation.
import os
os.chdir(path_loc) # train and test path location
training_set = train_datagen.flow_from_directory('/content/drive/MyDrive/DeepLearning_MRI_Dataset/Train',
                                               target_size = (64, 64),
                                               batch_size = 32,
                                               class_mode = 'categorical')
test_set = test_datagen.flow_from_directory('/content/drive/MyDrive/DeepLearning_MRI_Dataset/Test',
                                          target_size = (64, 64),
                                         batch_size = 32,
class_mode = 'categorical')
# buliding model and performing model validation simultaneously
history=classifier.fit_generator(training_set,
                      steps_per_epoch = 40, # number of images to be taken from training data set.
nb_epoch = 50,
                      validation_data = test_set,
                      validation_steps = 10) # number of images to be taken from test data set.
```

Fig 6. Results screenshot

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Epoch	och 38/50	
40/40	/40 [======================] - 14s 352ms/step - loss: 0.4710 - accuracy: 0.7977 - val_1	loss: 0.4251 - val_accuracy: 0.6962
Epoch	och 39/50	
40/40	/40 [=======================] - 12s 301ms/step - loss: 0.4938 - accuracy: 0.7940 - val_1	loss: 0.4788 - val_accuracy: 0.7656
Epoch	och 40/50	
40/40	/40 [======================] - 11s 285ms/step - loss: 0.4579 - accuracy: 0.8090 - val_1	loss: 0.1394 - val_accuracy: 0.7440
Epoch	och 41/50	
40/40	/40 [======================] - 12s 298ms/step - loss: 0.4497 - accuracy: 0.8043 - val_	loss: 0.6165 - val_accuracy: 0.7437
Epoch	och 42/50	
40/40	/40 [======================] - 12s 289ms/step - loss: 0.4810 - accuracy: 0.8070 - val_1	loss: 0.1260 - val_accuracy: 0.7679
Epoch	och 43/50	
40/40	/40 [======================] - 12s 306ms/step - loss: 0.4307 - accuracy: 0.8289 - val_1	loss: 0.5867 - val_accuracy: 0.7844
Epoch	och 44/50	
40/40	/40 [======================] - 11s 283ms/step - loss: 0.4552 - accuracy: 0.8145 - val_3	loss: 0.8243 - val_accuracy: 0.7816
Epoch	och 45/50	
40/40	/40 [=======================] - 12s 305ms/step - loss: 0.4438 - accuracy: 0.8164 - val_1	loss: 0.3129 - val_accuracy: 0.8250
Epoch	och 46/50	
40/40	/40 [=======================] - 12s 290ms/step - loss: 0.4156 - accuracy: 0.8390 - val_1	loss: 1.2564 - val_accuracy: 0.7270
Epoch	och 47/50	
40/40	/40 [=======================] - 12s 302ms/step - loss: 0.4205 - accuracy: 0.8295 - val_1	loss: 0.8527 - val_accuracy: 0.7594
Epoch	och 48/50	
40/40	/40 [=======================] - 12s 288ms/step - loss: 0.4376 - accuracy: 0.8180 - val_1	loss: 0.7462 - val_accuracy: 0.7782
Epoch	och 49/50	
40/40	/40 [=======================] - 12s 309ms/step - loss: 0.4410 - accuracy: 0.8078 - val_	loss: 0.6439 - val_accuracy: 0.7563
Epoch	och 50/50	
40/40	/40 [========================] - 11s 285ms/step - loss: 0.4293 - accuracy: 0.8319 - val_l	loss: 0.2665 - val_accuracy: 0.7850

Fig 7. Results screenshot

```
if result[0]==0:
    print("This image belongs to glioma category")
elif result[0]==1:
    print("This image belongs to menigioma category")
elif result[0]==2:
    print(" This image belongs to pituitary category")
```

This image belongs to glioma category

Fig 8. Results screenshot

```
# check the accuracy on the training set
print(svc_model.score(X_train, y_train))
print(svc_model.score(X_test, y_test))
```

0.7248134328358209 0.7402173913043478

Fig 9. Results screenshot

V. CONCLUSION

Experimental results from the three classifiers namely, Linear SVM, Polynomial SVM and CNN for the classification of Brain Tumour using MR images are tabulated as shown in Table II. Here, value of recall, precision and accuracy is highest for CNN. The bar graph of the accuracy of all classifiers over four parameters namely: overall accuracy, and three class specific accuracy like Specific Meningioma, Specific Glioma and Specific Pituitary shown in Fig 8. It is observed that Polynomial SVM is marginally better than Linear SVM but CNN perform much better than Polynomial SVM. So it is concluded that CNN is the best option for the most Fig. 8: Accuracy Graph precise and reliable classification

VI. FUTURE WORK

In the future work, accuracy of the SVM model can be increased by suitable features selection techniques.



Grading of tumour can also be classified with adequate available datasets. Other classifier can be used for better analysis.

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