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**Research Paper****CNN-based Binary and Categorical Model to Detect Tumor from MR Images****Aparna Datta<sup>1\*</sup>**, **Pritam Mukherjee<sup>2</sup>**, **Gourab Paul<sup>3</sup>**<sup>1,2,3</sup>Master of Computer Application, Meghnad Saha Institute of Technology, Kolkata, India\*Corresponding Author: [sarkar23aparna@gmail.com](mailto:sarkar23aparna@gmail.com)

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**Abstract:** Detecting Brain tumors through human eye inspection has a probability of errors in analysis and a higher number of MRI reports cannot be inspected in a feasible amount of time. Thus, we need an easier automated approach towards this, that can be easily used and can give accurate results in Tumor detection. In this paper, we have implemented a Machine Learning Model based on Convolutional Neural Network, with the help of Global Average Pooling to fulfill this goal. Here we have two models, where one can do a binary classification of the images to detect if they have a trace of tumor in the MR Images or not, and another model that can detect the type of Tumor categorically among 3 types which are Glioma, Meningioma, and Pituitary. This model has acquired an accuracy score of 96.02% and 99.46% in the Binary and Categorical Models respectively.

**Keywords:** CNN, Neural Network, Global Average Pooling, MRI, Batch Normalization, Max Pooling, Dropout, Dense layer.

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**1. Introduction**

Cells are the smallest unit of a living organism. In order to carry out the chores of the body, every cell has a specific function. Cells increase in numbers by dividing themselves in an orderly manner with limited recursions. The new cells either replace the old cells around them or fulfill the requirement of newer cells. But in case of a cell becoming defective or outgrowing and dividing excessively, programmed cell death comes into play. For a cell that is damaged or not repairable, it can be helped to self-destruct by its lysosome, and the process by which this happens is called Programmed cell death or apoptosis. But when this programmed death of the cell or apoptosis does not occur, the cells keep on dividing without any order. The masses of tissues that are formed from all these cells are called tumors. Tumors can be either Benign or Malignant, depending upon the formation, position, and state. Malignant tumors may lead to the formation of cancer, while benign tumors are not cancerous. As malignant tumors form and begin invading other organs, tissues, and even the bloodstream, cancer develops and spreads. Such Tumors can occur inside our skull which are called brain tumors. For the rigidity and limited volume of the human skull, depending on the affected part of the brain, abnormal growths will affect the functions of the human body.

From the head, it can also spread into other necessary organs throughout the body affecting all the necessary functions to stay alive.

The vital fields of diagnosis of brain tumors include various imaging processes such as X-Ray, MRI, CT-Scan, PET/CT

scan, etc. For general identification, Magnetic Resonance Imaging (MRI) is one of the most popular and accurate methods, also feature detection is much easier for general identification.

Magnetic Resonance Imaging (MRI) is a non-invasive imaging technique to image the organs and soft tissues of our body. As it uses non-ionizing radiation, the tissues are not subjected to any form of radiation defects. The MR Image is generated from magnetic field vectors of appropriately excited hydrogen atoms of the water molecules in our cells, using a strong magnetic field upon the human body, and then the image is generated by passing radio frequency pulses through those hydrogen atoms' nuclei.

Currently, an inspection of MRI via human eyes is a conventional method of detecting tumors, but this method is excessively time-consuming and totally infeasible, especially in the case of higher numbers of data sets. Thus, to analyze larger numbers of MRI scans in a feasible time, accurately and irrespective of the noise levels, Automated Tumor Detection systems are needed with extremely high accuracy levels being a matter of human life.

When it comes to MR image classification, A variety of supervised learning methods, such as ANNs (Artificial Neural Network), SVM (Support Vector Machine), and unsupervised learning techniques such as SOM (Self-Organization Map), FCM (Fuzzy C-Means), etc. are used by various researchers of this field.

In this paper, a Supervised Automated Machine Learning model is discussed to first identify if the MRI contains

symptoms of a Brain Tumor, and then identify which sort of tumor it is among Glioma, Meningioma, and Pituitary adenoma.

## 2. Related Work

Working with MRI reports of various patients is not a new field of interest, instead, there were various previous approaches in this field of study using multiple different types of Neural Networks and Machine Learning algorithms. A few of them are discussed in short below, -

Table 1. Related Work

Ref. No.	Authors	Publication	Date	Method/Algorithm	Accuracy	Data set Size
1.	Phaye SS, et al.	IIT Ropar, Punjab, India	10 May, 2018	DCNet and DCNet++	93.04%/95.03%	3064
2.	M Siar, et al.	ICCKE 2019, Mashhad, Iran	24 Oct, 2019	CNN	99.12%	1321
3.	Zhao, et al.	INRC, Italy	26 Nov, 2021	CNN	94.64%	2870
4.	Ercan, et al.	Çukurova University, Turkey	11 Dec, 2019	Faster R-CNN	91.66	3064
5.	M.O. Khairandish, et al.	IRBM 2020	26 April, 2020	CNN-SVM	98.49%	285
6.	Abdu Gumei, et al.	IEEE Access 2019	15 Feb, 2019	PCA and RELM	91.51%-94.23%	3064
7.	Ali Ari, et al.	TJEECS 2018, TÜBİTAK, Turkey	02 Jan, 2018	ELM-LRF	97.18%	~212
8.	Chen g J, et al.	PLOS one 2015	8 Oct, 2015	SPM	87.54%, 89.72% and 91.28%	3064
9.	W. Gao, et al.	SAI Computing Conference 2016	13 Jul, 2016	2D and 3D CNN	95%	~3600
10.	Yan Xu, et al.	ICASSP 2015, South Brisbane, Australia	19 April, 2015	CNN	97.5%	101

## 3. Theory/Calculation

Knowing all that we know from the literature review on this field of research, a fully automated machine learning model to detect tumors from MRI reports, is utterly needed and being studied. Detection of specific tumor types or the MRIs that do not contain any kind of tumor, requires feature extraction and classification techniques using various machine learning algorithms. In this paper, one such mechanism is discussed. To discuss the Methodology and

Procedural Designs of the proposed model, we first must know a few key theories and calculations, such as, -

**Conv2D:** The convolutional layer is a fundamental element of the CNN model. It employs a mathematical technique to produce a modified feature map by means of a dot product between two matrices. A total of 4 Conv2D layers are used here without changing the padding of any of them to avoid loss of details. The following equation describes the convolutional layer, -

$$c(h, d) = (k * f)(h, d) = \sum_i \sum_j k(h - i, d - j) f(i, j)$$

Formula 1. Conv2D

where, K is the image with a size of (h, d), and (i, j) corresponds to the kernel size value with a f-number of filters. The way the convolutional approach to generate the feature map, -

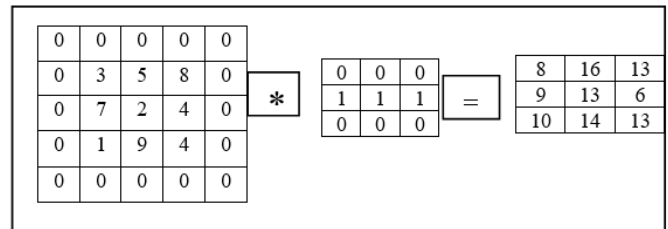


Fig 1. Matrix Multiplication in Conv2D layer

As a means of activation function, the Rectified Linear Unit (ReLU) is implemented, which carries out non-linear operations within the convolutional layer. Through the backpropagation process, the utilization of the ReLU activation function facilitates the resolution of the gradient vanishing predicament.

**Batch Normalization:** Batch normalization constitutes a layer that lets neural networks every layer have a greater degree of independence in their learning processes. It serves the purpose of standardizing the output of the preceding layers, thereby normalizing the activations in the input layer. Leveraging batch normalization contributes towards enhancing the efficiency of learning, while also serving as a regularization technique to mitigate the overfitting of the model. Here, 4 layers of Batch Normalization is used after each convolutional 2D layer.

**Max Pooling 2D:** Max pooling is a type of pooling operation whereby the highest element within a particular region of the feature map that is covered by the filter is selected. As a result, the output that follows the max-pooling layer will comprise a feature map that is replete with the most salient features of the preceding feature map.

$$f(z) = \max(0, z)$$

Formula 2. Max Pooling 2D

**Global Average Pooling 2D:** Global Average Pooling is a pooling mechanism that has been formulated to supplant the fully connected layers in conventional Convolutional Neural Networks. Before inputting the data into the dropout layer,

the GlobalAveragePooling2D layer is employed here to transform the multidimensional data into a one-dimensional vector.

**Dropout:** The Dropout layer is a mechanism that eliminates the contribution of certain neurons toward the next layer while leaving others unaltered. It can be applied to the input vector to nullify some of its characteristics, or to a hidden layer to nullify some hidden neurons.

**Dense:** The resultant output of the dense layer comprises an 'm' dimensional vector, primarily utilized for dimensionality alteration. Moreover, the dense layer applies various operations, such as rotation, scaling, and translation, to the vector

### 4. Experimental Method

The continuous experiments on the topic at hand has led us to this specific model that is proposed bellow, -

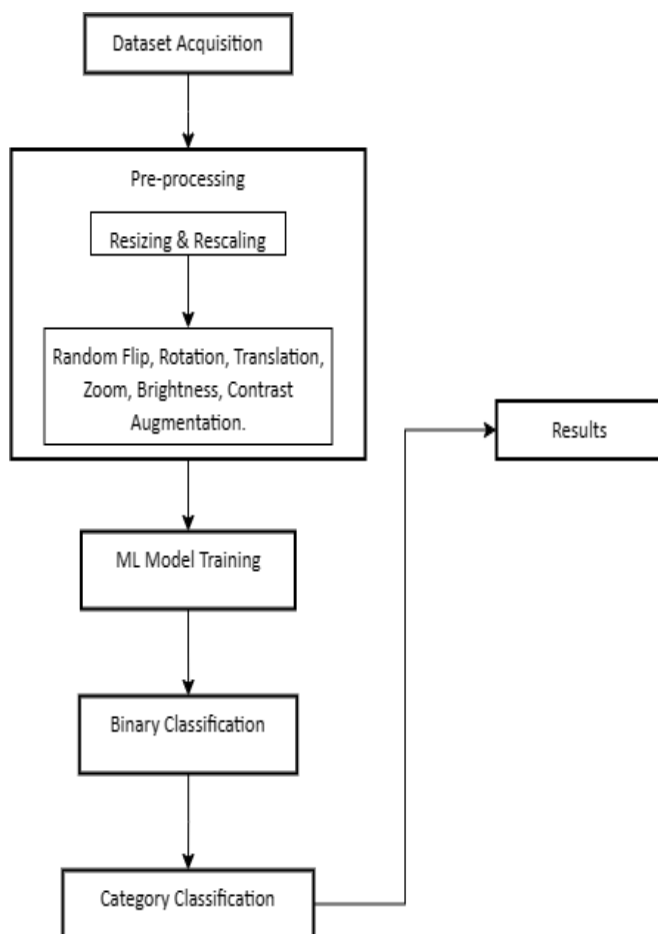


Fig 2. Method Diagram

**A. Dataset Acquisition:** The MR Images are acquired with the help of open libraries of online databases (here <https://www.kaggle.com/datasets/masoudnickparvar/brain-tumor-mri-dataset?select=Training>), DOI: 10.34740/kaggle/dsv/2645886.

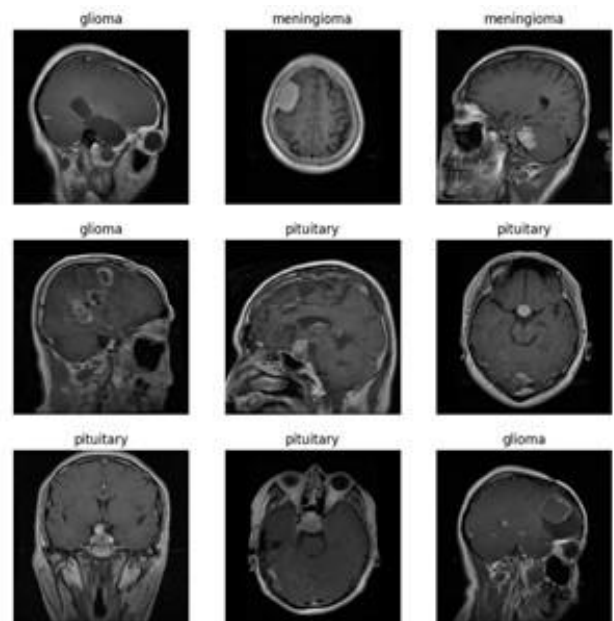


Fig 3. Partial Categorical Dataset

The dataset being comparatively smaller than the industrial-level approaches, it was determined to segregate a dataset segment for the purpose of creating a validation dataset, while utilizing the remaining portion for a training dataset. A total of 5712 images are there in Categorical Training Set, including MRIs of Glioma, Meningioma, and Pituitary tumors. In the case of the Binary model, it is 6117 in Training Set. In the Testing Set, there are a total of 1311 images of different categories and 906 for the binary model. In total 7023 MRIs of various patients. The no-tumor class images were taken from the Br35H dataset.

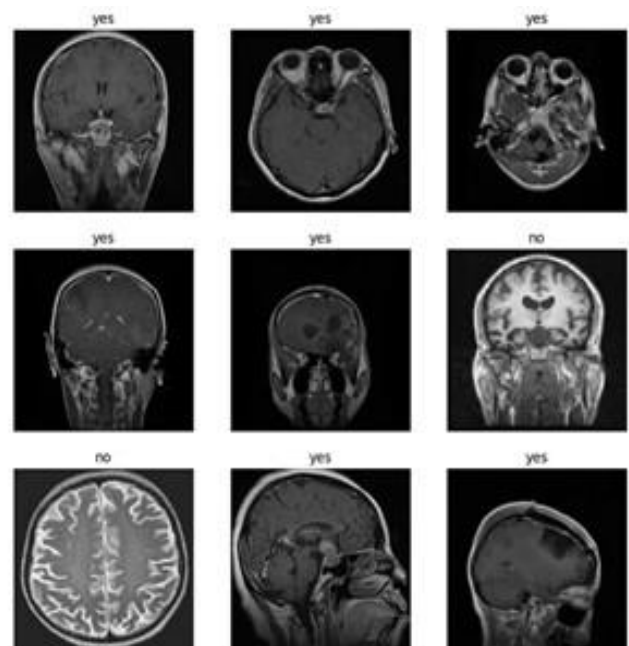


Fig 4. Partial Binary Dataset

In the first ML model we are detecting if the testing images contain any sort of tumor and in the second ML model, we

used these same images to classify which specific kind of tumor the MRI contains.

**B. Pre-processing:** Preprocessing was used for providing improvement in feature detection of the ML model, which is done here by providing different perspectives to the ML model to extract as much features possible from every single image. There are two levels of Pre-processing done in this model, -

i. **Image-Preprocessing:** Here, the images are first resized to (64,64) to provide an even size to compare all the images impartially. Then the images are rescaled by providing a value between 0 to 1, by dividing every pixel by 255, the maximum value for it being completely white. This provides ease in arithmetic calculations and comparisons and also more digestible data.

ii. **Data-Augmentation:** Here, the images are randomly Flipped, Rotated, Translated, Zoomed, Brightened, and Contrasted to feed more and more variable data from every image to the ML model. This also helps in providing a real-life like scenario where provided images can sometimes be distorted or falsely taken or placed.

**C. ML Model Training:** After Pre-processing all the images, training the model will be done with Conv2D, MaxPooling2D, and Batch Normalization layers, and finally a GlobalAveragePooling2D layer is used before the dropout and dense layer. After the training ends, certain activation functions finally create the connection between nodes by activating neurons to actually predict the result.

These Activation Functions play a pivotal role in determining the activation status of a neuron, here only two are needed, one is sigmoid, in case of binary classification and another is softmax, in case of categorical classification.

**Sigmoid** - The utilization of the sigmoid function is primarily justified by its domain existing within the interval of (0 to 1). The Sigmoid function is as follows, -

$$\text{Formula 3. Sigmoid} \\ \sigma(z) = \frac{1}{1 + e^{-z}}$$

**Softmax** - The softmax function is a more generalized logistic activation function which is used for multiclass classification. The Softmax function is as follows, -

$$s(y)_i = \frac{\exp(y_i)}{\sum_{j=1}^n \exp(y_j)}$$

Formula 4. Softmax

And finally, Adam optimizer is used to optimize the outputs which is an extended version of the Stochastic Gradient Decent.

## 5. Results and Discussion

After going through the dataset using both the algorithms mentioned earlier, we have two sets of results, where one is

of our binary classification of MRIs where the result is either the MRI contains a tumor or not. And another classification is categorical where the MRI contains a specific type of tumor and that is classified by the machine learning model.

Here we have different architectures and hyper-parameters tested and tied before reaching the final model, -

Table 2. Architectures and Hyper-Parameters

Factors	Values
Number of Convolutional + ReLU Layers	3,4,5,6
Number of Dropout Layers	1
Maximum epochs	50,100,150,200,500
Number of Convolutional Kernel	16,32,64,128,256,512
Kernel Size	3.5
Pooling Layer	MaxPooling,GlobalAveragePooling
Pooling Layer Window Size	2
Optimizer	Adam
Mini-Batch Size	8,16,32
Dropout Rate	0.2,0.3,0.4
Initial Learning Rate	0.001

In the following figures we have the Training and Validation Accuracy report and Loss report of the Binary Classification Model, -

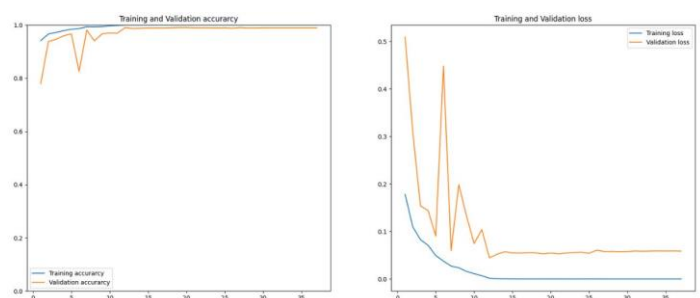


Fig 5. Accuracy Chart (Binary)

In the following figures we have the model summary of the Binary Classification Model, -

Table 3. Model Summary (Binary)

Layer (type)	Output Shape	Param #
sequential (Sequential)	(None, 64, 64, 3)	0
resizing (Resizing)	(None, 64, 64, 3)	0
rescaling (Rescaling)	(None, 64, 64, 3)	0
conv2d (Conv2D)	(None, 64, 64, 32)	896
batch_normalization (Batch Normalization)	(None, 64, 64, 32)	128
max_pooling2d (MaxPooling2D)	(None, 32, 32, 32)	0
conv2d_1 (Conv2D)	(None, 32, 32, 64)	18496



batch_normalization_1 (Batch Normalization)	(None, 32, 32, 64)	256
max_pooling2d_1 (MaxPooling 2D)	(None, 16, 16, 64)	0
conv2d_2 (Conv2D)	(None, 16, 16, 128)	73856
batch_normalization_2 (Batch Normalization)	(None, 16, 16, 128)	512
max_pooling2d_2 (MaxPooling 2D)	(None, 8, 8, 128)	0
conv2d_3 (Conv2D)	(None, 8, 8, 256)	295168
batch_normalization_3 (Batch Normalization)	(None, 8, 8, 256)	1024
max_pooling2d_3 (MaxPooling 2D)	(None, 4, 4, 256)	0
global_average_pooling2d (Global Average Pooling 2D)	(None, 256)	0
dropout (Dropout)	(None, 256)	0
dense (Dense)	(None, 3)	771

In the following figures we have the Training and Validation Accuracy report and Loss report of the Categorical Classification Model, -

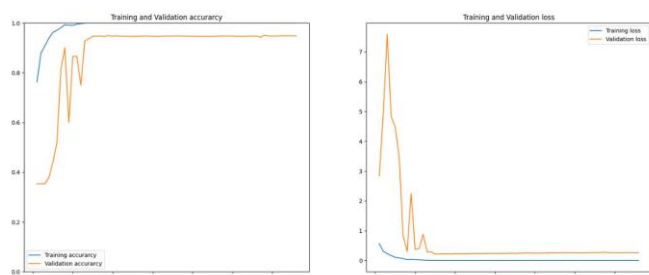


Fig 6. Accuracy Chart (Categorical)

In the following figures we have the model summary of the Categorical Classification Model, -

Table 4. Model Summary (Categorical)

Layer (type)	Output Shape	Param#
sequential (Sequential)	(None, 64, 64, 3)	0
resizing (Resizing)	(None, 64, 64, 3)	0
rescaling (Rescaling)	(None, 64, 64, 3)	0
conv2d (Conv2D)	(None, 64, 64, 32)	896
batch_normalization (Batch Normalization)	(None, 64, 64, 32)	128
max_pooling2d (MaxPooling 2D)	(None, 32, 32, 32)	0
conv2d_1 (Conv2D)	(None, 32, 32, 64)	18496
batch_normalization_1 (Batch Normalization)	(None, 32, 32, 64)	256
max_pooling2d_1 (MaxPooling 2D)	(None, 16, 16, 64)	0
conv2d_2 (Conv2D)	(None, 16, 16, 128)	73856
batch_normalization_2 (Batch Normalization)	(None, 16, 16, 128)	512

max_pooling2d_2 (MaxPooling 2D)	(None, 8, 8, 128)	0
conv2d_3 (Conv2D)	(None, 8, 8, 256)	295168
batch_normalization_3 (Batch Normalization)	(None, 8, 8, 256)	1024
max_pooling2d_3 (MaxPooling 2D)	(None, 4, 4, 256)	0
global_average_pooling2d (Global Average Pooling 2D)	(None, 256)	0
dropout (Dropout)	(None, 256)	0
output (Dense)	(None, 1)	257

Finally, the Testing Accuracy in the Binary Model came up to 99.46% with loss of 2.50, -

```
Found 1311 files belonging to 2 classes.
Test accuracy: 99.46605563163757
Test loss: 2.5080887600779533
```

Result 1. Testing Accuracy of Binary Model

Total Params: 390,593

Trainable Params: 389,633

Non-Trainable Params: 960

And, the Testing Accuracy in the Categorical Model came up to 96.02% with loss of 14.87, -

```
Found 906 files belonging to 3 classes.
Test accuracy: 96.02649211883545
Test loss: 14.870122075080872
```

Result 2. Testing Accuracy of Categorical Model

Total Params: 391,107

Trainable Params: 390,147

Non-Trainable Params: 960

## 6. Conclusion and Future Scope

Concluding the study, we have come to the agreement that medical analysis can be tremendously helped with the help of these kinds of Classification Models in a wide spectrum. Our excellent test accuracy is dependent on the use of CNN in this model. This accuracy could further be upscaled with better and more organized datasets that could be archived from hospitals and other medical centers.

Still, we maintained a higher range of accuracy against most of the recent models, thus this gives hope for planning future scopes around this model. This machine learning model can later be implemented in mobile applications or stationary devices to scan MR Images directly from their electro-magnetic input devices and prov

### Data Availability

The MR Images are acquired from a publicly available online database here, -

<https://www.kaggle.com/datasets/masoudnickparvar/brain-tumor-mri-dataset?select=Training>

DOI: 10.34740/kaggle/dsv/2645886.

### Conflict of Interest

There is no conflict of interest.

### Funding Source

None

### Authors' Contributions

Aparna Datta- Detailed Analysis of various approaches on this topic.

Pritam Mukherjee –Collection of information and build material, mathematical explanations, and core methodologies.  
Gourab Paul – Understanding the mechanics of Machine Learning and implementing the methods with various tries and error-checking, Finding resources and datasets, and improvement in base code.

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