Brain Tumor Classification Using Modified ResNet50V2 Deep Learning Model

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Abstract: Accurate diagnosis and categorization of brain tumours are very necessary for establishing optimal treatment choices and forecasting the patient's probable prognosis. The histopathological analysis of biopsy specimens is still the gold standard for identifying and categorizing brain tumours in today's medical environment. The strategy that is now being used is one that is invasive, time-consuming, and prone to human error. Because of these limitations, it is essential to use a completely automated method for multi-classification of brain tumours. The objective of this paper is to create a multi-classification of brain tumours using modified ResNet0V2 deep learning model. The accuracy of the traditional model has been improved by the addition of dropout layers, max pooling, and batch normalisation. Batch normalisation is used to normalise the activations of the preceding layer by scaling and changing their values to have zero mean and unit variance. This is accomplished by altering the scaling factor. Because of this, the impact of the internal covariate shift is reduced, training is sped up, the stability of the model is improved, and the performance of the model in generalization is elevated. The use of max pooling helps to minimise the number of parameters in the model, which in turn makes the model more computationally efficient. Max pooling also helps to improve the model's resilience to relatively minor shifts in the input. Dropout, on the other hand, helps to minimize overfitting by reducing the co-adaptation between neurons. This, in turn, forces the network to acquire characteristics that are more robust and generalizable. The proposed model was able to attain an accuracy in classification of 96.34% as a consequence of these adjustments.

Keywords: Brain tumor classification, ResNet50V2, batch normalization, maxpooling, droupout

1. INTRODUCTION (HEADING 1)

Brain tumour is an abnormal proliferation of cells in the brain [1]. It can be either benign (non-cancerous) or malignant (cancerous). The symptoms of a brain tumor may vary greatly depending on where the tumour is located and how large it is. Headaches, seizures, abnormalities in vision or hearing, trouble with coordination and balance, changes in mood or behaviour, and memory or cognitive issues are some of the more prevalent symptoms [2]. Imaging examinations, such as MRI or CT scans, and occasionally a biopsy or other tests are required to diagnose a brain tumour. The kind of tumour and its grade may be determined from the results of these tests. The treatment of a brain tumour is dependent on a number of criteria, the most important of which are the kind, location, and severity of the tumour, as well as the patient's age and general state of health. Surgical intervention, radiation therapy,

chemotherapy, and/or targeted therapy are some of the potential treatment options.

Brain tumors are a significant health concern in India, with an estimated incidence rate of around 2.5 to 3.5 per 100,000 population per year, according to the Indian Council of Medical Research (ICMR). After leukaemia, brain tumours are the form of cancer that affects children and young people in India. According to the National Cancer Registry Programme (NCRP) of India, the incidence of brain and nervous system tumors in India has been increasing over the years, with an estimated 36,000 new cases reported in 2020. Gliomas are tumours that originate in the brain or spinal cord and account for around forty percent of all brain cancers, are the most frequent kind of brain tumour. Survival rates for those diagnosed with brain tumours in India vary depending on the kind and stage of the disease, but in general, they are lower than in nations with higher levels of affluence. The five-year rate

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of survival for brain tumour patients in India is reportedly between 20 and 30 percent, according to certain estimates.

It is very important to discover a brain tumour as early as possible since doing so may enhance treatment results as well as the patient's quality of life [3]. It is critical to detect brain tumours as early as possible because this increases the number of treatment options available to the patient. Some of these options include surgical removal of the tumour, radiation therapy, chemotherapy, or a combination of these treatments. Early detection of brain tumours is extremely important. These treatments can be more effective when the tumor is smaller and has not yet spread to other areas of the brain. Early detection can improve the prognosis for a person with a brain tumor. With a smaller tumor size, the chances of successful treatment and recovery are higher. If a brain tumor is not detected early, it can grow and press on surrounding brain tissue, leading to complications such as seizures, memory loss, and difficulty with speech and movement. Those who have brain tumours may benefit from earlier diagnosis and treatment, which may lessen the severity of their symptoms and enhance their quality of life. This can include managing pain, reducing the risk of disability, and improving cognitive and emotional well-being.

There is active research being done in the domain of deep learning for the identification and classification of brain tumours, which has the potential to increase the accuracy as well as the efficiency of tumour diagnosis [4-6]. Deep learning is a part of machine learning that makes use of neural networks to learn patterns as well as characteristics from data [7-8]. It has been demonstrated that it can achieve state-of-the-art performance across a variety of image recognition tasks, such as medical imaging. Deep learning is a branch of machine learning that makes use of neural networks to learn patterns as well as characteristics from data.

Deep learning presents a number of challenges when it comes to the detection and classification of brain tumours. These obstacles include the requirement for large amounts of annotated data, the possibility of class imbalance (that is, more examples of one type of tumour than another), and the possibility of both false positives and false negatives. Addressing these challenges typically involves using techniques such as data augmentation, class weighting, and ensembling multiple models. In spite of these obstacles, there have been a number of promising studies on brain tumour detection and categorization using deep learning, and it is probable that this field of study will continue to expand and develop over the next several years.

2.   LITERATURE

Arshia Rehman et al [9] conducted three tests to identify brain malignancies such meningiomas, gliomas, and pituitary tumours using three different convolutional neural network designs (AlexNet, GoogLeNet, and VGGNet). After that, each researcher studies the transfer learning procedures, also known as fine-tune and freeze, utilising the MRI slices of such brain tumour dataset that can be found on Figshare. The data augmentation techniques are applied to the MRI slices in order to enhance the dataset samples as well as lower the chance of over-fitting.

Zar Nawab Khan Swati et al [10] We used a deep CNN model that had previously been trained, and we proposed a strategy to fine-tuning that was block-by-block and based upon transfer learning. The proposed method is evaluated with the use of a dataset consisting of T1-weighted contrast-enhanced magnetic resonance imaging (CE-MRI).

Sarah Ali Abdelaziz Ismael et al [11] provided a better strategy for categorising different kinds of brain tumours using residual networks. The authors put the suggested model to the test using a standard dataset that contains 3064 MRI images of three distinct types of brain tumours (Meningiomas, Gliomas, as well as Pituitary tumors). A table-based critical examination of the Deep Learning algorithms provided in the aforementioned research publications (2015–2020) will be carried out. In conclusion, this section will discuss both the positive and negative aspects of deep neural networks [12].

Jyostna Devi Bodapati et al [13] proposed a concept for a two-channel deep neural network which is more malleable and would be more effective at classifying tumours. At the beginning, InceptionResNetV2 and Xception networks' convolution blocks are used to extract local feature representations, which are then vectorized using suggested pooling-based approaches. A suggested attention mechanism allows for greater emphasis on tumour areas and decreased focus on non-tumor parts, thereby assisting in identifying the kind of tumour that is present in the pictures. The end-to-end cooperative training of two different sets of tumour image presentations is made possible by the two-channel model that was introduced. This helps the model achieve great generalisation.

Mohamed A. Naser et al [14] introduced a deep learning technique that combines transfer learning with a pre-trained convolution-base of Vgg16 and a fully connected classifier that makes use of convolutional neural networks (CNN) dependent on the U-net for the purpose of tumour segmentation and tumour grading. For the purposes of training and validating the segmentation and grading models, almost an identical pipeline of T1-precontrast, fluid attenuated inversion recovery (FLAIR), as well as T1-postcontrast MRI images of 110 patients with lower-grade glioma (LGG) is employed.

Javaria Amin et al [15] provided a comprehensive brain tumour detection literature for researchers. In this investigation, we looked at the histology of brain tumours, as well as publicly available datasets, enhancement techniques, segmentation, feature extraction, deep

learning, classification, transfer learning, as well as quantum machine learning.

Muhammad Imran Sharif et al [16] proposed an innovative method of automated deep learning for the classification of multiclass brain tumours. In order to put the recommended technique into action, the Densenet201 Pre-Trained Deep Learning Model is first modified, and then it is trained using a deep transfer of imbalanced data learning. The features of the trained model are obtained from the average pool layer, which has the very comprehensive information about each kind of tumour. This layer also contains the information that was used to train the model. Due to the unfortunate fact that the qualities of this layer are insufficient for producing an appropriate classification, two methods for selecting features are discussed below. The first and second strategies, respectively, are known as Entropy-Kurtosis-based High Feature Values (EKbHFV) as well as a Modified Genetic Algorithm (MGA) Depending on Metaheuristics. The newly offered threshold function is an additional step in refining the GA's selected properties.

Navid Ghassemi et al [17] presented an innovative deep learning approach for the categorization of tumours using MR images. A deep neural network has its convolutional layers originally pre-trained as a discriminator in a generative adversarial network (GAN) on many datasets of magnetic resonance (MR) images in order to extract robust features and comprehend the structure of MR pictures. After this, the fully connected layers of the deep network are altered, and the network as a whole is taught to act as a classifier so that it can discern between three distinct types of tumours. Six layers and around 1.7 million weight parameters are included in the deep neural network classifier. It is possible to avoid the network from overtraining on a very small dataset by pre-training a GAN to act as a discriminator. This may be done in combination with other methods, such as data augmentations (picture rotation and mirroring), and dropout.

Rajat Mehrotra et al [18] suggested that an AI-based classification of BT utilising Deep Learning Algorithms might be employed in the classification of various types of brain tumours by trying to make use of datasets that are openly accessible to the general public. This would allow for the classification of different types of brain tumours. The following categories are used to classify BTs within these datasets: (malignant and benign). The T1-weighted images that are included in the datasets come in a total of 696 pieces for the sake of testing.

S. Deepak et al [19] designed a new combination of features from a support vector machine (SVM) and features from a convolutional neural network (CNN) in order to classify the medical images. The completely automated method is assessed by utilising an available dataset from Figshare that contains MRI scans of all three different kinds of brain tumours. CNN was designed specifically for the purpose of gleaning information from MRI images of the human brain. In order to get better overall performance, a multiclass SVM is used after being paired with CNN features. For the whole of the testing and evaluation that was performed on the integrated system, a method known as fivefold cross-validation was used.

R. Vimal Kurup et al [20] investigated how the categorization of diseases is affected by the approaches used to preprocess data. The condition of concern for this particular piece of research is a brain tumour. There are three major categories of brain tumours that have the potential to form. These include gliomas, meningiomas, and pituitary tumours. The possibility that a successful therapy might be achieved by early detection of a certain form of brain tumour serves as the impetus behind this endeavour. From the point of view of image processing, there are a few different approaches that may tackle the issue of illness categorization. On the other hand, one of the most cutting-edge and well-known deep learning algorithms is referred to it as Convolutional Neural Networks (CNN), as well as its principal application is the task of classifying photographs. The traditional CNN needs a significant quantity of data that has been annotated, which presents a problem in the medical industry. This disadvantage can be solved with Capsulenet. As a result, the capsulenet was chosen as the categorization method for brain tumours in this study.

3. PROPOSED MODIFIED RESNET50v2 DEEP LEARNING MODEL

Deep learning Convolutional neural networks (CNNs) are used to examine MRI scans of the brain in order to identify the presence of malignancies. The objective of the classification is to determine with a high degree of precision, the kind of tumour that may be seen in the MRI image (for example, glioma, meningioma, or pituitary adenoma). It is necessary to have a big dataset of MRI pictures together with their accompanying labels (which indicate the existence and kind of tumour) in order to train a CNN for the classification of brain tumour MRI images. The images may be preprocessed using techniques such as normalization, intensity normalization, or cropping to ensure they are consistent in size and quality. After this step, the dataset is partitioned into a training set, a validation set, as well as a test set.

The CNN is trained with the help of the training set as well as the labels that correlate to it. The CNN is made up of many layers, including fully connected layers, pooling layers, and convolutional layers. The final image categorization is carried out by the dense layers, whereas the convolutional layers are responsible for extracting features from the MRI images. After that, the accuracy of the CNN is assessed with the help of the validation set, and the hyper parameters of the CNN are adjusted accordingly. Once the CNN has been trained and validated, it can be

tested using the test set to evaluate its performance on new, unseen data.

A. *Proposed modified ResNet50V2 Models*

In the proposed framework, image classification is performed with the help of ResNet50v2, which is an architecture that falls under the category of CNN. It is a modification of the ResNet50 framework that was first released in the year 2015. The ResNet50v2 design has 50 layers, and it makes use of skip connections to prevent the network from facing the vanishing gradient problem while it is learning deeper representations. By the use of skip connections, the output of one layer may be connected to the input of a layer that is located two or three levels further down in the network. This permits information to avoid layers that may otherwise cause the gradient to become too narrow during backpropagation, which can slow down or even prevent learning from occurring.

In some of its layers, ResNet50v2 makes use of an architecture known as a "bottleneck," which is one of the most important new features. The operations that make up a bottleneck layer are performed in the following order:

1) a 1x1 convolution, which decreases the number of channels in the input;

2) a 3x3 convolution, which applies a filter to the decreased number of channels in the input;

3) another 1x1 convolution, which increases the number of channels to the number that they were initially.

The use of bottleneck layers cuts down on the total number of parameters utilised by the network, which may assist in the prevention of overfitting.
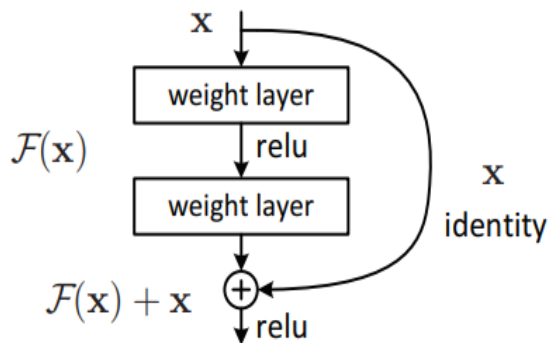

Figure 1. Identity mapping

ResNet50v2 also incorporates a number of other techniques to improve performance, including:

Identity Mappings: The network uses identity mappings to preserve the input signal and help ensure that gradients can flow smoothly through the network. This helps to prevent the vanishing gradient problem.

Pre-activation: The activation function is applied before the convolution operation in each layer, rather than after it. This helps to prevent the saturation of the activation function, which can also cause the vanishing gradient problem.

Weight Decay: A weight decay term is introduced to the loss function in order to encourage the network to utilise lesser weights, which may assist to minimise

overfitting. This is done in order to prevent the network from being too accurate.

The residual block has a specific structure, which includes three convolutional layers and a skip connection:

The input to the residual block is denoted by x.

The first layer is a 1x1 convolution that applies a set of filters to the input, reducing the number of channels. This layer is denoted by H(x).

The second layer is a 3x3 convolution that applies another set of filters to the output of the first layer. This layer is denoted by $F(H(x))$.

The third layer is another 1x1 convolution that expands the number of channels back to the original number. This layer is denoted by $G(F(H(x)))$.

5. To construct the final outcome of the residual block, the outcome of the third layer is combined to the input from the beginning of the process. The ultimate output, which will be indicated by the symbol y, will be specified as follows:

$$y = x + G(F(H(x)))$$

In this scenario, the channel count in the input is decreased by the function H(x), however the channel count is increased by the function G(F(H(x))) to return it to its initial state. The function F(H(x)) applies a filter to the reduced input, and it is the main source of non-linearity in the residual block.

Input layer
Convolution layer
Max pooling layer
Block 1
Block 2
Block 3
Block 1
Block 2   X 2
Block 3
Block 1
Block 2 X 4
Block 3
Block 1
Block 2 X 2
Batch Normalization layer
ReLu layer
Max pooling layer
Dense layer
Dropout layer
Dense layer
Dropout layer
Dense layer

(a)   Proposed ResNet model
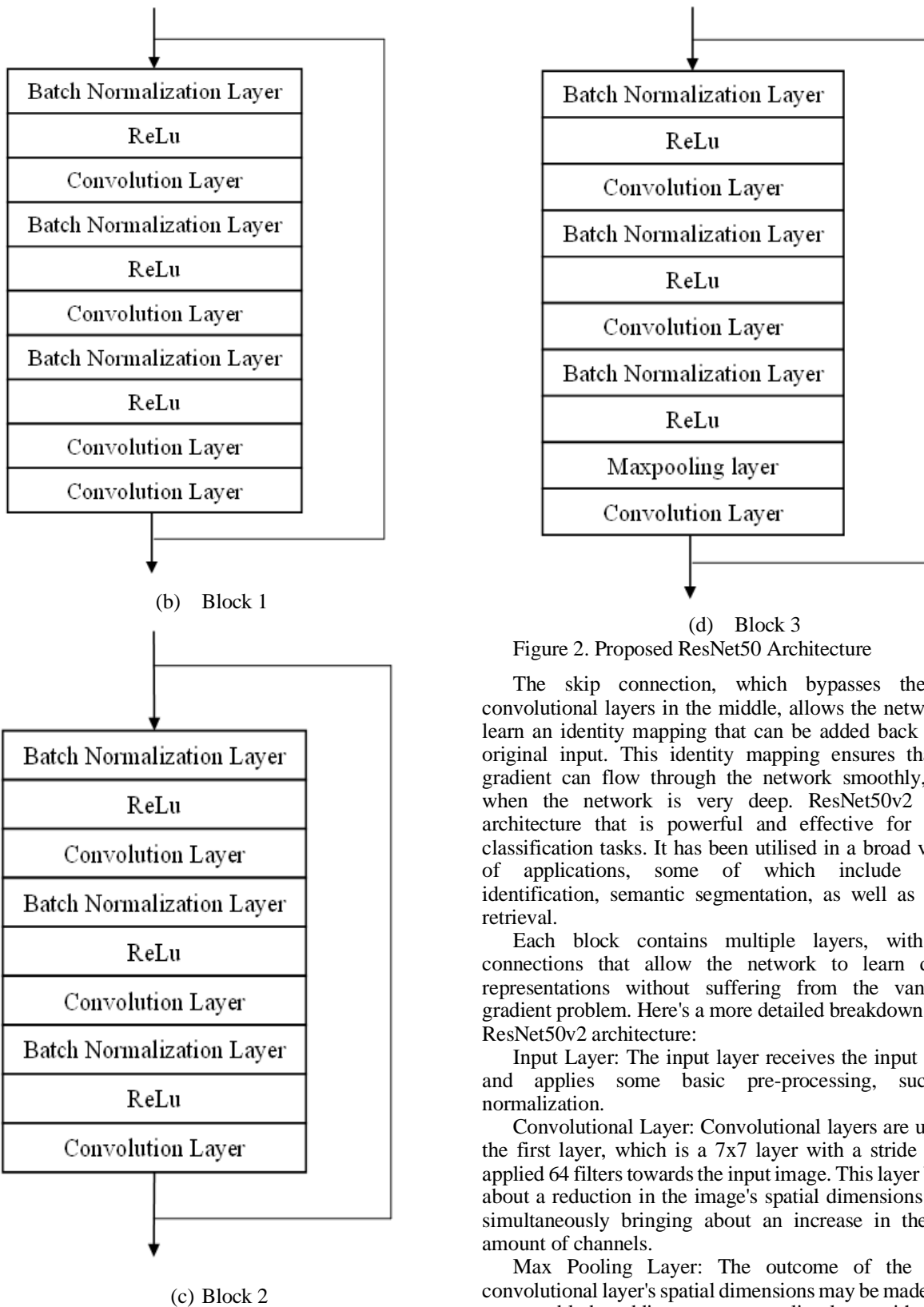
(b)   Block 1

(d)   Block 3

Figure 2. Proposed ResNet50 Architecture

The skip connection, which bypasses the two convolutional layers in the middle, allows the network to learn an identity mapping that can be added back to the original input. This identity mapping ensures that the gradient can flow through the network smoothly, even when the network is very deep. ResNet50v2 is an architecture that is powerful and effective for image classification tasks. It has been utilised in a broad variety of applications, some of which include object identification, semantic segmentation, as well as image retrieval.

Each block contains multiple layers, with skip connections that allow the network to learn deeper representations without suffering from the vanishing gradient problem. Here's a more detailed breakdown of the ResNet50v2 architecture:

Input Layer: The input layer receives the input image and applies some basic pre-processing, such as normalization.

Convolutional Layer: Convolutional layers are used in the first layer, which is a 7x7 layer with a stride 2 that applied 64 filters towards the input image. This layer brings about a reduction in the image's spatial dimensions while simultaneously bringing about an increase in the total amount of channels.

Max Pooling Layer: The outcome of the initial convolutional layer's spatial dimensions may be made more manageable by adding one max pooling layer with such a pool size of 3x3 and a stride of 2.

(c) Block 2

The ResNet50v2 design is made up of 16 different types of residual blocks as its core component. Each block of leftover material has its own unique structure:

The first layer of each residual block consists of a 1x1 convolution, which lessens the total amount of channels with in intake.

The second layer is a 3x3 convolution that applies a filter to the reduced input.

The third layer is another 1x1 convolution that expands the number of channels back to the original number.

While creating the final outcome of the residual block, the outcome of something like the third layer is joined to the input from the beginning of the process.

Each residual block also includes skip connections that bypass one or more layers and allow the network to learn deeper representations without suffering from the vanishing gradient problem.

Global Average Pooling Layer: A global average pooling layer condenses the spatial dimensions of something like the outcome of the last residual block into a single vector.

Fully Connected Layer: In order to construct the final network outcome, a fully connected layer will first take the output of a global average pooling layer and then apply a weight matrix to that output.

The conventional ResNet model is modified by the addition of batch normalization, maxpooling, dense and dropout layers as shown in figure 2 (a). The training of something like the proposed methodology has been greatly sped up thanks to the use of batch normalisation, which has cut down on the number of iterations necessary to obtain convergence. This is due to the fact that it helps to alleviate the vanishing gradient issue, which is a problem that might slow down the entire learning process. By normalizing the inputs to each layer, batch normalization helps to keep the activations within a certain range, which makes it easier to optimize the weights of the network. By lowering the degree to which the network was dependent on the initial values of its weights, it made the process of training deep neural networks more resistant to the effects of initialization. This is due to the fact that the process of normalising helps to minimise the variation in the inputs that are sent to each layer, which in turn makes the network steadier and simpler to optimise. Because of this, the generalisation functionality of deep neural networks was significantly enhanced as a result of the reduction in the impacts of overfitting. By reducing the internal covariate shift, batch normalization can help to regularize the network, making it less prone to overfitting.

The size of the feature maps may be reduced via maxpooling, which does this by picking the largest value in each pooling zone. As a result, the number of parameters in the network as well as the computational burden of the layers that followed were both decreased. It was also helpful in preventing overfitting, which was improved by limiting the number of parameters. It does this by choosing the activation level that is the highest inside each pooling zone. This gives the network some degree of translational invariance. This indicates that the network is less sensitive to minor translations of the input picture, which might result in an improvement in the network's performance regarding generalisation.

Regularization techniques like dropout, which assist prevent neural networks from becoming too "smart," are called "dropouts." Dropout is a method of training neural networks that works by randomly removing part of the network's units such that the remaining units are forced to acquire more robust features that are less reliant on specific inputs. This resulted in an improvement to the network's generalisation performance and a reduction in the risk of it overfitting. It also reduced co-adaptation between units in the network, by forcing each unit to learn useful features independently. This improved the diversity of the features learned by the network, and make it less sensitive to small changes in the input.

4.   EXPERIMENTAL RESULTS

This dataset contains 7023 images that were collected from MRI scans that were performed on human brains. The images have been divided into four different classifications: glioma, meningioma, no tumour, as well as pituitary. This dataset is a mixture of the three datasets, which are as follows:

- figshare
- SARTAJ dataset
- Br35H

The three categories of brain tumor present in the database include:

- Glioma is a kind of brain tumour that develops from glial cells inside the brain or spinal cord and may spread to other parts of the body. Glial cells, which are found in the spinal cord and brain, are responsible for providing support as well as protection for nerve cells. Nevertheless, glial cells have the potential to develop cancer and expand uncontrolled, leading to the formation of tumours.
- Meningioma is a kind of brain tumour that develops from of the meninges, which are the membranes that serve as a protective covering for the brain and spinal cord. • Meningiomas are relatively rare. Meningiomas are typically slow-growing tumors, and they are usually benign, although they can sometimes be malignant. They can occur anywhere along the meninges, and the symptoms of meningioma depend on the location and size of the tumor.
- Pituitary tumour is a form of brain tumour that develops in the pituitary gland. The pituitary gland is a tiny gland that sits at the base of the brain and is responsible for producing hormones that govern a variety of processes throughout the

body. Pituitary tumors can be either benign or malignant, and they can produce excess hormones or compress nearby structures in the brain, causing a variety of symptoms.

The input photos of the Glioma type are shown in Figure 3. The input photos of the meningioma type are shown in Figure 4. The input photos of the pituitary type are shown in Figure 5. The input pictures of a typical MRI scan are shown in Figure 6.
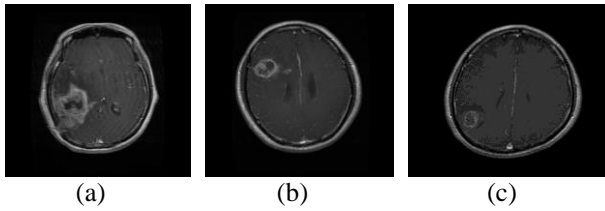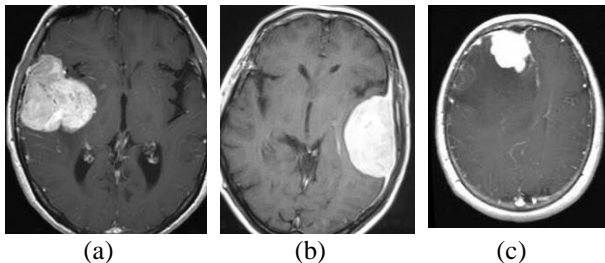

| (a) | (b) | (c) |

Figure 3. Input images type- Glioma

| (a) | (b) | (c) |

Figure 4. Input images type- meningioma
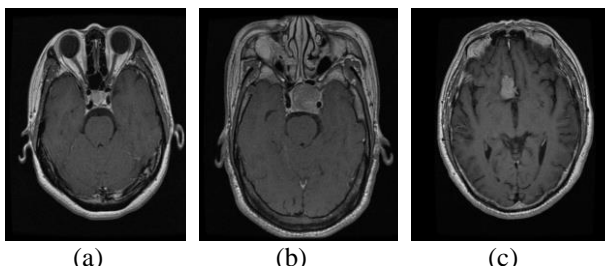

| (a) | (b) | (c) |

Figure 5: Input images type – pituitary
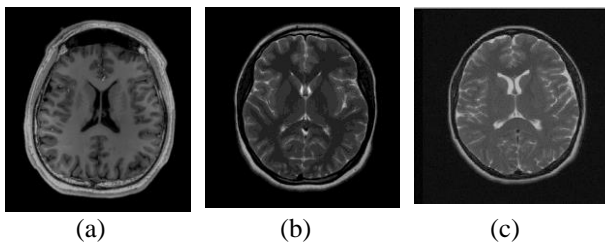

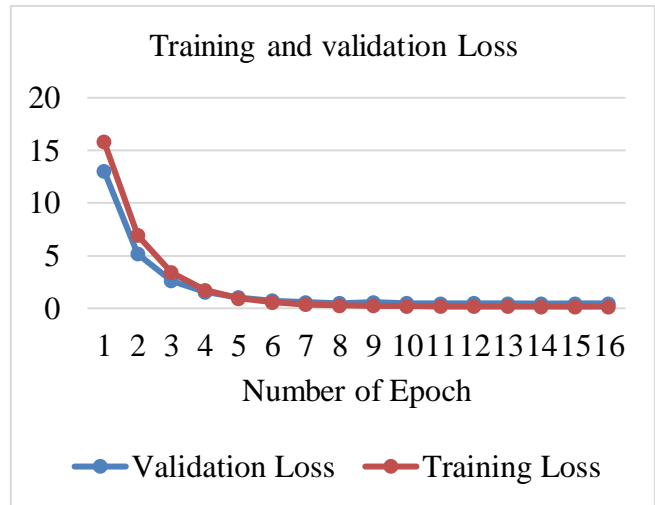| (a) | (b) | (c) |

Figure 6. Input images type - normal MRI

Figure 7. Training and Validation loss

Figure 7 illustrates the amount of time spent during training and validation. During training, the model is given a set of training data to process, and the objective is to optimise the model's parameters so as to reduce the amount of loss that occurs during training. The variation between the output that was predicted by the model as well as the output that was actually generated by the training data is what is used to determine the training loss. When the training loss is modest, the model performs very well when it comes to predicting the outcome of the training data. On the other side, validation loss is used as a tool for determining how well a model generalises its results. The model is validated by being tested on a distinct collection of data, which is referred to as the validation data, which it did not see when it was being trained. The validation loss is determined by subtracting the projected model's final outcome from the actual results of the validation data and using this difference as the starting point for the calculation. The model's ability to generalise to new data is said to improve in direct proportion to the model's validation loss.

Accuracy in both training and validation is shown in Figure 8. Throughout the training phase, a model's performance may be evaluated by measuring both its training accuracy and its validation accuracy. During training, the model is given a set of training data to process, and the objective is to optimise its parameters in order to achieve the highest possible level of accuracy in the training. The proportion of the training data which the model properly predicts is what constitutes the training accuracy when it is computed.
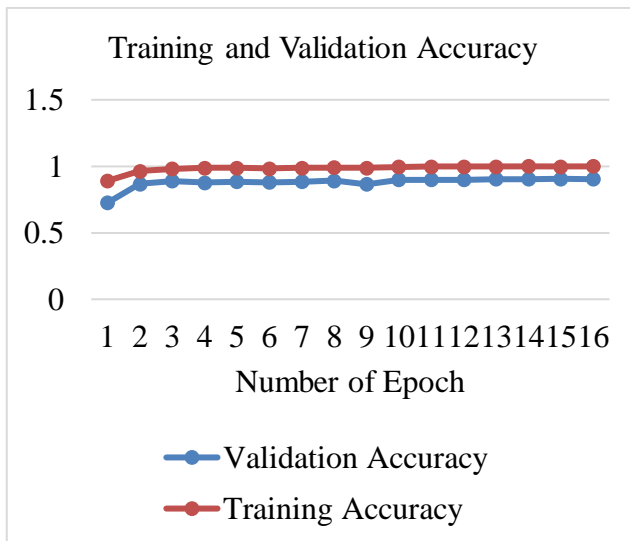
Figure 8: Training and Validation Accuracy

The accuracy of the model's predictions of the results of the training data is directly correlated to the level of the training accuracy. On the other hand, validation accuracy is what's utilised to assess the model's capacity for generalisation in the real world. The model is validated by being tested on a distinct collection of data, which is referred to as the validation data, which it did not see when it was being trained. The proportion of the validation data which the model properly predicts is the measure that is used to determine the validation accuracy. The model's ability to generalise to new data will be enhanced in direct proportion to the validation accuracy.

The validation parameters used in the experimental analysis are:

- Validation loss: The validation loss is commonly computed by taking the loss function over all of the cases that make up the validation set and averaging the results. The loss function determines how well the model is able to predict outcomes based on the validation set in relation to the actual labels.
- Validation Accuracy: Validation accuracy is a statistic that is used to assess how well a machine learning model performs on a validation set while it is being trained. This evaluation takes place throughout the training process. It is helpful to prevent overfitting to the training data by using the validation set, which is a subset of the whole dataset that is used to test the performance of the model on data that it has not previously seen.
- Precision: When evaluating the effectiveness of a machine learning model in performing binary or multiclass classification tasks, one of the metrics that is used is precision. It determines how many

of the model's positive predictions really turn out to be accurate compared to the total number of positive predictions generated by the model. In binary classification, precision is determined by the following formula:

$$precision = \frac{true\ positives}{(true\ positives + false\ positives)}$$

- Recall: The success of a binary classification model may be measured via the use of a performance indicator known as recall. To be more specific, recall measures the percentage of positive instances out of the total number of positive cases that really exist in the dataset that were properly detected by the model.
- Sensitivity: is a measurement that determines how well a machine learning model performs in binary or multiclass classification tasks. It calculates the percentage of accurate positive predictions produced by the model relative to the total number of cases in the dataset that are positive in reality. In binary classification, sensitivity is calculated as:

$$sensitivity = \frac{true\ positives}{(true\ positives + false\ negatives)}$$

- Specificity: The performance of a machine learning model in binary or multiclass classification problems may be evaluated using a statistic called specificity. It estimates the percentage of accurate negative predictions provided by the model relative to the total number of real negative cases included in the dataset. In binary classification, specificity is calculated as:

$$specificity = \frac{true\ negatives}{(true\ negatives + false\ positives)}$$

- F1 score: is a metric that determines how well a machine learning model performs in binary or multiclass classification works. It is a harmonic mean of precision as well as recall, which tries to balance the trade-off between the two aspects of accuracy. In the context of binary classification, the F1 score is determined by the following formula:

$$F1\ score = 2 * \frac{(precision * recall)}{(precision + recall)}$$

- Cohen's kappa: Cohen's kappa is a statistical measure that is used to estimate the amount of agreement between the two raters for a categorical or nominal variable. It is named after the statistician who first developed the measure. It gives a more realistic measure of inter-rater

reliability than just looking at the percentage of agreeing ratings given by each rater since it takes into consideration the potential that an agreement might be the result of chance.

TABLE 1. VALIDATION PARAMETERS

Metric	Value
loss	0.2364
Accuracy	0.9634
Precision	0.9641
Recall	0.9611
Sensitivity	0.9611
Specificity	0.9741
F1 Score	0.9610
Cohen's kappa	0.9478

The evaluating parameters of the suggested model are shown in Table 1. The value derived for the loss is 0.2364. The accuracy of the model that has been presented is equal to 0.9634. The precision produced is 0.9641. The recall obtained is 0.9611. The Sensitivity of the proposed model is 0.9611. The specificity obtained is 0.9741. The F1 Score obtained is 0.9610. The Cohen's kappa obtained is 0.9478.

TABLE 2: CONFUSION MATRIX

	glioma	meningioma	NoTumor	pituitary
glioma	292	5	0	3
meningioma	1	278	13	14
NoTumor	3	7	391	4
pituitary	0	1	0	299

The confusion matrix associated with the suggested model is shown in Table 2. The diagnostic process identifies four distinct types of tumour based on the examination of the photos.

TABLE 3. PRECISION, RECALL AND F1-SCORE OF EACH CATEGORY

	precision	recall	F1-score
glioma	0.99	0.97	0.98
meningioma	0.96	0.91	0.93
NoTumor	0.97	0.97	0.97
pituitary	0.93	1.00	0.96

The levels of accuracy, recall, and F1-score for each category are shown in Table 3. The glioblastoma has a precision score of 0.99, a recall score of 0.97, and an F1 score of 0.98 correspondingly. Meningioma has an accuracy of 0.99, recall of 0.91, and an F1-score of 0.93 correspondingly. The NoTumor algorithm has an accuracy score of 0.97, a recall score of 0.97, and an F1 score of 0.97 correspondingly. The pituitary has a precision score of 0.93, a recall score of 1.0, and an F1 score of 0.96, respectively.

TABLE 4. COMPARATIVE ANALYSIS

Method Name	Accuracy
NASNetMobile	0.81846
VGG19 [21]	0.90999
MobilenetV2 [22]	0.93593
InceptionV3 [23]	0.95957
Proposed modified ResNet50V2	0.96339

Table 4 shows the accuracy obtained by the existing models. NASNetMobile produced an accuracy of 81.84%. VGG19 obtained an accuracy of 90.99%. The MobilenetV2 obtained an accuracy of 93.59%. The InceptionV3 produced an accuracy of 95.95. The proposed modified ResNet50V2 produced an accuracy of 96.33%.

5. CONCLUSION

The categorization of brain tumours by the use of deep learning is a fast-expanding area of study that seeks to enhance the precision and effectiveness of brain tumour diagnosis. Deep learning is a subfield of machine learning that makes use of artificial neural networks in order to discover and comprehend intricate data patterns. This paper presents a modified ResNet50V2 based deep learning model to classify the four categories of images. The conventional resNet model is modified with the addition of batch normalization, maxpooling and dropout layers. Batch normalisation may assist to enhance the convergence behaviour of the network by minimising the risk of getting trapped in local minima or plateaus. This is one of the ways in which the likelihood of getting stuck can be reduced. This is because the normalization process helps to make the optimization landscape smoother, making it easier to navigate. Since it enables the network to learn additional abstract and high-level features, maxpooling has the potential to enhance the capability of the network to learn new features. This is due to the fact that maxpooling decreases the size of the characteristic maps, which in turn compels the network to learn features that are more informative and discriminative. Dropout can be particularly useful on small datasets, where overfitting is a common problem. Dropout is a technique that may assist enhance a network's generalisation performance on data it has not previously seen by prohibiting the network from learning and remembering the training data. The proposed model obtained an accuracy of 96.33%.

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