

Classification of Brain Tumors from MR Images Using a New CNN Architecture

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ABSTRACT

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Accurately classifying brain tumors is a crucial factor in combatting, intervening, and treating the disease. By automating the tumor diagnosis process without the involvement of human factors, it is possible to decrease the occurrence of human errors during the diagnosis process. In a new deep convolutional neural network architecture was developed to tackle the brain tumor classification problem, resulting in the successful classification of three distinct types of brain tumors - meningioma, glioma and pituitary. With the propose CNN architecture, a classification accuracy of 98.69% was achieved in brain tumor classification. The recommend model is simple and very fast. It was observed that giving high kernel size and strides values in the first layers and low values in the middle layers of the convolutional layers, and keeping the strides value small in the pooling layer had greatly increased on the model performance. The recommend CNN architecture was compared with studies using the same dataset and transfer learning models in the literature. As a result of these comparisons, high-scoring results were obtained with the recommend model. The classification success achieved by the model is state-of-the-art among stand-alone models.

1. INTRODUCTION

Brain tumors are a health issue that results from the growth of abnormal cells in brain and spinal cord tissue. Tumors can spread from the tissues in the brain to other parts of the body and cause symptoms by disrupting brain functions [1].

The World Health Organization (WHO) categorizes brain tumors according to their cell origin, cellular behavior, and tumor severity. In this classification, the development process of the tumor is taken into consideration. Classification and determination of the tumor grade are used to predict the behavior of the tumor. Imaging methods are very important in the diagnosis of brain tumors and the most commonly used ones are MRI, CT scan, and X-ray [2-8].

Brain tumors are a serious and destructive illness, and the accurate diagnosis of these tumors is vital. Incorrect diagnosis can lead to inappropriate medical response and reduce the patients' chances of survival. Creating an appropriate treatment plan and improving the condition of patients with brain tumors depend heavily on an accurate diagnosis. The advanced stage of the disease reduces the chances of treatment [9].

Tumors can be divided into two groups: cancerous (malignant) and benign. If left undetected in its early stages, malignant tumors can result in fatality by damaging the brain tissue. Malignant tumors can be categorized as pituitary, meningioma and glioma tumors. Meningiomas grow in the cells that surround the brain and can be difficult to diagnose. Gliomas are tumors that originate from glial cells, which can be categorized as either low-grade or high-grade depending on their severity. Pituitary tumors form in the pituitary gland, which is situated at the base of the brain and often known as

the master gland. Timely identification and treatment of brain tumors are essential since they tend to damage brain tissue and result in various side effects, regardless of whether they are malignant or benign [1].

Brain tumor symptoms can differ from individual to individual and may shift based on the tumor's size, location, and type. MRI imaging is utilized to detect and determine the size, location, and shape of brain tumors.

The process of magnetic resonance imaging (MRI) involves utilizing the variations in magnetic fields within the body's tissues to generate images. This technique allows for the imaging of tissues inside the body without using harmful rays such as X-rays or radiation. MRI can be used for the diagnosis and monitoring of various health conditions, particularly in the examination of brain and spinal cord functions.

Brain tumors can be detected using MRI images. The MRI technique creates images using the changes in magnetic fields in the body's tissues. This technique is a sensitive method that can be used to detect brain tumors and can help determine the size, location, and shape of tumors.

Meningiomas are the most frequently occurring benign tumors, commonly observed in adults. These slow-growing, spherical masses affect approximately 20% of individuals. Typically, slowly growing meningiomas can be followed over time. Glioma tumors are generally malignant. However, even benign meningioma tumors can cause other medical damage, as can benign pituitary tumors [10].

The membranes surrounding the brain and spinal cord can develop benign tumors known as meningiomas, which are the most frequently occurring. Tumors that grow in brain tissue are referred to as gliomas, and abnormal growth of brain cells in the pituitary gland in the brain are called pituitary tumors.

These tumors can arise anywhere in the brain, have a uniform shape and internal structure [11].

Computer-aided medical diagnosis is a method used to accurately diagnose a patient using their symptoms, test results, and other data. This method is used to speed up the diagnostic process and increase accuracy for doctors. It is implemented using software that analyzes data and supports the doctor's experience-based decision-making process. The timely and precise identification of brain tumors is crucial to apply an efficient treatment strategy. The stage, pathological type, and degree of the tumor play important roles in the selection of treatment methods. Some of the studies on computer-assisted medical diagnosis are described in the literature section of this study.

Recently, artificial intelligence technology has been used in the field of computer-aided medical diagnosis. Artificial intelligence aims to give machines human-like thinking and learning abilities using various algorithms and data sets.

Machine learning is a commonly used method in artificial intelligence studies. Deep learning, a subset of machine learning, finds application in numerous areas such as brain tumor classification and segmentation. These areas include industries such as food, healthcare, and IoT [12-16]

In deep learning technology, Convolutional Neural Networks (CNNs) are heavily used to extract features from images. In the case of MRI images, it is necessary to identify the size and location of a tumor in order to make a diagnosis. A skilled doctor can visually identify these data from the image and make a diagnosis. In computer-aided systems, it is necessary to work with expert doctors and identify the points to be considered in the images in order to obtain successful results from the system. In CNN technology, these processes are automated.

A clinical decision support system has been developed in the study to assist healthcare professionals who do not have enough experience in diagnosing or identifying the type of brain tumor in the image they are looking at from MRI images.

As mentioned in the literature section, transfer deep learning models are widely used in current studies. Nevertheless, transfer deep learning models consist of an extensive number of parameters, possess large sizes, require slower and more computationally intensive model training, and demand more expensive hardware and lengthier training periods. Therefore, estimation is done more slowly. Therefore, a simpler, faster, more effective, less parameterized, less computationally intensive, more flexible, less complex, and lower-capacity CNN architecture is proposed in this study. The proposed model is more generalizable and less detailed.

In this study, a simple, fast, and high-performance CNN architecture is proposed for the detection of three different types of brain tumors. The features of the tumor regions were automatically extracted with CNN networks using the recommend architecture, and the images were classified with high accuracy by correctly extracting the features.

The main contributions of this study are:

- The model has small parameters, low capacity, and requires less hardware computation, making it a simple and effective model. These features provide flexibility to the model, ensuring that it is fast and efficient. The model is more generalizable and less detailed.
- The recommend model has been compared to frequently used transfer deep learning models in the

literature, and it has been found that the recommend model outperforms deep transfer learning models.

- The success of the parameters used in the CNN architecture varies according to the dataset. The most critical parameter values for effective results have been identified. Many different experimental studies have been conducted to identify the most effective parameters for the convolution and pooling layers.
- The effects of the pooling layer and convolutional layer parameters in the recommend CNN model were determined,
- The recommend method showed the best classification accuracy compared to stand-alone models.

The study conducted a thorough comparative analysis and evaluation using evaluation metrics.

2. LITERATURE

Cheng et al. [17] developed a method for classifying brain tumors. The method proposed by them increases the tumor region using the image expansion method (ROI) and then divides this region into smaller sub-regions in a ring shape. Due to the varied shapes and sizes of brain tumors, this method was discovered to be more efficient than conventional methods. The study employed three feature extraction methods - histogram of proximity, gray level co-occurrence matrix, and bag of words model - on a large dataset to assess the efficacy of this method. The results showed that using the density histogram increased accuracy rates from 71.39% to 82.31%, GLCM from 78.18% to 84.75%, and the BoW model from 83.54% to 88.19%.

Ismael and Abdel-Qader [18] presented a method for classifying brain tumors. The proposed method combines statistical features with neural network algorithms to develop a brain tumor classification system for MRI images. By utilizing a combination of 2D Discrete Wavelet Transformation (DWT) and 2D Gabor filter techniques, the researchers were able to accomplish feature selection and achieve an accuracy of 95.66%.

In their study, Gumaei et al. [19] presented a classification approach for brain tumors using a hybrid feature extraction method and a regularized extreme learning machine (RELM). They introduced a new hybrid feature method called PCA-NGIST, which incorporates PCA and Normalized GIST. The experimental results demonstrated that their approach outperformed the current state-of-the-art methods, with the classification accuracy improving from 91.51% to 94.233% in the random holding technique test.

In their research, Kaplan et al. [20] introduced two feature extraction techniques (nLBP and α LBP) for brain tumor classification. The classification process employed KNN, ANN, RF, AIDE, and LDA methods. Using the Figshare dataset, the KNN model and LBPd=1 feature extraction method achieved the highest success rate of 95.56% in classifying brain tumor.

Abiwinanda et al. [21] proposed an ideal CNN design for classifying brain tumors consisting of two convolutional layers, an activation layer (ReLU), a maximum pooling layer, and a 64 neuron layer. The convolutional layers in this architecture have 3×3 kernel and 32 filters. A classification accuracy of 84.19% was obtained with the proposed architecture.

Cheng [22] presented a two-stage method for tumor classification, which involves offline database creation and online retrieval. During offline database creation, sequential processing steps are used to segment the brain tumor images, extract features, and learn distance metrics. The input brain image is processed in a similar way during the online retrieval stage, and its extracted features are compared to the learned distances stored in the online database. Despite not utilizing a neural network approach, this method attains a remarkable classification accuracy of 94.68%.

Toğaçar et al. [23] utilized a feed-forward CNN model called BrainMRNet, which incorporates a novel Hypercolumn technique for improving classification performance by selecting the most effective features from the input and minimizing computational cost. Their experiments on the Figshare dataset resulted in an overall classification accuracy of 96.57%.

Pashaei et al. [24] utilized an 8-layered CNN network for feature extraction and performed experiments with various classifiers. The results of their experiments demonstrated that the use of Kernel Extreme Learning Machines (KELM) achieved a superior classification performance of 93.68%, surpassing the performance of other classifiers.

Öksüz et al. [25] utilized a novel feature fusion technique to classify brain tumors. The approach involved combining features extracted from two distinct models, namely ResNet18 and ShallowNet, before feeding them into an SVM model for classification. The methodology yielded an overall accuracy of 97.25% on the Figshare dataset.

3. MATERIALS AND METHOD

3.1 Dataset

Figshare is a dataset introduced by Cheng in 2015 and its current version was presented in 2017 [26]. This dataset is publicly available and includes three common brain tumors (glioma, meningioma and pituitary tumor). The dataset consists of a total of 3064 images, comprising 1426 glioma, 930 pituitary tumors and 708 meningioma. Pituitary tumors are alternatively referred to as tumors of the pituitary gland. The dataset's number of tumor types is depicted in Figure 1. Each of the three different brain tumors is exemplified in Figure 2 with an image.

The dataset was partitioned into three categories: training, validation, and test sets. The training set comprised 85% (2604 images) of the dataset, while 15% (460 images) was allocated to the test set. Of the images in the training set, 15% (391) were reserved for validation, leaving 2213 images for model training.

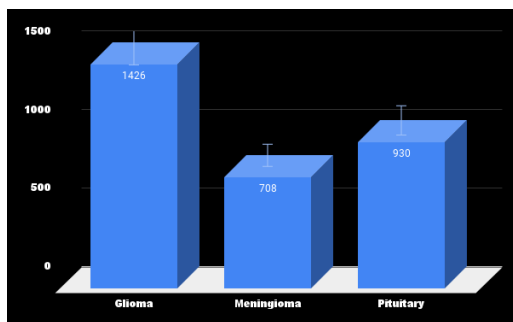


Figure 1. Distribution of the number of images for each class in the data set

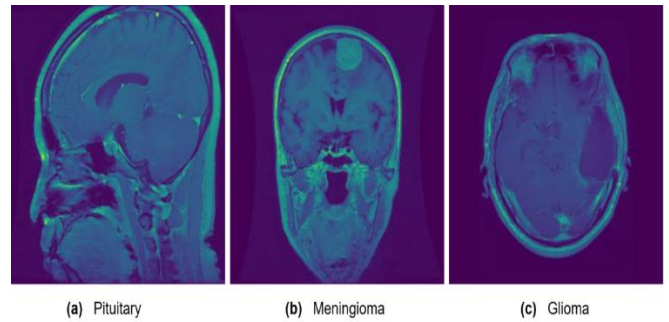


Figure 2. Types of brain tumors

3.2 Method

The Figshare dataset was used in this study to propose a novel CNN architecture for the separation of three distinct brain tumors. Before the images are given to the CNN architecture, various preprocessing is performed on these images. In the preprocessing stage, for the images allocated for the training data set, random 15% rotation, horizontal flipping, 15% zoom and scaling operations are applied. Only scaling operation is applied to the test data set. The brightness of the images was not increased (brightness_range) as this operation worsened the results in the preprocessing stage.

To choose the most appropriate model for the dataset, numerous experimental studies have been undertaken. Specifically, a significant number of experimental studies have focused on selecting optimal parameters for the layers of the model architecture, which have been identified and applied. Figure 3 depicts the CNN architecture suggested for the classification of brain tumors.

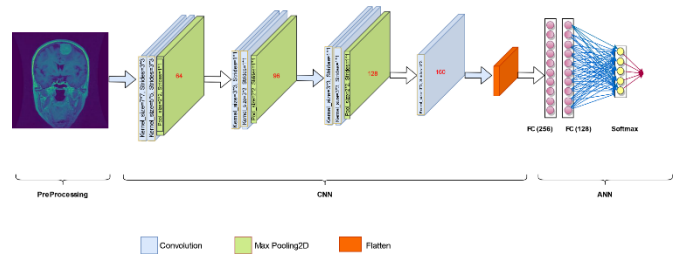


Figure 3. Suggested CNN architecture

The architecture for brain tumor classification using deep learning comprises three groups, as illustrated in Figure 3. The summary of operations performed in each group is provided below.

PreProcessing: In this stage, all images in the dataset have been preprocessed. For the training images in the preprocessing stage, 15% random rotations, 15% horizontal flips, zooming and scaling operations were applied. Only scaling operation was applied on the test dataset. Reducing the size of images can accelerate processing time in deep learning methods due to their high mathematical operations. All images were resized to 256×256 due to variations in size and high resolution.

CNN: The preprocessed images are given to the CNN group. All kinds of information and features related to the images, including the edge information, are extracted in this block.

ANN: The model is trained using the features obtained from CNN. Two dense layers were used in this block. The dense layers utilized the "relu" activation function. In addition, dropout was used after each dense layer to prevent overfitting.

As shown in Figure 3, the proposed CNN architecture is divided into 4 groups. Each group has 2 convolution and 1 pooling layers. The pooling layer is used to prevent the model from overfitting and reduce the computational load of the subsequent layers. In experimental studies on the selection of the pooling layer, better results were obtained using the max pooling method. The pool_size value is 2 and the strides value is 1 in the three pooling layers. This is mainly due to the fact that high histogram values in the images are distinctive features.

The CNN architecture consists of 4 groups. The first group consists of 2 convolution layers (kernel_size=7×7 for the first convolution layer, 5×5 for the second convolution layer, and strides=3×3 for both) and a max pooling pooling layer with 64 filters, the second group consists of 2 convolution layers (kernel_size=3×3, strides=1×1) and a max pooling pooling layer with 96 filters, the third group consists of 2 convolution layers (kernel_size=3×3, strides=1×1) and a max pooling pooling layer with 128 filters, and the fourth group consists of a convolution layer with 160 filters (kernel_size=3×3, strides=3×3).

In the convolution layers, the activation function used is ReLU. The flatten layer is used after the CNN architecture to obtain features before feeding them to the ANN. The flatten layer readies the outputs for transmission to the fully connected layer. In the flatten layer, multidimensional data is reduced to one dimension. Then the obtained features are given to the ANN. In the ANN architecture, there are two fully connected layers comprising 256 and 128 neurons respectively, and they employ the ReLU activation function. The Softmax activation function is utilized in the classification layer to generate a probability score ranging from 0 to 1, indicating the class membership.

The model's output is compared with the actual output, and the optimization function is utilized to update the model's weights through backward propagation. This process continues until the minimum error is obtained. In the proposed study, the "adam" function was used as the optimization function.

Kernel size and strides are variables that determine the characteristics of the convolutional layers used in the ANN model. These variables determine the filter sizes used to filter the input data and how many steps to take during filter application. In general, kernel size and strides values have an effect on the performance, speed, and accuracy level of the model. Therefore, choosing these values correctly can significantly affect the functionality and performance of the model. Kernel size and strides values are used to filter the features in the images. In this study, the model was tried to be measured by testing various combinations of kernel size and strides values. The model was created by finding the parameters where the highest performance values were obtained.

3.3 Performance metrics

This study assessed the accuracy of the proposed architecture's results by comparing them to the true results determined by experts, using metrics such as sensitivity, specificity, and accuracy. The performance metrics can be found in Table 1.

The sensitivity rate shows the proportion of patients with cancer that are also detected by the model. This metric measures the proportion of correctly detecting the disease and

shows the proportion of those who are actually sick being detected as sick by the model. It is used in places where the classification of positives is of high priority.

Table 1. Performance metrics

	Predicted (P)	Predicted (N)	N= Negative P= Positive	T=True F=False
Actual (P)	TP	FN	$Recall = \frac{TP}{TP + FN}$	
Actual (N)	FP	TN	$Specificity = \frac{TN}{TN + FP}$	
	$Precision = \frac{TP}{TP + FP}$		$Accuracy = \frac{TP + TN}{TN + TP + FP + FN}$	

The specificity rate measures the probability that the model's predictions will be negative in cases where cancer is actually absent. This metric shows the probability of the model wrongly detecting the disease and measures the proportion of those who are not sick being detected as not sick by the model. It is used in places where the classification of negatives is of high priority, for example, making a diagnosis for a health condition before treatment.

Accuracy rate is calculated by the proportion of correct predictions (positive and negative) in the total data set by the model. It can become less useful in imbalanced data.

Precision rate shows how many of the total positives were correctly classified as positive. Precision is a way to measure how many of our model's predictions are correct predictions out of all the predictions made.

The F1 score rate combines sensitivity and recall metrics in a single metric. It works well on imbalanced data.

$$F1\ Score = \frac{2 * (precision * recall)}{precision + recall} \quad (1)$$

Sensitivity and recall allow you to consider the type of errors made by your model (false positives or false negatives), so they are more appropriate performance metrics when you have imbalanced data.

4. EXPERIMENTAL STUDIES

A new CNN architecture is recommended for the Figshare dataset consisting of 3 classes and 3064 MR images. Different preprocessing techniques have been applied to improve the performance of the proposed CNN architecture on the dataset. Different studies have been conducted to select the best architecture.

There are numerous parameters that determine the performance of a model, and many of these parameters interact with each other. The optimal values of these interacting parameters depend on the dataset used. Hence, numerous experimental studies have been undertaken to ascertain the optimal parameters for this dataset.

In experimental studies, experimental work has been carried out to determine which pooling layer would be used after the architectural design is completed. Default values were used for the parameters of the layers in the study architecture. No fine-tuning process (such as kernel size, strides, etc.) was performed for the pooling layer in the experimental studies. In the experimental studies conducted for the selection of the pooling layer, it was observed that the maximum pooling layer

performed relatively better than the average pooling layer. The results of the experimental study for the pooling layer are shown in Table 2.

Table 2. Pooling layer results

	Accuracy	Precision	Recall	F1-Score
MaxPooling	93.26%	92.77%	92.07%	92.35%
AvgPooling	92.24%	92.48%	91.97%	92.22%

As a result of experimental studies, the architectural design shown in Figure 3 has been created. The results of the experimental study on the convolutional layer parameters used in the proposed CNN architecture are shown in Table 3.

Table 3. Kernel size=3×3, strides=1×1

Accuracy	Precision	Recall	F1-score
85.43%	85.63%	84.19%	84.80%

As seen in Table 3, when the convolutional layer parameters are given as kernel size 3×3 and stride value 1×1, the accuracy rate is determined as 85.43%.

It has been observed that using larger filter, kernel size, and strides values in the first block of the designed architecture helps to extract the most decisive features from the dataset and better results are obtained. In the first block, 2 convolutional layers and 1 pooling layer are used. Kernel_size is taken as 7×7 and strides value as 3×3 in the first convolutional layer, and kernel_size is 5×5 and strides value is 3×3 in the second convolutional layer. Thus, obtaining larger features is ensured in the first block. Strides value is specifically set to 3×3 to contribute to the computation cost and to preserve the interrelated information for the 7×7 and 5×5 kernel_size values.

Smaller kernel sizes were used in the convolutional layers of the second and third blocks to capture more precise and smaller features. In these blocks, 2 convolutional layers and 1 pooling layer were used. Since the stride values were smaller in these blocks, a more detailed feature map was created. In the second and third blocks, the kernel size was taken as 3×3 and the strides as 1×1.

Leaving the values of the convolutional layer in the fourth and final block standard allowed for better capture of higher-level features. While the kernel size was taken as 3×3 in the convolutional layer, the stride value was also taken as 3×3.

A maximum pooling layer was added to the end of each block. The pooling layer decreases the quantity of feature maps and model parameters, while still retaining the predominant information present in the feature maps.

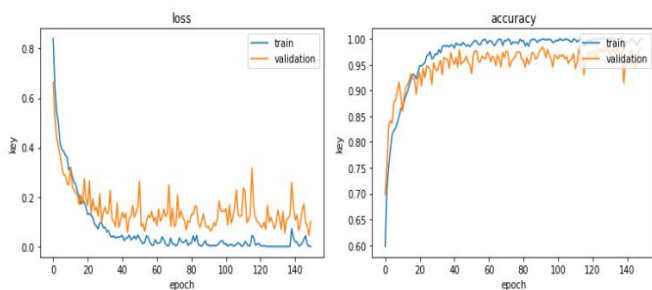


Figure 4. Loss and accuracy representation of the proposed model

True Label	Meningioma	111	0	1
	Glioma	3	221	2
	Pituitary	0	0	122
		Meningioma	Glioma	Pituitary
		Predicted Label		

Figure 5. Confusion matrix

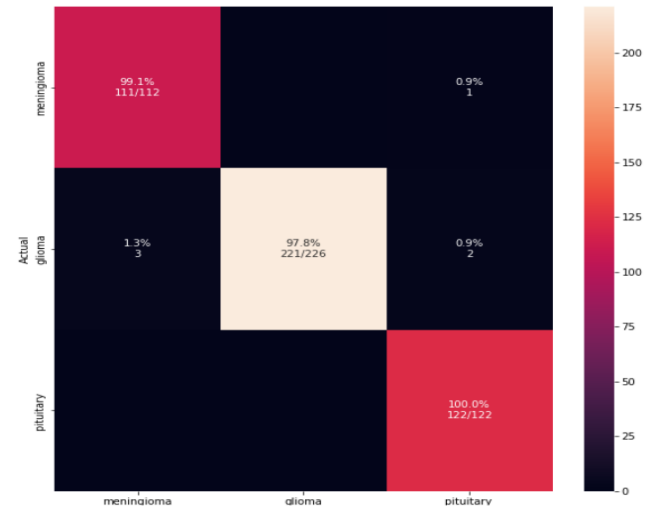


Figure 6. Confusion matrix

Following the CNN architecture design, the model was trained using the dataset, and Figure 4 depicts the loss and accuracy graph of the proposed model during the training process.

Figure 5 presents the Confusion Matrix showing the success of the model on the test data, after it was trained on the dataset.

The Confusion Matrix of the test data's actual results and the predicted values of the proposed model are presented in a distinct manner in Figure 6.

Table 4 displays the classification report of the results achieved through the CNN architecture proposed in the study.

Table 4. Classification report

	Precision	Recall	F1-Score
Meningioma	0.97	0.99	0.98
Glioma	1	0.98	0.99
Pituitary	0.98	1.0	0.99
Accuracy		0.99	0.99
Macro Avg	0.98	0.99	0.99
Weighted avg	0.99	0.99	0.99

As seen in Table 4, the proposed model reaches an accuracy rate of 98.69%.

Precision is the proportion of images predicted by the model as cancer that are actually cancer. The proposed model has achieved a precision rate of 97% for meningioma tumors, 100% for glioma tumors, and 98% for pituitary tumors.

Recall is the proportion of images that are actually cancer and predicted by the model as cancer. The proposed model has achieved a recall rate of 99% for meningioma tumors, 98% for glioma tumors, and 100% for pituitary tumors.

In the literature, widely used transfer learning models were compared to the proposed architecture to evaluate its performance. The results of these experimental studies are presented in Table 5. The same parameter values, including pre-processing stages, were used in all of the experimental studies conducted.

As seen in Table 5, transfer learning models performed similarly, but the ResNet50 transfer learning model showed better performance than the other models. Our proposed deep learning model outperformed all of these models. While ResNet50 deep transfer learning model classified images with an accuracy rate of 98.43%, our proposed model classified images correctly with a rate of 98.69%.

As seen from the results, high performance results have been obtained in all metrics. It is seen that all three types of tumors have been classified with a high performance rate.

Table 5. Comparison of the proposed model with transfer learning models

	Accuracy	Precision	Recall	F1-score
InceptionV3	97.82%	97.52%	97.77%	97.64%
DenseNet201	98.26%	98.29%	97.79%	98.02%
MobileNetV3	96.08%	96.44%	94.94%	95.53%
VGG16	98.04%	97.95%	97.64%	97.78%
ResNet50	98.43%	98.14%	98.36%	98.25%
Our Model	98.69%	98.32%	98.96%	98.63%

Table 6 shows the studies conducted in the literature using the Figshare dataset, the feature extraction methods used in these studies, the classification and classification success.

Table 6 shows that our proposed deep learning model outperformed previous studies conducted on the Figshare dataset in terms of performance scores.

Table 6. Methods and results used in studies with Figshare dataset

References	Feature extraction	Model	Acc
Deepak and Ameer [5]	GoogleNet	SVM	97.10%
Swati et al. [6]	Fine-tune VGG19		94.80%
Cheng et al.[17]	Bag of words	SVM	91.28%
Kaplan et al. [20]	nLBP ve α LBP	KNN	95.56%
Pashaei et al. [24]	CNN	ELM	93.68%
Öksüz et al. [25]	ResNet18+ShallowNet	SVM	97.25 %
Ari et al. [26]	AlexNet and VGG16	ELM	97.64%
Cheng et al. [27]	Local features using Fisher Vector	SVM	94.68%
Abir et al. [28]	GLCM	PNN	83.33%
Afshar et al.[29]	Capsule networks (CapsNet)		86.56%
Deepak and Ameer [30]	CNN	SVM	95.82%
Kaur and Gandhi [31]	Fine-tuned AlexNet		96.95%
Ayadi et al. [32]	DSURF and HoG	SVM	90.27%
Bodapati et al. [33]	Xception and InceptionResNetV2	Softmax	95.23%
Türkoğlu [34]	AlexNet,DenseNet201	Bayes optimization based SVM	98.04%
Our recommend model	CNN	Softmax	98.69%

5. RESULTS

In this study, a novel CNN architecture is suggested for categorizing three types of brain tumors using brain MR images. The dataset comprises 3064 MR images, with 85% of the data utilized for training, 15% for testing, and 15% of the training images reserved for model validation. After being trained on the training data, the model correctly classified the images on the test data with a highest accuracy rate of 98.69%. Accurate classification of tumors is important because it affects the type of treatment method used, and can help doctors decide how to treat the tumors. It can also increase the effectiveness of treatment and reduce potential side effects.

The Kernel size and strides values used in the convolutional layer of CNN architectures can vary depending on the characteristics of the model and the input data. To select these values correctly, the input data for the model has been carefully analyzed according to the purpose of the model, and the most suitable values have been determined through experimental studies. In the recommended architecture, it has been observed that the use of high kernel_size values in the first convolutional layers has a positive impact on the results. Large kernel size values have enabled the extraction of large features. As the kernel size increases, the filter covers a wider area and captures wider features. This allows the model to detect higher-level features and achieve higher performance.

The transfer deep learning models trained with the dataset were compared in terms of performance with recommend model, and higher scoring results were obtained with recommend model.

According to Table 6, the proposed CNN architecture achieved superior results compared to other studies that utilized different methods but the same dataset. The model accurately classified tumors with a precision rate of 98.69%.

The CNN architecture we propose is small, fast, and effective in terms of parameter count. Therefore, it is a CNN architecture that requires less computational power, is more flexible, less complex, and has less capacity.

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