

## Brain Cancer Tumor Classification from Motion-Corrected MRI Images Using Convolutional Neural Network

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**Abstract:** Detection of brain tumors in MRI images is the first step in brain cancer diagnosis. The accuracy of the diagnosis depends highly on the expertise of radiologists. Therefore, automated diagnosis of brain cancer from MRI is receiving a large amount of attention. Also, MRI tumor detection is usually followed by a biopsy (an invasive procedure), which is a medical procedure for brain tumor classification. It is of high importance to devise automated methods to aid radiologists in brain cancer tumor diagnosis without resorting to invasive procedures. Convolutional neural network (CNN) is deemed to be one of the best machine learning algorithms to achieve high-accuracy results in tumor identification and classification. In this paper, a CNN-based technique for brain tumor classification has been developed. The proposed CNN can distinguish between normal (no-cancer), astrocytoma tumors, gliomatosis cerebri tumors, and glioblastoma tumors. The implemented CNN was tested on MRI images that underwent a motion-correction procedure. The CNN was evaluated using two performance measurement procedures. The first one is a  $k$ -fold cross-validation testing method, in which we tested the dataset using  $k = 8, 10, 12,$  and  $14$ . The best accuracy for this procedure was  $96.26\%$  when  $k = 10$ . To overcome the over-fitting problem that could be occurred in the  $k$ -fold testing method, we used a hold-out testing method as a second evaluation procedure. The results of this procedure succeeded in attaining  $97.8\%$  accuracy, with a specificity of  $99.2\%$  and a sensitivity of  $97.32\%$ . With this high accuracy, the developed CNN architecture could be considered an effective automated diagnosis method for the classification of brain tumors from MRI images.

**Keywords:** Classification; convolutional neural network; tumor classification; MRI; deep learning;  $k$ -fold cross classification



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## 1 Introduction

Brain cancer is one of main causes of death globally [1]. If detected early, the progress of this disease can be controlled and fatality due to it can be prevented. Cancerous brain tumors are classified into pre-carcinoma tumors or malignant tumors [2].

Brain tumors that are classified by computerized methods usually fall into three types: gliomas, which affect brain tissues, meningiomas and pituitary, which both affect brain membranes. While meningiomas are typically benign brain tumors, pituitary tumors induce lumps inside the skull [3–6]. Clinical diagnosis can separate between these types of tumors and aid in assessing medical cases efficiently.

Other brain tumor types include astrocytoma tumors, gliomatosis cerebri tumors, and glioblastoma tumors. Those types are our concern in this research for two reasons; The first one is that they are diffused types of tumors where their classification is very difficult manually. The second is that there are very few previous researches exist that classify them using computerized methods.

The diagnosis of brain tumors is performed through magnetic resonance imaging (MRI). Although MRI is an important tool in detecting brain tumors, it is not that helpful in early detection. Early detection from MRI requires an experienced medical expert. With the new technology in image analysis and processing as well as deep learning, it is now feasible to develop a computerized identification tool for discerning brain tumors in MRI images [7]. However, MRI as a tool is not able to show whether a tumor is benign or malignant. As such, an MRI must be followed with an invasive biopsy procedure, which is in fact a brain surgery [8].

Deep learning and image analysis techniques can be useful in identifying brain tumors in MRI images. Many MRI image databases are available, such as BRATS [9,10], which is available to the public and contains around 290 MRI images with their diagnosis and tumor detection. In [11], MRI images for real patients with and without tumors are stored with their manual diagnoses.

One of the main problems with MRI image classification via CNN is how many images are in the dataset. The larger the database, the better the classification procedure, especially for the CNN classifiers with no pre-processing and when feature extraction is required.

In [12], the authors devised a classification methodology based on deep learning techniques. They classified brain tumors into normal, metastatic bronchogenic carcinoma, glioblastoma, and sarcoma tumors. The authors in [13] performed tumor classification by enhancing the region of interest and the image ring segmentation. Feature extraction was attained using histograms of intensity levels and a co-occurrence matrix.

The authors in [14] performed brain tumor classification utilizing capsule networks, which requires smaller datasets. In [15], the authors utilized the capsule-net neural network architecture for brain tumor classification from MRI images. They proved an assumption that data pre-processing plays an important part in the classification improvement. In [16], the authors proposed a CAD architecture for brain tumor classification of gliomas tumors into three grades utilizing a custom deep neural network structure. The authors in [17] presented a new method for brain tumor classifications using CNN with preprocessing and denoising based on Discrete Wavelet Transform (DWT); their method gained a high accuracy of 93.5%–96.7%.

In [18], the authors classified brain tumors by transfer learning and fine-tuning techniques for the MRI images. They achieved better accuracy and less execution time. The authors in [19] utilized a machine learning technique for classifying brain tumors through the implementation of transfer learning method. In [20], the authors presented a non-invasive technique for brain

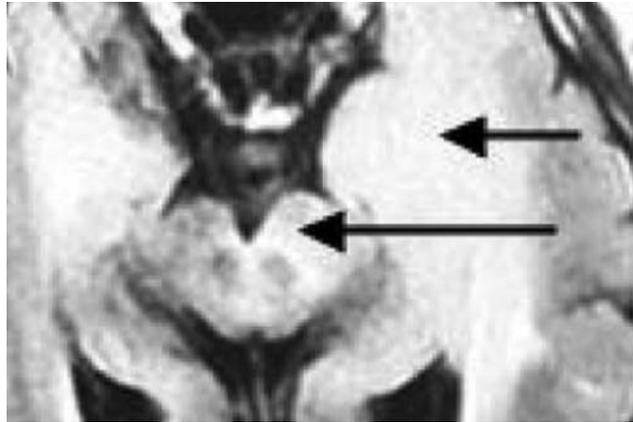
tumor grading using textural-based features. They achieved a high accuracy of 96.8%. The authors in [21] utilized a back-propagation technique to classify brain tumors through extracting statistical features. In [22], the authors used MRI-based brain tumor grading through CNN and genetic-based algorithms. They claimed that this achieved better accuracy than CNN alone. In [23], the authors utilized fast R-CNN to classify brain tumors with a high speed and an average accuracy of 97.8%. However, the smallness of the dataset was considered as a drawback of this research.

A comparison of recent research in brain tumor classification using deep learning techniques is depicted in Tab. 1.

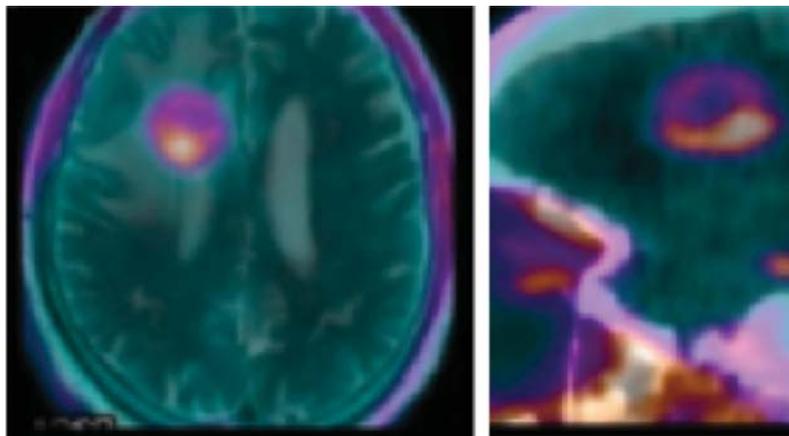
**Table 1:** Recent research in brain tumor classification using deep learning techniques

Ref.	Achievement	Method	Dataset	Results (Average accuracy) (%)
Cheng et al. [13]	Classification of meningioma, pituitary, and glioma	Spatial pyramid matching	Contrast-enhanced MRI, T1-weighted MRI dataset	91.28
Afshar et al. [14]	Brain tumor identification	Capsule neural networks	3,064 MRI of 233 patients	86.56
Kurup et al. [15]	Classification of meningioma, pituitary, and glioma	Capsule neural networks	3,170 images	92.6
Sultan et al. [16]	Classification of glioma tumors into three grades	Custom deep neural network structure	3,044 slices of 233 patients	98.7
Kutlu et al. [17]	Brain and liver tumor classifications	Using CNN and DWT	3,064 brain images	93.5–96.5
Swati et al. [18]	Brain tumor classification	Transfer learning and fine-tuning methods	572 MRI images	97.3 with less execution time
Rehman et al. [19]	Brain tumor classification	Deep learning technique through implementation of transfer learning method	3,215 MRI images	96.67
Tripathi et al. [20]	Brain tumor grading	Non-invasive technique for using textural based features	640 MRI images	96.8
Ismael et al. [21]	Brain tumor classification	Back-propagation technique and statistical feature extraction	320 patients with 1,580 slices	92.8
Anaraki et al. [22]	MRI-based brain tumor grading	CNN and genetic-based algorithms	Not specified	Gives better accuracy than CNN alone.
Kaldera et al. [23]	Classification of brain tumor with high speed	Fast R-CNN	32 MRI images	97.8, with small dataset drawback

In this paper, we devise and implement a CNN network for the automated classification of brain tumors. We classify these types of tumors into gliomatosis cerebri tumors, astrocytoma tumors, and glioblastoma tumors. Gliomatosis cerebri tumors have a diffusion pattern and can cause extensive growth and infect multiple brain lobes (Fig. 1). Astrocytoma brain tumors can be aggressive and can grow at a fast pace (Fig. 2). Therefore, it is very important to identify astrocytoma tumors when they first occur. Glioblastoma is a fast-growing tumor and is considered a grade IV astrocytoma (Fig. 3).



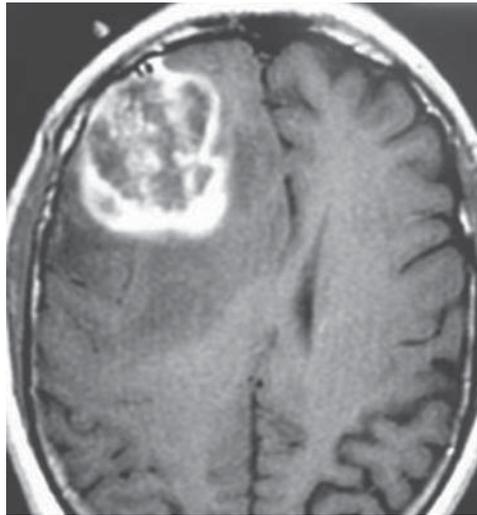
**Figure 1:** Gliomatosis cerebri diffusion pattern



**Figure 2:** MRI images showing astrocytoma brain tumor in AC-PC and sagittal planes. The tumor is outlined with a pink mark

These three types of tumors are our concern in this research because very few research efforts have tried to classify them using computerized methods.

The rest of the paper is as follows: Section 2 describes the methodology and the dataset used. Section 3 presents the validation and testing, while Section 4 discusses the experimental results. Section 5 presents the conclusions of this research.



**Figure 3:** Glioblastoma grade IV astrocytoma

## 2 Methods

### 2.1 MRI Dataset

MRI images for real patients with and without tumors were taken from the database in [11]. The dataset we used included 680 MRI images of astrocytoma tumors, 520 MRI images of gliomatosis cerebri tumors, and 700 MRI images of glioblastoma tumors. Another 680 MRI images of normal-cell brains without tumors are also included in our dataset. All images are captured in the sagittal plane and the anterior commissure–posterior commissure (AC–PC) plane, which is an axial MRI plane that is widely used. Fig. 2 presents an example of MRI images showing a brain tumor in the AC–PC and sagittal planes.

### 2.2 Pre-Processing Stage

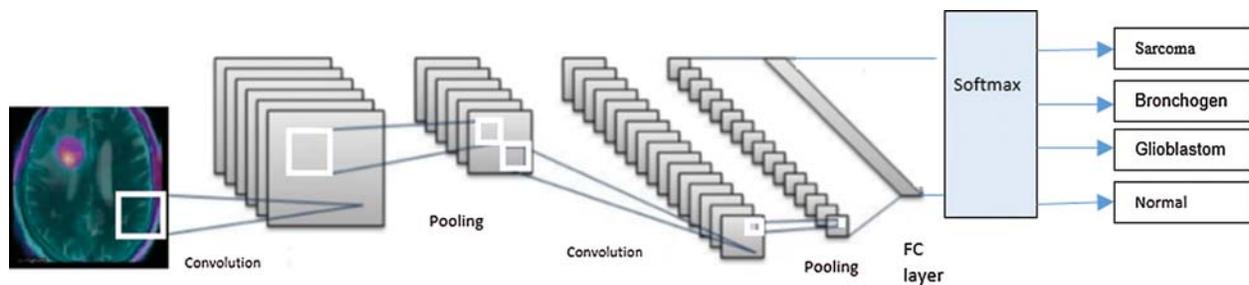
The normalization of the acquired MRI images for the dataset used in our research was necessary because they were sized differently. All MRI images were normalized into  $512 \times 512$  pixels.

We applied pre-processing steps to the MRI images prior to any image analysis being done. The pre-processing steps included:

- Distortion rectification: Spatial distortions, especially near the anterior frontal lobe, were eliminated through high-pass filters.
- Motion correction due to head movement during the MRI using motion compensation techniques from a set of MRIs taken at time slices via minimizing a cost mean-squared difference error function.
- Noise elimination, which was done by applying low-pass filtering that could output spatial smoothing for the MRI images.
- Spatial smoothing was also accomplished through the averaging of adjacent pixels and the removal of noises that were above the average standard deviation.

### 2.3 The CNN Architecture

We classified brain tumors from the MRI images through deep learning by utilizing CNN. As shown in Fig. 4, the implemented CNN was comprised of: 1) an input layer; 2) several blocks (C-P blocks) that included a convolution layer followed by a pooling layer; 3) a classifier layer; and finally 4) an output layer. Each C-P block contained convolutional and pooling layers. The convolution layer converted the input image into a smaller image with the ratio of 4:1 from the input image. The convolutional layer was tailed with the pooling layer. The pooling layer utilized a max pooling strategy to reduce the image further to a quarter of the input's size. The classifier block consisted of two fully connected layers, representing the output of the latest pooling layer (max) and the identification of the tumor class. The CNN layers and their properties are depicted in Tab. 2.



**Figure 4:** The CNN network, including the input layer, two convolution/pooling layers, the classification layer, and the output layer

**Table 2:** CNN neural network layers

Layer #	Layer type	Properties
1	Input layer	$512 \times 512$ images
2	First convolutional layer	$330 \times 5 \times 1$ convolutions
3	First pooling layer	Max pooling
4	Second convolutional layer	$64 (3 \times 3 \times 16)$ convolutions
5	Second pooling layer	$2 \times 2$ max pooling
6	Third convolutional layer	$128 (3 \times 3 \times 32)$
7	Third pooling layer	$2 \times 2$ max pooling
8	Fully connected (FC) layer	1,024 hidden neurons
9	Softmax feature extraction layer	Softmax
10	Classifier output layer	Three output classes: 1. Astrocytoma tumor 2. Gliomatosis cerebri tumor 3. Glioblastoma tumor

### 3 Validations and Testing

We devised experimental validation using  $k$ -fold cross-validation testing and hold-out testing. We conducted the experiments on MRI images without motion correction and on motion-corrected MRI images.

#### 3.1 $K$ -Fold Cross-Validation

In the experiments, we utilized a  $k$ -fold cross-validation to assess the performance of the implemented CNN neural network.

We divided the data into  $k$  partitions of approximately equal size (equal folds). CNN training and validation was performed in  $k$  iterations. For each iteration, one fold was utilized for testing and  $k-1$  folds were utilized in the training phase. The accuracy was measured in every iteration, and the average accuracy over all of the iterations defined the model accuracy. To have a well-accepted accuracy, data stratification is a must. Stratification is the rearrangement of data in each fold to become an acceptable representation of the data as a whole.

The first set of experiments used MRI images without motion correction and its results are depicted in [Tab. 3](#). The second set of experiments was performed on motion-corrected images and its results are depicted in [Tab. 4](#).

**Table 3:** Cross-validation testing for MRI images without motion correction

Testing method	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)
8-fold	87.41	85.10	86.17	85.73
10-fold	93.60	91.43	92.02	91.91
12-fold	90.00	89.46	89.12	89.86
14-fold	86.48	85.13	85.32	84.95

**Table 4:** Cross-validation testing for MRI images with motion correction

Testing method	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)
8-fold	94.30	93.71	94.17	93.83
10-fold	97.26	95.41	96.23	96.01
12-fold	91.45	91.40	92.72	91.86
14-fold	89.98	89.93	89.82	89.95

The results of this experiment found  $k$ -fold cross-validation with  $k = 10$  to have the best accuracy, with a classification error as low as approximately 2.7% for motion-corrected MRI, as shown in [Tab. 4](#), and with a classification error of more than 7% for MRI without motion correction, as shown in [Tab. 3](#). The confusion matrix for the 10-fold testing procedure for motion-corrected MRI is depicted in [Tab. 5](#).

#### 3.2 Hold-Out Testing

Hold-out testing is used to remove the over-fitting that can be seen in the  $k$ -fold testing method where the testing folds have a statistical resemblance to the training folds. The MRI data is partitioned into two not necessarily equal non-overlapping partitions. While the first partition is

specifically used for training only, the second (hold-out partition) is utilized in testing and validation. The problem with hold-out validation is the over-fitting, especially if the data that is utilized in the learning model is not distributed properly. In spite of the over-fitting problem, though, this method has the advantage of taking less learning time than the  $k$ -fold cross-validation.

**Table 5:** Confusion matrix for the utilized dataset with 10-fold cross-validation for MRI images with motion correction

		Predicted cases				Total	Average accuracy (%)	FN (Having cancer and predicted as normal) (%)
		Astrocytoma	Gliomatosis cerebri	Glioblastoma	Normal			
Actual cases	Astrocytoma	648	2	0	8	680	95.29	1.17
	Gliomatosis cerebri	3	510	2	5	520	98.00	0.96
	Glioblastoma	7	1	690	3	700	98.50	0.42
	Normal	1	2	1	676	680	99.40	–
	Total	–	–	–	–	2,580	97.80	0.62

Therefore, we used an intermediate approach between hold-out testing and the  $k$ -fold testing. To increase the randomness of the partitions while avoiding the over-fitting problem, we divided the data into  $k$  nearly equal portions in a random fashion. This mechanism is utilized in order to examine the capability of the CNN generalization procedure in medical diagnosis [24,25]. This will aid in forecasting the brain cancer diagnosis based on the data that has no observations in the training model. Therefore, a constraint in dividing the partitions must be that no subjects in the training shall be included in the test set. We tested the hold-out method by dividing the data into two partitions, three for validation, and nine for training.

**Table 6:** Confusion matrix for the utilized dataset with hold-out test validation for motion-corrected MRI images

		Predicted cases				Total	Average accuracy (%)	FN (Having cancer and predicted as normal) (%)
		Astrocytoma	Gliomatosis cerebri	Glioblastoma	Normal			
Actual cases	Astrocytoma	164	2	1	3	170	95.29	1.17
	Gliomatosis cerebri	3	125	0	2	130	98.00	0.96
	Glioblastoma	2	1	171	1	175	98.50	0.42
	Normal	0	1	1	168	170	99.40	0.60 (FP)

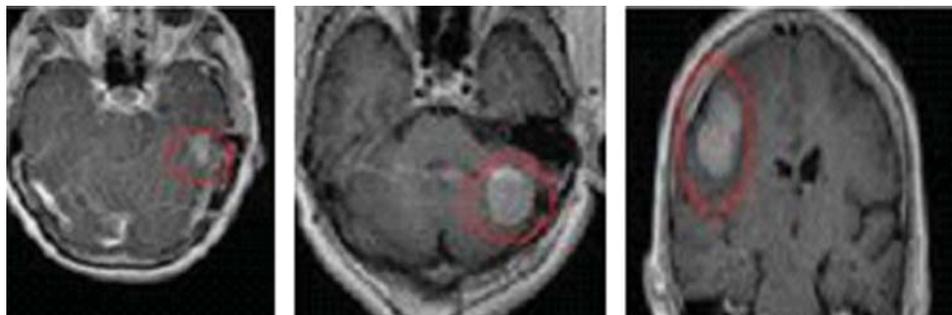
The CNN is trained using a stochastic gradient descent optimizer with data shuffling for every iteration. It finalizes the training process by tuning into one epoch. The training process will end with the start of the increase of loss. We set the regularization factor to 0.006 and the rate of the initial learning to 0.0003. Xavier initializer was used to initialize the convolutional layers' weights [26].

We devised the testing procedure to end the training at the event that the loss was greater than the previous lowest loss for 10 consecutive iterations. The confusion matrix for the utilized dataset with hold-out test validation (for motion-corrected MRI images) is depicted in Tab. 6.

#### 4 Experimental Results Discussion

The experimental results of the implemented CNN using  $k$ -fold cross-validation with  $k$  equal to 8, 10, 12, and 14 folds are depicted in Tabs. 3 and 4, for MRI images without motion correction and for motion-corrected MRI images, respectively. Average precision, average recall, and average F1-score are displayed, which helped overcome the classes' imbalance of the number of tumors in the dataset.

Instances of tumors classified from the used dataset via 10-fold cross-validation testing are displayed in Fig. 5. (The tumors are marked in pink outlines.)



**Figure 5:** Instances of classified tumors from the used dataset using 10-fold cross-validation testing

A classifier is usually evaluated by measuring its accuracy, sensitivity, and specificity. Eqs. (1)–(3) are the metrics to measure the accuracy, sensitivity, and specificity of this classifier, respectively. The classifier attains 97.5% average accuracy, 99.44% average sensitivity, and 97.15% average specificity over 20 runs. These numbers are for the dataset of motion-corrected MRI images.

$$\text{accuracy} = \frac{TP + TN}{TP + FP + FN + TN} \quad (1)$$

$$\text{sensitivity} = \frac{TP}{TP + FP} \quad (2)$$

$$\text{specificity} = \frac{TN}{TN + FN} \quad (3)$$

where TP (true positives) is the number of correctly predicted positive cases, TN (true negatives) is the number of correctly predicted negative cases, FP (false positives) is the number of incorrectly predicted positive cases, and FN (false negatives) is the number of incorrectly predicted negative

cases. The accuracy of a classifier is the percentage of correctly predicted cases among the test set, the sensitivity is the rate of true positives, and the specificity is the rate of true negatives.

Two figures show our experimental results:

- Fig. 6 shows the distribution of the different cases. The total number of cases and the numbers of normal and cancerous cases are plotted. In addition, the output of our proposed CNN is presented, showing the different types of brain cancer cases in the testing set.
- Fig. 7 shows the accuracy, sensitivity, and specificity of five runs of the classifier. It also shows the average accuracy, sensitivity, and specificity of 20 runs of the classifier, each with a different set of input data and a different set of tested data.

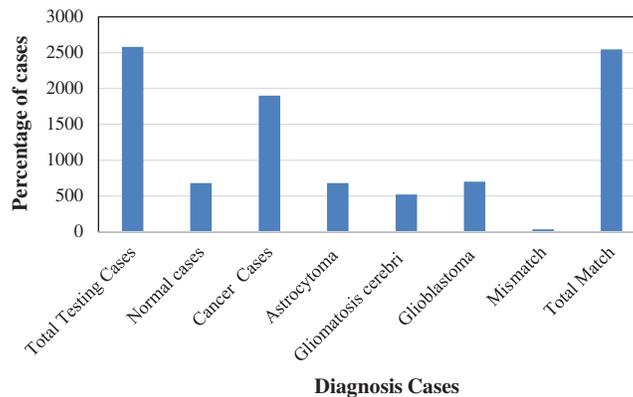


Figure 6: Percentage of patient cases using 10-fold cross-validation

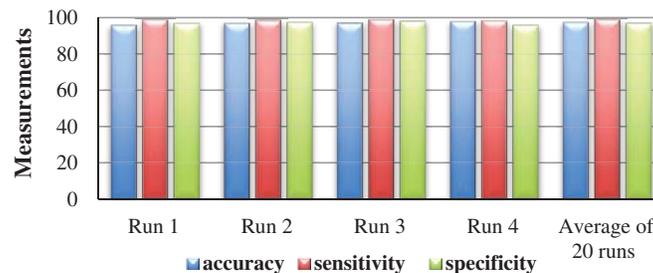


Figure 7: The accuracy, sensitivity, and specificity of 4 different runs and the average accuracy, average sensitivity, and average specificity of 20 runs

#### 4.1 Performance Comparison

Several researchers have used the database in [11] to classify brain tumors using CNN technique. The CNN architectures that used MRI images with motion correction as input for classification were compared to our proposed architecture using  $k$ -fold cross-validation, as shown in Tab. 7.

**Table 7:** Comparison of the results of the CNN, which used motion-corrected MRI images as input for classification, and our proposed architecture using  $k$ -fold cross-validation

Reference	$k$ -Fold cross-validation method/data division	Accuracy [%]	Sensitivity [%]	Specificity [%]
Rehman et al. [19]	8-fold: training set (80%), testing set (20%)	94.03	95.80	92.30
Tripathi et al. [20]	10-fold: training set (70%), testing set (30%)	91.68	92.10	93.00
Ismael et al. [21]	10-fold: training set (70%), testing set (30%)	93.68	94.60	91.43
Proposed	10-fold: training set (80%), testing set (20%)	97.50	99.44	97.15

#### 4.2 Limitations

Improvement of the quality of the utilized visual feature is very essential to produce better classification results that can lead to augmenting the tumor region.

The performance of our proposed algorithm can be enhanced using clustering techniques as a preprocessing stage; K-means and C-means algorithms might be very helpful [27]. Both algorithms are unsupervised clustering algorithm that will lead to better segmentation of regions of interest which will lead to better classification. Also, Sparse coding can be combined to enhance the classification performance of our model especially that we have datasets with labeled images. Sparse coding can lead to better discriminative classifier.

Another aspect that may hinder the performance is that MRI images are vulnerable to noise, so more complicated inhomogeneity correction should be applied. Also, more advanced motion correction algorithms can enhance the performance especially for pediatric patients. Other limitation that hindered our experiments is the unavailability of larger datasets.

#### 5 Conclusions

In this paper, we demonstrated the importance of automated methodology for brain cancer tumor diagnosis. We developed and implemented a CNN for brain tumor classification. The proposed CNN can distinguish between normal (no-cancer), astrocytoma tumors, gliomatosis cerebri tumors, and glioblastoma tumors. We chose these types of aggressive cancerous classifications in order to shed light on the need to automatically diagnose them.

The implemented CNN utilized motion-corrected MRI images and was evaluated using two performance measurement procedures. The first one is a  $k$ -fold cross-validation testing method, using  $k = 8, 10, 12,$  and  $14$ , in which  $k = 10$  was determined to achieve the best accuracy of 96.26%. Generalization of the CNN architecture is very important, as it proves that the algorithm's accuracy does not depend on a specific dataset. Therefore, we also used a hold-out testing as a second evaluation procedure. The results succeeded in attaining 97.8% accuracy with a specificity of 99.2% and a sensitivity of 97.32%. With the high accuracy in the classification procedure, the developed CNN architecture is considered to be an effective automated diagnosis method for the classification of brain tumors from MRI images.

In future extension of the work, the proposed methodology can be extended for other brain tumor classification such as gliomas and pituitary. The diagnosis of other brain tumors types can lead to detect other brain abnormalities.

Other contribution that can stem from our proposed system is to participate effectively in the early diagnosis of other types of cancers such as breast and lung cancers that can benefit from our classification scheme, especially for cancers with high mortality rate. We can extend our approach in other image classification of diseases especially with the problematic accessibility of large image datasets.

Also, the practicality of the proposed method can be utilized in devising an automated diagnostic tool that can help in tumor classification at an early stage. The motion correction aspect of our methodology can be incorporated in a pediatric diagnostic tool to compensate for head motion of small children.

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