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Research Article

Multiple classification of brain tumor images using a new and efficient convolutional neural network-based model

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ABSTRACT

In conventional methods, the detection of tumour disease from brain images using magnetic resonance imaging is a difficult and human error-prone field of study that requires an expert medical doctor. Incomplete or inaccurate detection of brain tumours can have significant undesirable consequences such as shortening of human life. In order to overcome these difficulties, many researchers are working on autonomous disease detection supported by artificial intelligence. The aim of this study is to utilise brain magnetic resonance images with deep learning architectures for fast and reliable autonomous cancer detection. In this study, brain images are classified using two different datasets and a convolutional neural network infrastructure, which are widely used in the publicly available literature. The results obtained as a result of experiments with similar parameters in training, validation and testing processes are compared in detail with other studies in the literature and the differences between them are presented. The new convolutional neural network-based model proposed in the study achieved 99.76% classification result in the accuracy evaluation metric. The results obtained showed that the model proposed in the study can be used with high accuracy in brain tumour detection and can shed light on other fields of study.

Introduction

Anomalies in cell growth within the human brain or spinal canal result in the formation of brain tumors. These tumors pose significant challenges and are among the most formidable and lethal irregularities to address, impacting individuals across all age groups and genders. Swift identification of brain tumors is imperative to impede their progression to advanced stages. These growths can be classified as either non-cancerous (benign) or cancerous (malignant), with symptoms varying based on their size and cerebral placement. Glioma brain tumors are acknowledged as the most fatal type. The survival rate for high-grade gliomas is less than 5% over a span of five years [1]. Brain tumors rank among the ten leading factors contributing to mortality in both males and females. Additionally, they stand as the second primary contributor to cancer-induced fatalities in individuals under 20 years old, following leukemia. According to data from the year 2020, approximately 251.329 individuals across the globe lost their lives due to malignant brain tumors [2]. Some common symptoms of brain tumors include headaches, seizures, vision and hearing problems, difficulty understanding speech and language, mood or personality changes [3].

The manual evaluation of brain tumors on raw MR images is an extremely challenging task for radiologists. To overcome this situation, computer-aided diagnosis (CADx) is required to assist in the evaluation of MR images. In medical image analysis, many researchers have carried out different studies in this field. These studies can be classified as identification, detection and segmentation [4]. These studies are mainly carried out with traditional machine learning approaches and DL approaches belonging to the artificial intelligence (AI) class.

In addition to providing solutions to engineering problems that can be modeled as various systems, AI also helps to produce solutions to human-related problems, which are the most complex of systems. A very large part of these solutions is undoubtedly medical applications. Today, AI is utilized in almost every field of medicine. Detection of many types of cancer (lung, breast, central nervous system tumors, etc.), hypertension control during anesthesia, and calculating the volume and depth of brain tissues in MR images are examples of these applications. As a result, accurately assessing the size, shape and location of the tumor within brain tissue is an extremely difficult process. This also negatively affects treatment planning procedures. In medical science, any disease that may occur in soft brain tissue is one of the most feared diseases. Detection of such tumors in the brain tissue, which serves as a vital organ for the individual, is of vital importance. This has led to the Brain Tumor Segmentation (BraTS) Challenge competition organized annually by Medical Image Computing and Computer-Assisted Interventions [5, 6]. The BraTS competition is specifically focused on the segmentation of tumor regions on MR images and is a competition that encourages studies in this field.

DL, a rapidly expanding domain within the realm of data science, pertains to a category of algorithms founded on artificial neural networks designed to handle unstructured data types like audio, images, videos, and textual content [7]. Its capacity to facilitate scalable interpretation of images makes DL adept at extracting intricate feature representations beyond human perceptibility. This, combined with the significance of managing extensive datasets to attain efficient and precise outcomes, introduces remarkable avenues for its application in the healthcare sector. One notable application is the utilization of deep learning for analyzing images, specifically in pinpointing tumor locations. DL serves a multitude of purposes, spanning from diagnostics and prognostics to real-time monitoring of analyses and the formulation of individualized treatment strategies. These possibilities unfold through the utilization of data collected and processed by deep learning models tailored for image analysis [8].

Recently, many studies have utilized CNN-based algorithms to classify brain tumors. Among these studies, the deep learning-based CNN model utilized to classify brain MR images into different classes stands out [9]. On the other hand, studies with extremely high accuracy rates were conducted with the use of net technologies such as AlexNet, GoogLeNet, etc. [10]. With evolving hardware and software infrastructure, CNNs will continue to play an important role for future academic research and industrial applications [11]. In this study on tumor detection and classification focusing on DL-based methods, we provide clinicians with a comprehensive overview of how to make accurate inferences from complex, heterogeneous and high-dimensional biomedical data.

Contribution

There is a good similarity in appearance between normal tissue and brain tumor cells, so segmentation of tumor sites becomes a challenging task. This may affect the appropriate medical treatment of the patient. Therefore, there is a necessity for a highly accurate automatic tumor detection and classification method. Deep ML-based methods allow this process to be performed faster and in a controlled manner with a low error rate. At this point, it is thought that the experimental results of the current study based on DL approaches provide significant contributions to support medical decision-making.

A review of the literature reveals that there are many studies on tumor segmentation, but fewer on tumor detection and classification. In this context, we propose a new and efficient CNN model from scratch for tumor detection and classification. Enhancing the creation of computer-assisted systems aimed at facilitating timely and precise brain tumor diagnosis holds pivotal significance in the realm of treatment procedures. Equally crucial is the refinement of previously suggested techniques to elevate the accuracy of medical image analysis, thereby expediting the process of accurate diagnosis and subsequent treatment. At this point, our model, which we built from scratch, significantly increases the classification accuracy compared to previous studies.

The consistent utilization of automatic classification methods employing ML and AI has consistently yielded superior accuracy when compared to manual classification. Thus, putting forth a system that undertakes detection and classification via DL algorithms like Convolutional Neural Networks (CNN), Artificial Neural Networks (ANN), and Transfer Learning (TL) holds the potential to make substantial contributions to medical professionals engaged in this domain.

The primary contributions of the present research can be succinctly outlined as follows:

- The study facilitates the creation of a novel and efficient CNN model right from its inception, utilizing the principles of deep learning.
- The study demonstrates experimental results obtained through datasets with high accuracy in identifying brain tumors.
- The developed system is one of the studies that achieved the best classification accuracy among all other related studies.
- The proposed model will help clinicians predict the type of tumor and provide the most suitable treatment for patients.

The subsequent segments of the study are organized in the following manner: In Section 2, the conceptual framework underlying brain tumor detection and classification is expounded, along with a comprehensive survey of the preexisting literature in this domain. Proceeding to Section 3, the study delineates the dataset and methodological approach employed, elaborating on the designed DL model for brain tumor detection. In Section 4, the experimental outcomes and associated observations are presented. Concluding the study, the final section encapsulates overarching concluding observations and engages in a discourse concerning the future trajectories of DL-driven image analysis within the domain of cancer research.

Brain tumor and classification

The word tumor is a synonym for "neoplasm", which is the result of the abnormal growth of cells. A "neoplasm" is an abnormal tissue that is capable of unlimited growth and movement beyond the control of the living organism. Brain tumors, which manifest as a prevalent and aggressive ailment, manifest as an accumulation of these anomalous cells within the cerebral region. Typically, their emergence is prompted by an abrupt and atypical augmentation of brain matter. The volume of these deviant cells is not static; instead, they undergo rapid proliferation and initiate dissemination [12]. A brain tumor can be malignant or benign depending on its morphological structure [13]. Benign tumors are less aggressive in terms of their normal appearance, with slow growth rates and regular borders, and can be surgically removed because they have good borders. Malignant tumors, on the other hand, contain cancer cells and can worsen the patient's condition as they rapidly spread to other tissues in the brain, have a very irregular shape and are aggressive to the point of being life-threatening. Furthermore, brain tumors are divided into primary and secondary tumors depending on their origin. Tumors that occur in the brain are considered primary tumors, while tumor types that arise in another part of the body and then progress to the brain are considered secondary tumors [14]. The approach to medical treatment predominantly relies on the specific types of tumors and their respective locations. Brain tumors can be divided into various groups according to their morphological structure, localization, growth rate and recently especially their genetic structure [15]. Figure 1 presents this grouping.

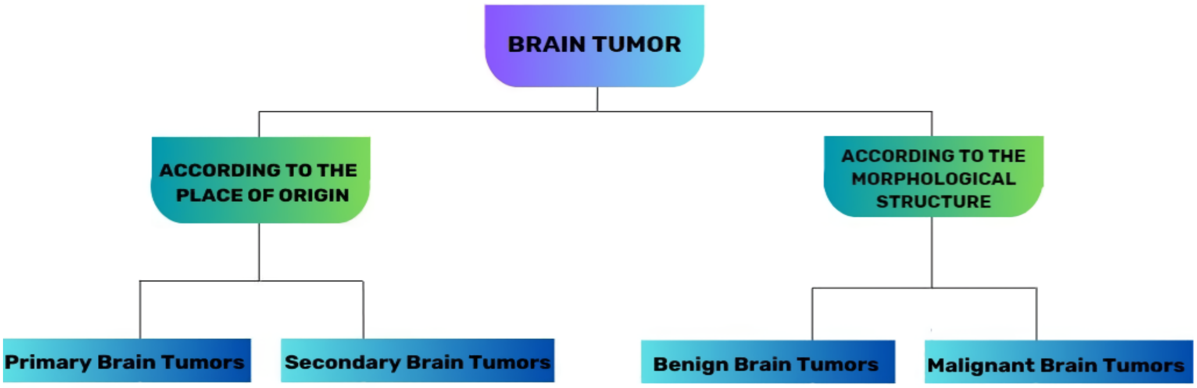


Figure 1. Brain tumor grouping

In 2016, the World Health Organization (WHO) released a revised edition of its brain tumor classification framework, encompassing significant revisions. The WHO introduced a classification into four distinct grades for malignant tumors, which considers both the physical and chemical attributes of the brain tumor. These grading criteria are visually represented in Figure 2.

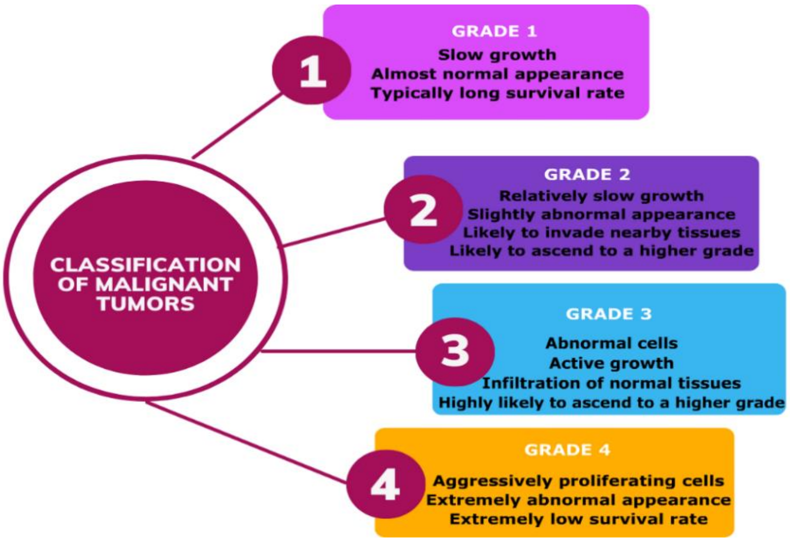


Figure 2. Brain tumor grading criteria

As can be seen in Figure 2, for the first time, the WHO classification of brain tumors is not based solely on histology. As a novelty, a "layered diagnosis" approach has been introduced to brain tumor classification. Within the revised 2016 WHO classification system for Central Nervous System (CNS) tumors, specific tumor types are delineated through a fusion of morphological, microscopic, molecular, and genetic considerations, while certain others persist in being characterized solely by their morphology. It is evident that the prevailing tendency favoring augmented integration of molecular and genetic components in tumor characterization, encompassing both CNS tumors and broader tumor classification, is likely to persist [16].

As per the National Brain Tumor Society, the spectrum of brain tumors encompasses over 120 distinct types. Within our study, we focused on Glioma, Meningioma, and Pituitary brain tumors, as these are the most frequently referenced categories in the literature. To provide a succinct overview, Glioma denotes a tumor category that originates within the brain and spinal cord, developing from glial cells that function as the brain's support structure. Gliomas encompass various subtypes, with the most prevalent being astrocytoma. Gliomas account for approximately 30% of all brain tumors and tend to be largely malignant [17]. Conversely, meningioma stands as one of the prevailing brain tumor types. Characterized by gradual growth, these tumors do not metastasize and are amenable to surgical removal. They are typically benign and do not adhere to brain tissue. This makes it possible to remove them completely with surgery. Meningiomas smaller than 2 cm or up to 5 cm in size can be encountered [18]. Pituitary tumors are benign tumors of the pituitary glands located in the lower part of the brain (skull base). They can be treated with medical and surgical methods. They often present with visual disturbances, hormonal disorders and headaches.

Causes and most common symptoms of brain tumor

Although the causes of brain tumors are unknown, it is accepted that some brain tumors are inherited. Moreover, there are some risk factors. These risk factors are briefly explained below [19]:

Gender: Brain tumors are more common in men, but meningiomas are more common in women.

Race: All types of brain tumors are more common in Caucasians.

Age: When the incidence of brain tumors is evaluated based on age, the incidence of tumors is higher in individuals over the age of 70, and in childhood, brain tumors in the cerebellum are more common in those under the age of 10.

Family History: Individuals with a family history of brain glioma are more likely to develop brain tumors. Apart from these, some viruses, radiation exposure, some chemical azo dyes, head trauma and various hormones can be counted as other risk factors in the formation of brain tumors.

The most common symptoms of brain tumors can be listed as follows:

-Headache (especially headache at night)
-Numbness, tingling or loss of strength in the arms and legs
-Gait and balance disorders
-Double vision, blurred vision, nausea, vomiting
-Fainting (epileptic seizures)
-Personality disorders, forgetfulness, speech disorders

Artificial intelligence and deep learning in brain tumor detection

Artificial intelligence (AI), which was developed based on the problem “How can machines be smarter?”, can be briefly defined as the ability of machines to imitate human cognitive and learning abilities and to realize human-specific reasoning abilities. For the first time in a 1985 study, artificial intelligence was used in brain tumor detection [20]. The frequency of brain tumors and the use of various sub-branches of AI in tumor detection and classification bring AI to an important point in the field of health informatics. These main sub-branches are shown in Figure 3.

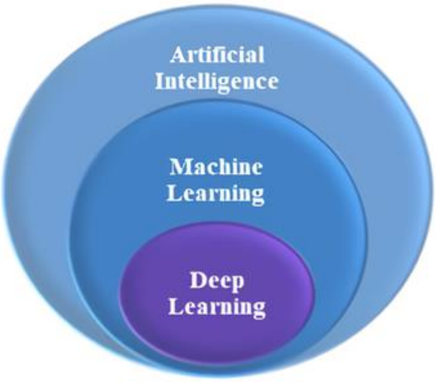


Figure 3. Artificial intelligence elements

DL is a machine learning approach that utilizes artificial neural networks (ANN), consisting of three or more layers [21]. ANN stand as a prominent technique within the domain of machine learning [22]. DL architectures have garnered preference over conventional Machine Learning (ML) algorithms due to their capacity for autonomous learning and adeptness in deciphering intricate image attributes. The landscape of DL continuously evolves with the emergence of novel models aimed at enhancing feature extraction, and finding utility across diverse medical domains. DL techniques encompass an array of methodologies extensively applied in tasks encompassing image processing, classification, and segmentation [23]. In building deep learning frameworks, three primary architectures are commonly employed: Convolutional Neural Network (CNN), Deep Belief Network (DBN), and Recurrent Neural Network (RNN). DBN finds utility in general classification tasks, while RNN is suited for sequential data formats. However, CNN holds sway in the domain of image, text, and audio classification [24].

Convolutional neural networks (CNN)

CNN constitutes a multi-layered, forward-propagating artificial neural network, notably employed in the realm of image analysis [25]. CNNs hold significance in image recognition and contribute substantially to the formulation and advancement of classification models rooted in natural language processing. CNN architecture has provided high success in diagnosing diseases in the fields of medicine, image and voice recognition, computer vision, text and video processing, and many other fields. The aim of artificial systems with CNN, which is based on the human visual system, is to perceive, identify and classify objects. Convolutional Neural Networks are a combination of the well-known convolution process and artificial neural networks.

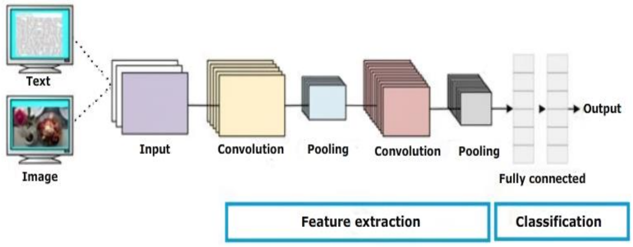


Figure 4. Convolutional neural network model

Upon scrutinizing the CNN architecture depicted in Figure 4, the model encompasses distinct components such as an input layer, convolution layers, pooling layers, a fully connected layer, and an output layer. Adhering to the conventional CNN structure as illustrated in Figure 4, each convolutional layer is succeeded by a rectified linear unit (ReLU), representing a nonlinear function, and subsequently, a pooling layer.

Related studies

Upon analyzing the literature, it becomes evident that numerous investigations rooted in deep learning have yielded promising experimental outcomes in the realms of diagnosing, classifying, and segmenting brain tumors. Of notable significance is the consensus that sophisticated deep CNN architectures have achieved impressive levels of automated brain tumor detection and accurate classification. Within this segment, the focus turns to a comprehensive review and presentation of recent studies centered around the deep learning methodology for brain tumor detection and classification.

Kumar, Prasad, and Metan [26] introduced a study focused on brain tumor detection and classification, where they proposed a model utilizing a Deep Convolutional Neural Network with a ResNet 152 Transfer Learning strategy. Their approach amalgamated CNN and Transfer Learning techniques. The research reported achieving remarkable accuracy along with a minimal error rate in tumor detection. In a separate endeavor, Bhanothu, Kamalakannan, and Rajamanickam [27] devised a swifter R-CNN deep learning algorithm for tumor detection. The algorithm employed the VGG-16 architecture as the foundational layer for both the region proposal network and the classifier network. The algorithm achieved an average precision of 77.60% across all classes. Çınar and Yıldırım [28] used CNN and ResNet50 architecture, which is a variant of CNN models. Their approach involved removing the last five layers of the ResNet50 model and then adding eight new layers. Vankdothu, Hameed and Fatima [29] proposed the combination of a CNN and Long-Short Term Memory (LSTM) in their work. The model's efficacy was tested against a Kaggle dataset comprising 3264 MR images, yielding a commendable accuracy of 92%. Conversely, Patil and Kirange [30] introduced a shallow Convolutional Neural Network (SCNN) and combined it with the VGG-16 network utilizing T1C modality MR images. Aslan [31] conducted a brain tumor detection study founded on deep learning principles. They employed the k-nearest neighbor (k-NN) algorithm in conjunction with the MobileNetV2 deep network model to identify brain tumors from MR images. The method garnered an accuracy rate of 96.44% in k-NN-based brain tumor detection. Deepak and Ameer [32] engaged deep CNN features in tandem with the transfer learning approach to classify brain tumors. Their study targeted a three-class classification problem, aiming to differentiate the major brain tumor types (glioma, meningioma, and pituitary). Nazir et al. [33] use a customized CNN model powered by three advanced explainable artificial intelligence (XAI) techniques. The proposed model achieved a remarkable training accuracy of 100% and validation accuracy of 98.67%. Goceri [34] designed an efficient network containing CNN and transformer blocks for glioma grading and brain tumor classification from MRIs. The proposed approach achieved a high accuracy of 99.21% in glioma grading and 98.66% in brain tumor classification.

Material and Method

This section describes the datasets utilized in the study and the preprocessing steps applied to the datasets. Then, detailed information about the proposed CNN architecture is given. We also discuss the reasons for choosing this method and the post-processing steps for training the model. The first dataset is the base dataset of our study. The second dataset is utilized while measuring the performance of the developed model when trained on a different dataset. Detailed information about the datasets is presented below.

Dataset-1

The brain tumor MR images processed in the current study were retrieved from the Kaggle web platform, which provides input for the use of metrics and ML algorithms for exploratory analysis. The dataset-1 is divided into two folders, the training folder and the test folder, containing a total of 7023 images [35]. 5712 data were allocated for training (81.3%) and 1311 for testing (18.7%) (Figure 6).

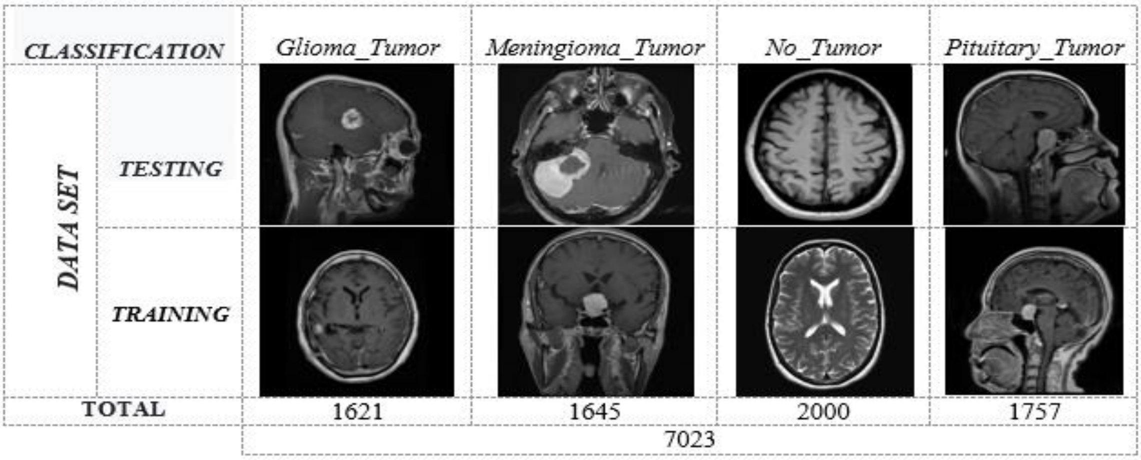


Figure 5. Examples of images and numbers of dataset 1

In Figure 5, 1621 images contain glioma tumors, 1645 images contain meningioma tumors, 2000 images contain no tumor and 1757 images contain pituitary tumors.

Dataset-2

Dataset 2 was downloaded for free from the Kaggle web platform, which provides publicly available data for scientific studies. The dataset-2 contains 3264 images in total [36]. 2870 images are reserved for training and 394 images are reserved for testing. Each folder has four subfolders (Glioma_tumor, meningioma_tumor, no_tumor, pituitary_tumor). These folders have MRIs of the respective tumor classes. A cross-section of the dataset is presented in Figure 7.

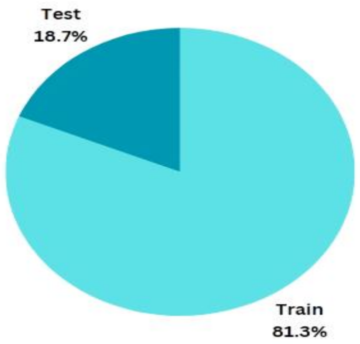


Figure 6. The distribution ratio of dataset 1

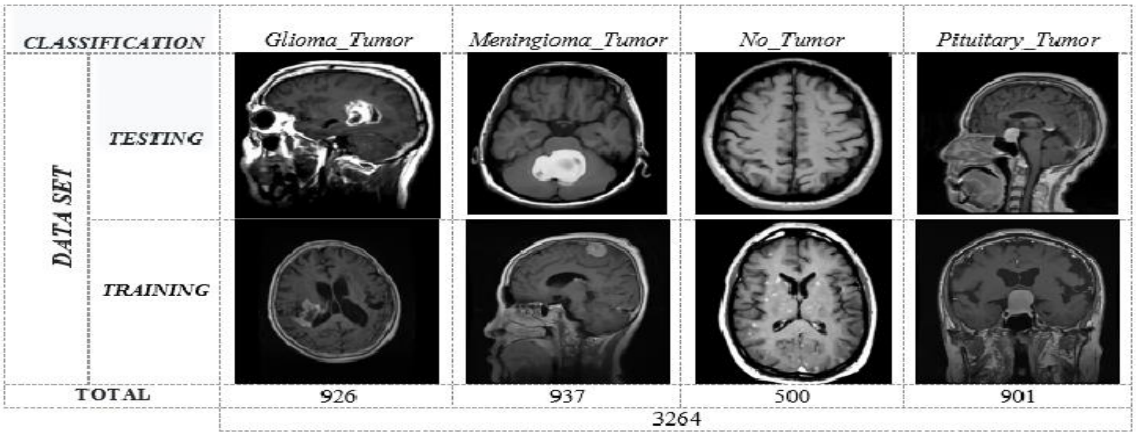


Figure 7. Examples of images and numbers of dataset 2

All images in the dataset are in two folders containing training and test images. To work with the data, the dataset was divided into glioma, meningioma, pituitary and no tumor folders. From the data divided into training and testing, 926 images contain glioma tumors, 937 images contain meningioma tumors, 500 images contain no tumor and 901 images contain pituitary tumors.

Pre-processing

Data quality is crucial to ensure that the study is free from incorrect analytical results and wrong business decisions. In this case, preprocessing is a necessary step to improve data quality. In particular, since it is difficult to classify images with complex texture structures such as the brain, it is imperative to have a certain level of image quality. For these reasons, images should be preprocessed before training. The images used in this study have undergone preprocessing such as normalization, some cropping and resizing to remove noise and improve image quality. These steps are briefly described below.

Normalization, image cropping and resizing

The different head size of each person makes the analysis difficult. To overcome this problem, a normalization process was performed to place the images on the same coordinate plane (Figure 8). In the normalization steps, OpenCV and Python were used to find the extreme north, south, east and west (x, y) coordinates along a contour.

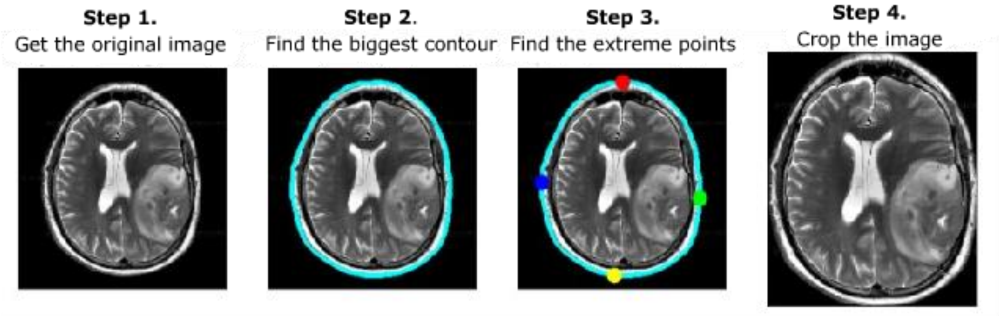


Figure 8. Normalization steps

In the next step, the images were resized to 224x224 pixels and the necessary preprocessing for CNN model input was applied (Figure 9).

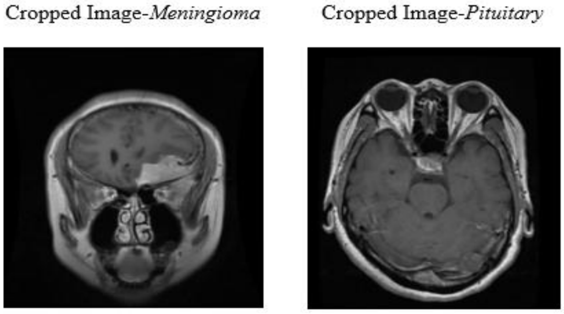


Figure 9. Examples of cropped and resized images in 224x224 pixels

In Figure 9, unnecessary and distorted areas as well as unnecessary backgrounds were removed from the images and the necessary processing steps were performed for the performance of the model and accurate classifications of images. To achieve this, the images were cropped and resized. Thus, the model is focused only on the regions where the features are present.

Proposed methodology

The deep learning architecture proposed for this study includes a Convolutional Neural Network (CNN). CNN is the most commonly used classifier as it produces remarkably successful results in the detection and classification of brain tumors. The study involves brain tumor diagnosis using MRI, classification as identification of type and tumor location. In this study, instead of using a separate model for each classification task, experiments were conducted using one model to classify brain images in different classification tasks. A new efficient CNN-based multi-task classification system built from scratch is developed for tumor detection and classification.

A thorough examination of the existing literature reveals a prevalent trend of conducting classification studies centered around the utilization of CNN architectures integrated with transfer learning models for the purpose of brain tumor detection. Although the use of this approach in classification studies offers different advantages, it may result in overfitting and inaccurate results. Given the feasibility of conducting brain tumor studies with modest datasets that do not necessitate an extensive array of class categories, the development of simpler CNN architectures proves adequate. In specific instances, research indicates the prevalence of two-class studies, such as distinguishing between tumor and non-tumor cases. To avoid over-learning and overfitting, we focused on training our model with more data and developing an efficient classical CNN network architecture. Figure 10 presents a diagram of the proposed model.

In our study, we undertook the task of enhancing the fundamental CNN model, culminating in the creation of an improved iteration. A new CNN model for brain tumor classification was crafted entirely from scratch. Our custom-designed model, stemming from modifications to the pre-existing CNN architecture, encompasses a total of 11 layers spanning from input to output layers. Within this structure, nine convolutional layers are interwoven with two fully connected layers. To facilitate training and evaluation, a dataset comprising 7023 brain MR images, sourced from the Kaggle platform, was employed—a dataset known for driving metrics and ML algorithms.

Figure 10. The architecture of the proposed CNN model

Central to CNN is the pivotal convolutional layer responsible for feature detection within images. It plays a fundamental role by executing convolution on input data. This process employs filters to scrutinize images, extracting both low-level and high-level features. Our novel CNN model commences with a convolutional layer featuring 64 filters, each possessing a filter size of 3×3. Subsequent to each convolutional layer, a pooling layer is introduced to mitigate network disparities. Among various pooling techniques, maximum pooling holds prominence due to its popularity. This technique trims down input data dimensionality while preserving critical information without compromising its integrity.

The utilization of normalization layers aids in refining the convolutional neural network's stability and regularity. Batch normalization, specifically, furnishes the advantage of expediting network learning while reducing data loss between processing layers by normalizing inputs. This enhancement significantly elevates accuracy across the network's expanse.

Recognizing the diverse array of features present in images and aiming to enhance the model's efficiency, adjustments were made to the number of filters in the third, fifth, seventh, and ninth layers. By augmenting the filter count, the network is equipped to better discern distinct image attributes. Following a similar methodology, these layers underwent the same sequence of operations: convolution, maximum pooling, and batch normalization. The outcome of these operations, in matrix form, necessitates flattening to facilitate utilization in the Fully Connected (FC) layer. To achieve this, a flattening layer was introduced, rendering the input ready for the FC layer.

Within our CNN neural network model, the FC layer follows the flattening layer. This layer garners its name from its comprehensive connection to all fields of the preceding layer, ultimately serving as the CNN architecture's terminal layer. To our model, we appended a 3×3 dimensional fully connected layer, endowed with 1024 filters. A dropout layer was then integrated to combat overfitting during model training. This layer operates by randomly deactivating certain neuron sets throughout the training phase. Post-experimentation, the optimal dropout value of 0.25 was determined based on model performance assessment.

Following the dropout layer, an additional fully connected layer with 3×3 dimensions and 512 features was incorporated. Ultimately, the model culminates in the final layer where the Softmax function is employed to generate class predictions based on the provided inputs, enabling multiple classifications. At this juncture, input data is classified into categories such as glioma, meningioma, pituitary, and non-tumor cases.

Table 1. Hyper-parameter used in the model

Hyper-parameter	Value
Input activation function	ReLU
Output activation function	Softmax
Loss	Categorical Cross-Entropy
Metrics	Accuracy
Optimizer	Adam
Epoch	60
Dropout rate	0.25
Initial learning rate	0.001
Learning rate decay	0.0001
Batch size	32
Train-test split	81.3%-18.7%

We ran our code in two different environments, first in the Python editor and then in the Google Colab platform, where we present our experimental results. Effective training of deep learning models requires careful selection of parameters and methods that optimize the accuracy and speed of the model [37]. In this study, all parameters were tested with different data partitions and tuned for optimal performance. The hyperparameters used in the model and their values are detailed in Table 1.

In this study, the determination of which layers to be used and which sections to be placed in the creation phase of the model, the hyper-parameters used and the parameters of the model were determined by examining successful methods in the literature and conducting experiments. Moreover, at this point, based on our experience, certain improvements have been made and optimum performance has been tried to be achieved. Adam optimizer was chosen as the optimizer of our model.

Taking into account the diverse factors influencing the efficacy of model training, the selection of an optimal number of epochs is paramount. An inappropriate epoch count may lead to memorization rather than genuine learning, and suboptimal updates to model weights. In our model, we determined the optimal epoch count as 60. To manage the training process, we employed categorical_crossentropy as the chosen loss function, coupled with an initial learning rate of 0.001.

The ReLU activation function was adopted for the input layer of our model, facilitating rapid learning. Conversely, the Softmax activation function was deployed for the output layer. Softmax operates by generating values within the 0-1 range, thereby ascertaining the probability of input membership in a particular class. A batch size of 32 was stipulated for training iterations. To gauge model performance, the accuracy metric was adopted—a well-recognized evaluation criterion within the literature. Furthermore, a pivotal parameter within our model is the dataset split: 81.3% of the available dataset was allocated for training, while the remaining 18.7% was reserved for testing purposes. This partitioning scheme plays a crucial role in the model's ability to generalize its learnings. The total number of parameters in the proposed CNN model is shown in Table 2 below.

Table 2. Total number of parameters in the proposed CNN model

Total parameters
Total params: 52.773.828 (201.32 MB)
Trainable params: 52.767.940 (201.29 MB)
Non-trainable params: 5.888 (23.00 KB)

As the number of parameters increases, the capacity of the model also increases, meaning it can learn more patterns. However, if the number of parameters is too high, the model can over-fit the training data and over-learn. In this case, it can perform poorly on the test data. Some techniques can be applied to the model to prevent over-learning. Examples of these techniques are regularization, dropout and data augmentation techniques.

In our study, we took some precautions to provide low time cost and high performance. When we look at the total number of parameters presented in Table 2, we see that the total number of parameters of our model is 52.77 million. 52 million parameters indicate a large capacity. At this point, risks such as over-learning may arise. We used the dropout technique to overcome this situation. This layer works by randomly disabling certain neuron clusters during the training phase. After the experiment, we determined the optimum dropout value as 0.25 according to the model performance evaluation. Since there were enough images in our dataset, we did not use the data augmentation technique. We aimed to reduce the time cost by running our model on a high-end computer system and observed its effect. We used Callback to speed up the training process of our CNN model and make it more efficient. In this context, we used early stopping to ensure time efficiency and prevent the model from being trained for unnecessary periods.

Almost all parameters in our model are trainable (52.76M). All layers of the model are open to learning. There are also 5.8K untrainable parameters in our model. These usually come from layers like Batch Normalization. This ratio is low, meaning almost all of the model is updatable.

When we compare the number of parameters of our model with some other popular CNN architectures; our proposed architecture has a total of 52.77 million parameters and a size of 201.32 MB, while VGG-16 architecture has 138 million parameters and a size of 528 MB. This architecture is quite large, time-consuming, and has many more parameters than our proposed model. In addition, ResNet50 architecture can be trained more deeply and is more efficient thanks to residual connections. In addition, EfficientNet-B0 is one of the popular CNN architectures that can work with fewer parameters such as 5.3 million and offer the same accuracy.

Our model has 52.77 million parameters, which is larger than ResNet50 but not as heavy as VGG16. This shows that our proposed model has high learning capacity and a strong architecture to capture complex patterns. A deep and wide architecture has the potential to learn complex visual features. Having more parameters compared to ResNet50 means that the model can learn more details. If trained with sufficient data, it can achieve high accuracy rates and show strong performance in challenging tasks. The high capacity of our model has become more efficient because it is well optimized. With some improvements, both the computational cost of the model has been reduced and the accuracy level has been increased. For example, the model has been made more balanced with techniques such as Dropout or Batch Normalization and Callback. In short, the good optimization of the training process has provided a strong model with high accuracy. The large capacity and deep structure of our model offers a powerful and flexible CNN architecture.

Results and Discussion

Within this section, we unveil the outcomes garnered from our experiments involving algorithms geared toward brain tumor detection and classification within MR images. Subsequently, we subject our proposed approach to a comprehensive evaluation utilizing suitable metrics. This evaluation culminates in a comparative analysis of the model's performance. Our novel CNN model, conceived as part of the proposed methodology, operates autonomously to detect and classify varying brain tumor types within the provided input dataset.

Evaluation metrics

The selection of appropriate metrics stands as a crucial stride in gauging the effectiveness and proficiency of the devised models. In this study, we employ established metrics such as accuracy, precision, recall, and F1 score to comprehensively assess the overall performance of our proposed model. These metrics are widely acknowledged and embraced in classification studies. The metrics used in the study are briefly explained below.

-*Accuracy:* Accuracy is a pivotal measure frequently employed to assess model performance. It represents the proportion of correctly classified samples, expressed as a percentage. The accuracy calculation, a paramount metric evaluating model adequacy, is articulated in Equation 1 below:

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \quad \textbf{(1)}$$

- *Precision:* Precision quantifies the proportion of positively predicted values that are indeed positive. The calculation of precision is outlined in Equation 2 below:

$$Precision = \frac{TP}{TP + FP} \quad \textbf{(2)}$$

- *Recall (Sensitivity):* Recall elucidates how proficiently the model identifies positive cases among the instances that should have been predicted as positive. The calculation for the recall is defined in Equation 3 below:

$$Recall = \frac{TP}{TP + FN} \quad \textbf{(3)}$$

- *F1 Score:* The F1 score represents the harmonic mean of precision and recall. It offers a consolidated measure of the test's accuracy. The F1 score calculation is presented in Equation 4 below:

$$F1\ Score = \frac{2 * Precision * Recall}{Precision + Recall} \quad \textbf{(4)}$$

Experimental results

Our study proposes a deep efficient CNN network that classifies the MR images in the dataset. These classes are meningioma, glioma, pituitary and no tumor. Firstly, all libraries required to perform the experimental phases were imported and experiments were performed.

Tumor types were classified with the CNN model built from scratch. The proposed model was validated by considering multiple stages and experiments. The proposed system provided high classification accuracy. The performance of the model was also analyzed via other metrics to determine the robustness of the system. The performance values obtained in our model are presented in Table 3 below.

Table 3. Performance metrics of the proposed CNN model based on Dataset-1

Tumor class	Precision	Recall	F1-score	Avg accuracy %
Glioma	0.99	1.00	1.00	99.76
Meningioma	1.00	0.99	1.00	
Pituitary	1.00	1.00	1.00	
No tumor	1.00	1.00	1.00	

The performance values in Table 3 are analyzed with the confusion matrix. In the following sections of the study, the confusion matrix created with actual values and predicted values is presented. All performance metrics of our study contain consistently high values. The accuracy value, which measures the adequacy of our model, was found to be 99.76%.

In the next step of our study, we trained our model with dataset-2 to measure the performance success of the system we developed. The model trained with a dataset of 3264 images with four classes provided high success. The classification success of the model with this dataset is 97.45%. This rate is another result that demonstrates that the model is robust and effective. It is also clear that our model performs quite satisfactorily in different experiments (Table 4).

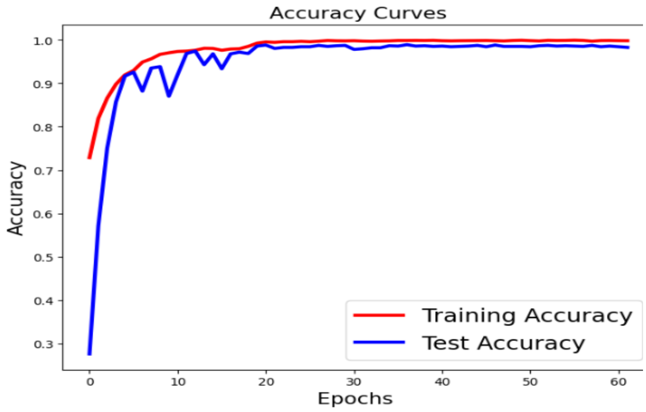
Table 4. Performance accuracy values in different datasets

Dataset	Method	Accuracy %
Dataset-1	Proposed model-CNN	99.76
Dataset-2	Proposed model-CNN	97.45

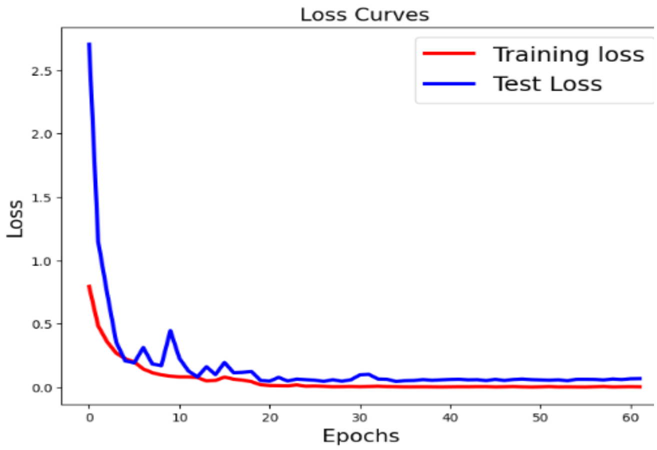
Validating the model's robustness and generalization capability

The generalizability of the model is one of the prerequisites for the model to be effective. To verify the generalization capability of our model that we built from scratch, the training and testing phases of two separate datasets were tested with different split ratios (9:1, 8:2, 7:3). We observed that splitting the training and dataset with different split ratios did not change the performance much. Moreover, the same dataset was trained with special CNN networks created with different numbers of layers and the results were analyzed. In the experimental results of the model, the highest performance values were obtained and presented in this study. Different classification functions were also tested. In classical CNN-based models, Softmax and sigmoid functions are the activation functions used in classification. Additionally, ML classifiers (Support Vector Machine, Decision Trees, Naïve Bayes et al.) In our study, K-NN, which uses the number of nearest neighbors and distance measure, was selected as one of the machine learning classifiers and we found the accuracy of K-NN in deep CNN features to be 98.21%. As a result of the experiments, it was determined that Softmax provided the best performance among other classifiers in multiclass classification.

Selecting the most suitable hyper-parameters and testing them is one of the important steps for building a robust model. The CNN model proposed in this study was finalized after many methods were tried. Figure 11 demonstrate the training/testing accuracy and training/testing loss graphs of the new CNN neural network model for 60 epochs.



(a) Training and testing accuracy curve



(b) Training and testing loss curve

Figure 11. Training and testing curves

The horizontal axis demonstrates the number of iterations and the vertical axis demonstrates the learning rate (Figure 11). By examining the learning curves demonstrating the step-by-step learning process of the model, it can be determined whether the model demonstrates an overfitting situation. Additionally, the compatibility between the data set and the model can also be interpreted through these curves. Considering Figure 11 (a), both the test and training accuracy curves demonstrate an increasing slope as the number of iterations increases. After a certain number of iterations, there is a very small change in the accuracy value, which increases up to a certain epoch. Accordingly, it can be stated that the training of the model takes place at this stage.

The loss curve depicted in Figure 11 (b) illustrates a steady decline in the error rate. Upon closer examination, the graph reveals a well-performing CNN model during the training process, signifying favorable learning dynamics of the network over epochs. With each iteration, the loss value diminishes, and the accuracy rate surges as the model learns from the provided training dataset. As showcased in Figure 11 (b), it's noteworthy that the loss value stabilizes after a certain number of epochs, indicative of the convergence of the training process. Moving on to Figure 12, it presents the confusion matrix of the deep CNN network model, revealing its proficiency with high accuracy. The confusion matrix encapsulates valuable insights into the model's predictive prowess across different classes.

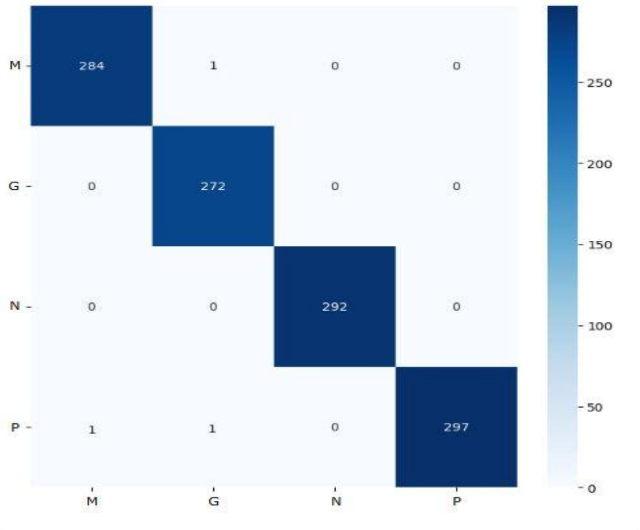


Figure 12. Confusion matrix of the model

In evaluating the performance of our brain tumor classification system, the confusion matrix serves as a pivotal tool. This matrix encapsulates a comprehensive summary of both accurate and erroneous classifications, presented in a structured table format. In our context, the abbreviations M, G, N, and P correspond to Meningioma, Glioma, No-Tumor, and Pituitary tumor, respectively, as depicted in Figure 12. A meticulous scrutiny of this matrix is imperative for a thorough assessment of the model's capabilities. Upon reviewing the confusion matrix pertaining to our proposed model, it becomes evident that out of the 285 Meningioma brain tumor images earmarked for testing, a striking 284 are accurately predicted by the model. This level of precision underscores the proficiency of the model in identifying Meningioma cases. However, out of 274 Glioma tumor images, 272 images were correctly classified as Glioma. According to the confusion matrix, images without tumors were classified as no tumors with high accuracy. Similarly, images belonging to the Pituitary tumor type are also classified with high accuracy.

Differences of our proposed model from canonical CNN architectures

Our proposed model is designed with optimized layer order, advanced convolution techniques and modern normalization methods, unlike traditional canonical CNN structures. These changes not only increase the accuracy of the model, but also enable it to work faster and more efficiently.

- Traditional CNN models usually have 3-5 convolution layers. Our proposed model contains 9 convolution layers, and each of them is optimized with different filter sizes and channel numbers.
- In addition to the Adam optimization algorithm, modern optimization techniques such as SGD and RMSprop were tested. RMSprop optimization increased the accuracy rate by providing a more stable learning process compared to SGD.
- The risk of overfitting the model was reduced with learning rate adjustments.

Ablation study

To highlight the importance of each component that increases the accuracy of our model, an ablation study was conducted. Table 5 below shows how the accuracy changes when certain components of the model are removed:

Table 5. Using different hyper-parameters in the model

Model configuration	Accuracy (%)
Recommended full model	**99.76**
Standard CNN (3 layers, ReLU, MaxPooling)	92.34
Sigmoid function instead of ReLu	95.32
Sigmoid function instead of Softmax	97.21
SGD instead of Adam optimization algorithm	96.12
RMSprop instead of Adam optimization algorithm	98.45
Epoch number 30 instead of 60	97.89
Epoch number 100 instead of 60	99.41
Learning rate is 0.0001 instead of 0.001	99.12
Batch size 16 instead of 32	98.41
Batch size 64 instead of 32	98.74
Split ratio 70%-30%	98.91

Table 5 clearly shows the response of the model to hyperparameter adjustments. It is seen that our proposed model provides the best performance with 99.76% accuracy. However, when the standard CNN architecture is limited to only three layers, the accuracy drops to 92.34%, indicating that deeper architectures can generalize better. While using ReLU instead of Sigmoid increases the model accuracy, it is observed that when SGD is used instead of Adam as the optimization algorithm, the accuracy drops to 96.12%.

Reducing the learning rate to 0.0001 decreased the model accuracy to 99.12% and could not provide optimal learning. Increasing the epoch number to 100 shows that the model increases its learning capacity with 99.41% accuracy, but carries the risk of overfitting. In addition, when the batch size is reduced to 16, the accuracy is measured as 98.41%, while when it is increased to 64, it is measured as 98.74%. When the training-test split was changed to 70%-30%, the accuracy dropped to 98.91%, indicating that more test data had little impact on the model performance. According to the results in Table 5, we can say that we obtained the best model configuration with rigorous hyperparameter tuning.

k-Fold cross validation

In the cross-validation test, the dataset was divided into 5 different layers (k=5) and the model was trained and tested in each layer. The results are presented in Table 6 below:

Table 6. k-Fold cross validation results

Number of floors (k)	Average accuracy (%)	Standard deviation
k=3	99.42	0.21
k=5	99.56	0.18
k=10	99.61	0.14

According to Table 6, we can say that our model provides a stable accuracy rate on different data sets and has high generalizability. As a result of testing the model with different layer numbers (k), the highest accuracy rate of 99.61% was obtained for k=10 layers. It was observed that as the number of layers increased, the generalization ability and accuracy rate of the model increased, but the computational cost could increase at extremely high layer numbers. However, when the standard deviation values were also examined, the lowest standard deviation (0.14%) value was obtained for k=10 and it was seen that the model produced more stable results.

Especially when compared with k=3, it is understood that the accuracy rate is 99.42% but the standard deviation value is the highest with 0.21%. This indicates that the model works less stably and the results may show more variability. The accuracy for k=5 was 99.56% and the standard deviation remained at a medium level with 0.18%. When evaluated in general, it can be said that k=10 is the most optimal choice as it offers the highest accuracy and the lowest variability.

Comparison to related studies

In our study, we evaluated the performance of our method in comparison with the other existing methods on the problem of diagnosing and classifying brain tumors. At this point, the comparison is made from two different perspectives. In the first case, we consider application studies with the first dataset. In the second case, we compare our proposed model with the results of papers published in prestigious journals with Dataset 2 that demonstrate high-accuracy classification from different deep learning architectures. The comparative results are summarized in Table 7 below.

Table 7. Comparative review of studies on brain tumors based on dataset 2

Reference	Method	Accuracy %
Vankdothu, Hameed, Fatima[29]	CNN-LSTM	92.00
Deepak et al. [38]	CNN and SVM	90.21
Badža et al. [39]	CNN	89.45
Abiwinanda et al. [40]	CNN	88.68
Sultan et al. [41]	DNN	90.21
Ayadi et al. [42]	CNN	95.71
Kumar et al. [43]	ResNet-50 and Global Average Pooling	95.10
Our proposed model (Dataset-2)	CNN	97.45
Our proposed model (Dataset-1)	CNN	99.76

This table shows various studies on the classification of brain tumors and the success rates of the proposed methods. Most of the studies used conventional neural networks (CNN) and deep learning techniques. In addition, some studies preferred combination methods such as CNN and LSTM (Long Short-Term Memory), support vector machines (SVM) and deep neural networks (DNN). According to Table 7, the success rates of brain tumor classification methods are generally high. For example, while 95.71% accuracy rate was obtained in Ayadi et al. [42] study, 95.10% accuracy rate was obtained in Kumar et al. [43] study. However, the proposed model (Dataset-2) reached the highest accuracy rates with a success rate of 97.45% and a success rate of 99.76% was obtained especially in Dataset-1. This shows that the proposed model performs better than most methods in the existing literature and provides high accuracy in brain tumor classification.

The differences between the accuracies of the methods used in various studies once again reveal how critical the model selection is. The high accuracy rate of the proposed model shows that the structural design, hyperparameters and training process of the model are effectively optimized. In addition, it has been observed that CNN-based methods generally work more efficiently with visual data and such deep learning models provide high success in the analysis of medical images such as brain tumors. This supports that the proposed model is the right choice in terms of the selected technique. The success of the model is directly related not only to the quality of the method used, but also to the quality and diversity of the dataset on which it was trained. For example, the presence of different accuracy rates in Dataset-1 and Dataset-2 indicates that factors such as the difficulty level of the images in the datasets, the size and diversity of the dataset can affect the performance of the model. At this point, the generalization ability of the datasets and the improvements made to prevent overfitting are also very important. It should be noted that high accuracy rates can be due to balanced, correctly labeled and sufficiently large datasets.

Table 7 clearly shows the previous studies on brain tumor classification and the superior performance of our proposed model. The high accuracy rates of the proposed model indicate that it will contribute to the advancement of research in this field and can be effectively used in future applications. In addition, it can be said that the model has the potential to generalize better compared to other methods. In terms of the robustness of the model, the consistently high accuracy rates of the proposed model show that it has a robust structure against noise and variability. The proposed model presents an innovative and effective solution by offering the best results in the current literature. The high accuracy rate of the model is supported by advanced optimization techniques, powerful network architecture and effective data processing strategies and can be an important reference point for future research.

Discussion

While formulating the methodology of our study, a pivotal consideration was the observation that CNN-based architectures offer the advantage of achieving high-accuracy classification while utilizing fewer parameters when contrasted with DNN architectures. Based on this point, we chose the CNN network architecture and while building our working model, we aimed to reduce the running time and achieve high efficiency by performing different experiments on the model. When we examined the literature, we found that some studies with the CNN approach indicated higher performance than many other DNN methods. The efficient CNN model we proposed in this study also outperformed many DNN models and indicated high classification accuracy.

We subjected our newly proposed CNN-based model to a diverse array of assessments, one of which involved evaluating its performance using various datasets. Recognizing the importance of gauging the model's adaptability to different data sources, we undertook the training process using distinct datasets. This approach aimed to provide a more comprehensive understanding of the model's capabilities. In pursuit of this objective, we explored the performance metric outcomes of our model using the four-class dataset-2. This dataset, sourced from the Kaggle platform, was acquired without cost and is widely employed in studies related to tumor detection. By applying our model to this dataset, we sought to gain insights into its performance across different data contexts, thereby enhancing our understanding of its overall robustness. When we examined the results of our model for two different datasets, we observed that it indicated high classification success rates. These results prove the efficiency and generalization capability of our model.

We have already mentioned that in general, all deep learning approaches successfully perform disease detection and classification. The performance of these deep methods varies and they have their advantages and disadvantages. When we compare our model with DNN's advantages, we see that it lags behind in generating continuous signals. To overcome this problem, we can increase the dimensionality of the CNN model. Additionally, problems such as overfitting can be avoided by stopping training at an earlier stage or increasing the data. In our study, to overcome this problem, we stopped training at different stages and observed the results. Furthermore, another disadvantage of this approach is that it takes a long training time even with small data sets. Apart from these disadvantages, one of the biggest advantages of our model is that the number of layers and parameters can be changed. In this way, the CNN model can achieve the most satisfactory structure while detecting and classifying tumors. After trying many different methods in our CNN architecture, which we created from scratch, we finalized it in the light of the most appropriate results.

Our model has 52.77 million parameters, which is a structure that brings both a strong learning capacity and some challenges. While a large number of parameters allows the model to learn complex patterns and achieve high accuracy, it may also require more computational resources. However, thanks to this large capacity, our model can show superior performance on detailed and feature-rich datasets. However, a large model size can increase the risk of overfitting, but this risk can be reduced by methods such as dropout, data augmentation and regularization. We used some of these techniques to reduce these risks in our study. If the model is well optimized, a large number of parameters can increase its generalizability to new datasets since it offers a wider learning capacity. In this context, we optimized our model with the most appropriate hyperparameters and applied it on a different dataset to discuss its generalizability and robustness. In addition, techniques such as pruning and quantization, recall can be applied to reduce the computational cost while preserving the complexity of the model. We provided time efficiency by using the early stopping method from recall techniques. In summary, the large number of parameters of our model provides a strong learning capacity and at the same time creates some computational costs, but these problems have been overcome with correct optimizations.

Conclusion

The rapid identification and classification of brain tumors hold paramount significance in extending an individual's life expectancy. This paper introduces a novel deep learning model rooted in CNNs, designed to autonomously classify brain tumors within MR images. The MR images of brain tumors used in this study were sourced from the Kaggle platform, offering invaluable resources for researchers. Our proposed model embarks on its journey with preprocessing steps dedicated to refining brain images. To enhance image quality and eliminate noise, preprocessing techniques are applied to the images. Subsequently, image features are extracted and processed through a convolutional network.

Although our initial model yielded an impressive accuracy output, further tuning of parameter values propelled us to achieve an ultimate accuracy of 99.76%, thereby enhancing performance accuracy. As a pivotal step to combat overfitting, a dropout layer was integrated after the fully connected layer in our model. This strategic inclusion safeguards against the model's tendency to overly specialize in the training data.

To affirm the efficacy of our model, we conducted a comparative analysis against successful studies conducted with brain tumor MR images available on the Kaggle platform, which boasts a publicly accessible dataset. Furthermore, we juxtaposed our model's performance against the experimental findings published in esteemed journals. The outcome of our endeavors revealed that our novel CNN-based neural network model significantly elevates the accuracy of tumor-type classification. Notably, our experimental results illustrate that our model surpasses numerous transfer learning methodologies across pivotal evaluation criteria, including accuracy, precision, and F1 score. This substantiates the remarkable potential of our proposed model in enhancing brain tumor classification methodologies.

Ethics committee approval and conflict of interest statement

“There is no need to obtain permission from the ethics committee for the article prepared.”
“There is no conflict of interest with any person / institution in the article prepared.”

Author contributions

"The authors declare that they have contributed equally to the article."

References

[1] K. D. Miller, Q. T. Ostrom, C. Kruchko, N. Patil, T. Tihan, G. Cioffi, ... & J. S. Barnholtz-Sloan, "Brain and other central nervous system tumor statistics", *CA: a cancer journal for clinicians*, vol. 71, no. 5, *pp.* 381-406, Sep. 2021, DOI: 10.3322/caac.21693.

[2] Cancer.Net, Brain Tumor_Statistics_Cancer, (2022). Date of Access: 12.06.2024 from https://www.cancer.net/cancer-types/brain-tumor/statistics

[3] Cancer survival rate: A tool to understand your prognosis - Mayo Clinic, (n.d.). Date of Access: 02.07.2024, from https://www.mayoclinic.org/diseases-conditions/cancer/in-depth/cancer/art-20044517

[4] K. M. Iftekharuddin, J. Zheng, M. A. Islam & R. J. Ogg, "Fractal-based brain tumor detection in multimodal MRI", *Applied Mathematics and Computation*, vol. *207, no.*1, pp. 23-41, Jan. 2009, DOI: 10.1016/j.amc.2007.10.063.

[5] L. M. DeAngelis, "Brain tumors", N. Engl. J. Med., vol. 344, no.2, pp. 114– 123, Jan. 2001, [CrossRef] [PubMed].

[6] D. N. Louis, A. Perry, G. Reifenberger, et al. "The 2016 World Health Organization Classification of Tumors of the Central Nervous System: A summary", *Acta Neuropathol*, vol. 131, pp. 803–820, May 2016. [CrossRef] [PubMed].

[7] V. Kotu & B. Deshpande, "Data science: concepts and practice", Morgan Kaufmann, 2nd ed. 2019.

[8] B. Janeczko & G. Srivastava, "”The use of deep learning in image analysis for the study of oncology", In *Internet of Multimedia Things (IoMT)*, pp. 133-150, 2022, Academic Press,[Online]Available:https://www.sciencedirect.com/science/article/abs/pii/B9780323858458000113

[9] R. Polikar, "Ensemble Learning", *Ensemble machine learning: Methods and applications*, Springer, New York, NY. pp. 1-34, Jan. 2012, https://doi.org/10.1007/978-1-4419-9326-7_1

[10] O. Sagi & L. Rokach, "Ensemble learning: A survey", WIREs Data Mining and Knowledge Discovery, vol. 8, no. 4, Jul. 2018, 8:e1249, DOI: 10.1002/widm.124.

[11] E. Aslan, "Classification of Brain Tumor from MRI Images with LSTM-CNN Hybrid Model", *Adıyaman University Journal of Engineering Sciences*, vol. 11, no. 22, pp. 63–81, 2024, doi: 10.54365/adyumbd.1391157.

[12] Brain tumor. (2019, April 27). Date of Access: 15.12. 2024, from https://www.mayoclinic.org/diseases-conditions/brain- tumor/symptoms-causes/syc-20350084.

[13] MD. Charles Patrick Davis, "Cancer Causes, Types, Treatment, Symptoms & Signs", MedicineNet, MedicineNet, Date of Access: 20.07.2023, from https://www.medicinenet.com/cancer/article.htm

[14] S. A. Swapnil & V. S. Girish (2020, March). Image Mining Methodology for Detection of Brain Tumor: A Review. Presented at ICCMC Annual Meeting. IEEE.[Online].Available:https://ieeexplore.ieee.org/abstract/document/9076409

[15] U. A. Dere. (2017). What is a brain tumor? Date of Access: 09.05.2024, from https://ankara.baskenthastaneleri.com/magazine/sayi30/files/assets/common/downloads/publication.pdf

[16] D. R. Johnson, J. B. Guerin, C. Giannini, J. M. Morris, L . J. Eckel & T. J. Kaufmann, "2016 updates to the WHO brain tumor classification system: what the radiologist needs to know", *RadioGraphics*, vol. 37, no. 7, pp. 2164-2180, Oct. 2017, DOI: 10.1148/rg.2017170037

[17] Acıbadem Web and Editorial Board (2019). Date of Access: 24.06.2024, from http://acibadem.com.tr/ilgi-alani/gliomlar/

[18] Y. Aras (2022). What are the types of brain tumors? Date of Access: 24.10.2024, from https://kolanhastanesi.com.tr/saglik-rehberi/beyin-tumoru-turleri-nelerdir

[19] Braın and Nerve Surgery (Neurosurgery) (2023). What are brain tumor symptoms? What are the treatment methods? Date of Access: 25.07.2024, from https://www.medicalpark.com.tr/beyin-tumorleri/hg-1539

[20] L. Sprincl, J. Vozenílek, J. Vedralová, et al, "Use of a computer program in the diagnosis of brain tumors", Cesk Patol, vol. 21, no. 4, pp. 218-222, Nov. 1985, PMID: 3905026

[21] E. Aslan, M. A. Arserim & A. Uçar, "Development of Push-Recovery control system for humanoid robots using deep reinforcement learning", *Ain Shams Engineering Journal*, vol. 14, no. 10, 102167, Oct. 2023, DOI: 10.1016/j.asej.2023.102167.

[22] A. Geçmez & Ç. Gençer (2021, June). Wind Energy Production Estimation with ANN and ANFIS, Presented at *icSmartGrid*, Setubal, Portugal, pp. 167-173. [Online]. Available:https://ieeexplore.ieee.org/abstract/document/9551254

[23] E. H. Houssein, M. M. Emam & A. A. Ali, "An optimized deep learning architecture for breast cancer diagnosis based on improved marine predators algorithm", *Neural Computing and Applications*, vol. *34, no.* 20, pp. 18015-18033, Jun. 2022, DOI:10.1007/s00521-022-07445-5.

[24] N. Ganatra & A. Patel, "A comprehensive study of deep learning architectures, applications and tools", Int. j. comput. sci. eng, vol. 6, no. 12, pp. 701-705, Dec. 2018, DOI: 10.26438/ijcse/v6i12.701705.

[25] F. Doğan & İ. Türkoğlu, "A compilation of deep learning models and application areas", Dicle University Engineering Faculty Journal of Engineering, vol. 10, no. 2, pp. 409-445, 2019.

[26] K. A. Kumar, A. Y. Prasad & J. Metan, "A hybrid deep CNN-Cov-19-Res-Net Transfer learning architype for an enhanced brain tumor detection and classification scheme in medical image processing", *Biomedical signal processing and control*, vol. *76*, 103631, Jul. 2022, DOI: 10.1016/j.bspc.2022.103631

[27] Y. Bhanothu, A. Kamalakannan & G. Rajamanickam (2020, March). Detection and classification of brain tumor in MRI images using deep convolutional network, Presented at *6th ICACCS,* Coimbatore, India, pp. 248-252, IEEE.[Online].Available: https://ieeexplore.ieee.org/abstract/document/9074375

[28] A. Çinar & M. Yildirim, "Detection of tumors on brain MRI images using the hybrid convolutional neural network architecture", *Medical hypotheses*, vol. *139*, 109684, Jun. 2020, DOI: 10.1016/j.mehy.2020.109684

[29] R. Vankdothu, MA. Hameed & H. Fatima, "A brain tumor identification and classification using deep learning based on CNN-LSTM method", Computers and electrical

engineering, vol. 101, 107960, Jul. 2022, DOI:10.1016/j.compeleceng.2022.107960

[30] S. Patil. & D. Kirange, “Community of Deep Learning Models for Brain Tumor Detection”, Procedia computer science, vol. 218, pp. 2468-2479, 2023.

[31] M. Aslan, “Deep learning based automatic brain tumor detection”, Fırat university journal of engineering sciences, vol. 34, no.1, pp. 399-407, Mar. 2022, DOI:10.35234/fumbd.1039825

[32] S. Deepak & P. M. Ameer, “Brain tumor classification using deep CNN features via transfer learning”, *Computers in biology and medicine*, vol. 111, 103345, Aug. 2019, DOI:10.1016/j.compbiomed.2019.103345

[33] M. I. Nazir, A. Akter, M. A. H. Wadud ve M. A. Uddin, "Utilizing customized CNN for brain tumor prediction with explainable AI," *Heliyon*, cilt. 10, sayı. 20, 2024.

[34] E. Goceri, "An efficient network with CNN and transformer blocks for glioma grading and brain tumor classification from MRIs," *Expert Systems with Applications*, cilt. 268, s. 126290, 2025.

[35] Math & Physics with Gus (2023). CNN Brain Tumor Classification. Date of Access:12.08.2023, from https://www.kaggle.com/code/guslovesmath/cnn-brain-tumor-classification-99-accuracy

[36] S. Bhuvaji (2020). Brain Tumor Classification (MRI). Date of Access:12.08.2023, from https://www.kaggle.com/datasets/sartajbhuvaji/brain-tumor-classification-mri

[37] E. Aslan & Y. Özüpak, “Detection of road extraction from satellite images with deep learning method”, *Cluster Comput*, vol. 28, no. 72, 2025, DOI:10.1007/s10586-024-04880-y

[38] S. Deepak & P. M. Ameer, “Automated categorization of brain tumor from mri using cnn features and svm”, *Journal of ambient intelligence and humanized computing*, vol. *12*, pp. 8357-8369, Oct. 2021, DOI:10.1007/s12652-020-02568-w

[39] M. M. Badža & M. Č. Barjaktarović, “Classification of brain tumors from MRI images using a convolutional neural network”, *Applied sciences*, vol. *10, no.*6, 1999, Mar. 2020, DOI:10.3390/app10061999

[40] N. Abiwinanda, M. Hanif, S. T. Hesaputra, A. Handayani & T. R. Mengko (2018, June). Brain tumor classification using convolutional neural network, Presented at WCMPBE, *Prague, Czech Republic, vol. 1,* pp. 183-189, Springer Singapore. [Online]. Available: https://link.springer.com/chapter/10.1007/978-981-10-9035-6_33

[41] H. H. Sultan, N. M. Salem & W. Al-Atabany, “Multi-classification of brain tumor images using deep neural network”, *IEEE access*, vol. *7*, pp.69215-69225, May. 2019, DOI: 10.1109/ACCESS.2019.2919122

[42] W. Ayadi, W. Elhamzi, I. Charfi & M. Atri, “Deep CNN for brain tumor classification”, *Neural processing letters*, vol. *53*, pp. 671-700, Jan. 2021, DOI: 10.1007/s11063-020-10398-2

[43] R. L. Kumar, J. Kakarla, B. V. Isunuri & M. Singh, “Multi-class brain tumor classification using residual network and global average pooling”, *Multimedia tools and applications*, vol. *80*, pp. 13429-13438, Jan. 2021, DOI: 10.1007/s11042-020-10335-4