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Deep Learning Based CAD System for Early Detection of Brain Tumor

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Benha 2024

ABSTRACT

A brain tumor is an uncontrolled growth of brain cells that occurs in brain cancer if it is not detected at an early stage, which is critical for treatment planning and patient survival. Brain tumors come in a variety of shapes, sizes, properties, and treatments. As a result, manual brain tumor detection is difficult, time-consuming, and prone to error. So, high-precision automated computer-aided diagnosis (CAD) is currently in demand. Using image processing techniques in magnetic resonance imaging (MRI) is difficult but important task for a variety of medical analysis applications. This thesis uses deep learning technology, especially the Convolutional Neural Network (CNN) model, for the early detection of brain tumors and rapid diagnosis due to the importance of this disease and the increasing number of people infected with it annually, which helps reduce the death rate.

This is done by applying this technique to MRI images, and it was applied to two different size of datasets (the first is large dataset "3264 images" and the second is small "253 images") in order to increase the number of the images and thus increase the accuracy and efficiency of the model by applying two methods to the CNN model.

The first method is to apply all the images on the network together. The network was trained on a large and different dataset consisting of 3517 images divided into a group of images that have tumors and others that do not have tumors. We recorded the results and obtained an accuracy rate of **94.6 %.**

The second method is to divide the images into 3 classes and enter them into the network, each group separately, that is, as if we had repeated the network 3 times until efficiency increased. Although the images were divided into 3 classes, it is expected to improve efficiency, reduce the model’s working time, and speed up the overall time. The accuracy of the model increases.

The accuracy rate in detecting this tumor has increased to **98.4 %.**

PUBLICATIONS

Ereny M.Abdel-malak, Ashraf Y.Hassan and Wael A.Mohamed "Deep Learning Based CAD System for Early Detection of Brain Tumor" The 13th International Conference on Information Communication and Management (ICICM), Egypt, November 2023.

ACKNOWLEDGMENTS

“The God of heaven will prosper us. Therefore we, his servants, will arise and build.” (Nehemiah 2:20)

First, all thanks to **ALLAH** the source of every success, I am grateful to my advisor **Professor Dr. Ashraf Yehya Hassan and Dr. Wael Abdel-Rahman Mohamed**, for their guidance and support throughout the work that led to this thesis, as well as, during the writing process. None of this would have been possible without their support, also, I wish to express my sincere, gratitude, thanks, and appreciation for their supervision, encouragement, valuable guidance, active advices, and indispensable help during this work.

I am grateful to the Electrical staff of **Benha faculty of engineering** for their help and suggestions throughout the research. My knowledge would have been inadequate without them.

I would like to thank my parents, my **husband**, my little **kiddy**, my brother, my sisters, my husband's family, and my closest friends for their help, encouragement, and support throughout my educational adventure. Their support means everything.

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List of Main Abbreviations

AI	Artificial Intelligence
ANN	Artificial Neural Network
CT	Computed Tomography
CAD	Computer- Aided Diagnosis
CD	Compact Disc
CNN	Convolutional Neural Network
CNS	Central Nervous System
DL	Deep Learning
FC	Fully Connected
FN	False Negative
FP	False Positive
GBM	Glioblastoma Multiform
GPU	Graphics Processing Unit
HGG	High-Grade Gliomas
JPEG	Joint Photographic Experts Group
LGG	Low-Grade Gliomas
LSTM	Long Short-Term Memory
MRI	Magnetic Resonance Imaging
MLP	Multi-Layer Perceptron
PET	Positron Emission Tomography
RGB	Red, Green and Blue

ReLU	Rectified Linear Unit
SGD	Stochastic Gradient Descent
TN	True Negative
TP	True Positive
VGG	Visual Geometry Group
WHO	World Health Organization

List of Symbols

B	Bias
W	Weight vector
β_k^i	The bias term
σ	The non-linearity
ω_{kj}^i	The convolutional layer's weight
X_j^{i-1}	The input term
ψ_k^i	The output of a convolutional layer

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Chapter 1

Introduction

1.1 Introduction

Nobody expects to hear the words "it's a brain tumor." Those words can elicit a wide range of emotions, and it may be difficult to process the complex information provided by your doctor. Making decisions regarding your course of therapy using this knowledge is an even bigger challenge. And at that moment, everything changes. In a relatively short period of time, you must process the diagnosis, master a new and difficult vocabulary, and make treatment decisions.

Figure 1.1 depicts the central nervous system and the parts it consists of and contains such as it's shown below. [1]

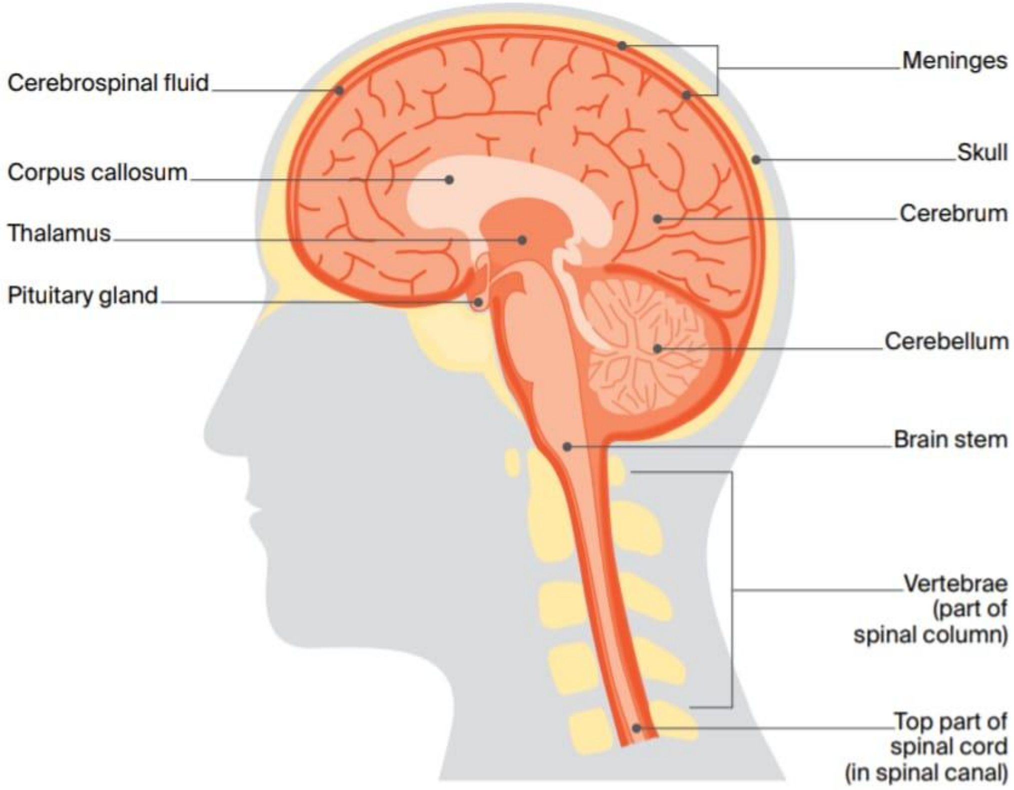


Fig 1.1 The central nervous system. [1]

1.2 The Brain

In a top view, the cerebrum is the biggest component of the brain. Hemispheres are the names of the two halves that make it up.

Each hemisphere is divided into four main areas – the frontal, parietal, occipital, and temporal lobes as it's shown in figure 1.2. [1]

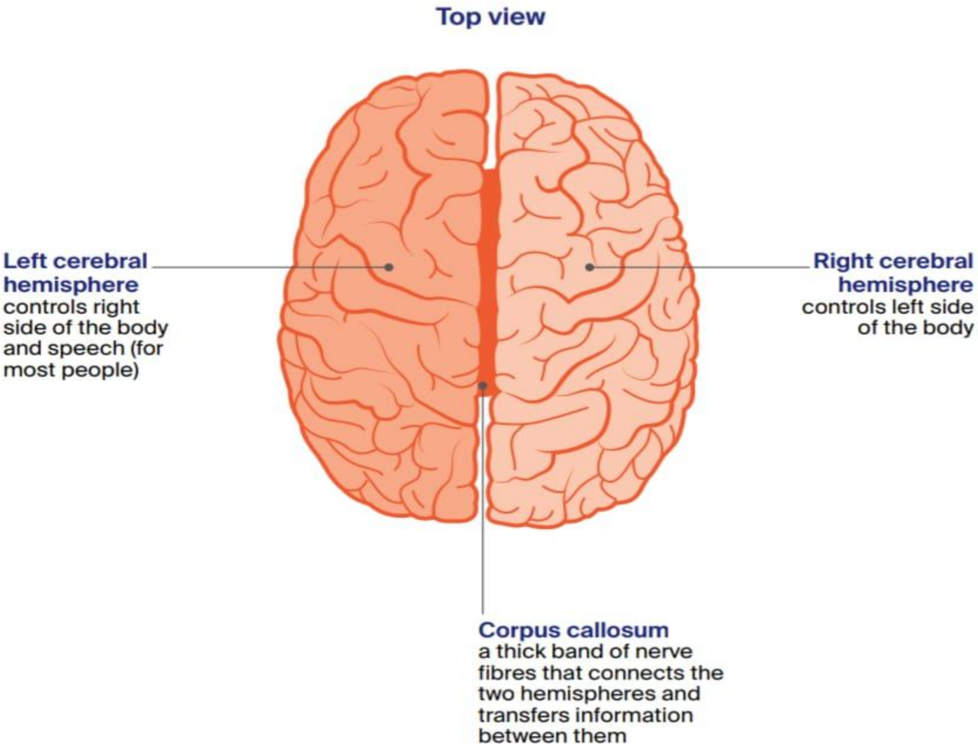


Fig 1.2 Top view of the brain. [1]

The cerebellum and brain stem are two other important parts of the brain. The cerebellum is located near the back of the brain. The spinal cord and brain are connected by the brain stem. Each part of the brain controls different bodily functions as it's shown in figure 1.3. [1]

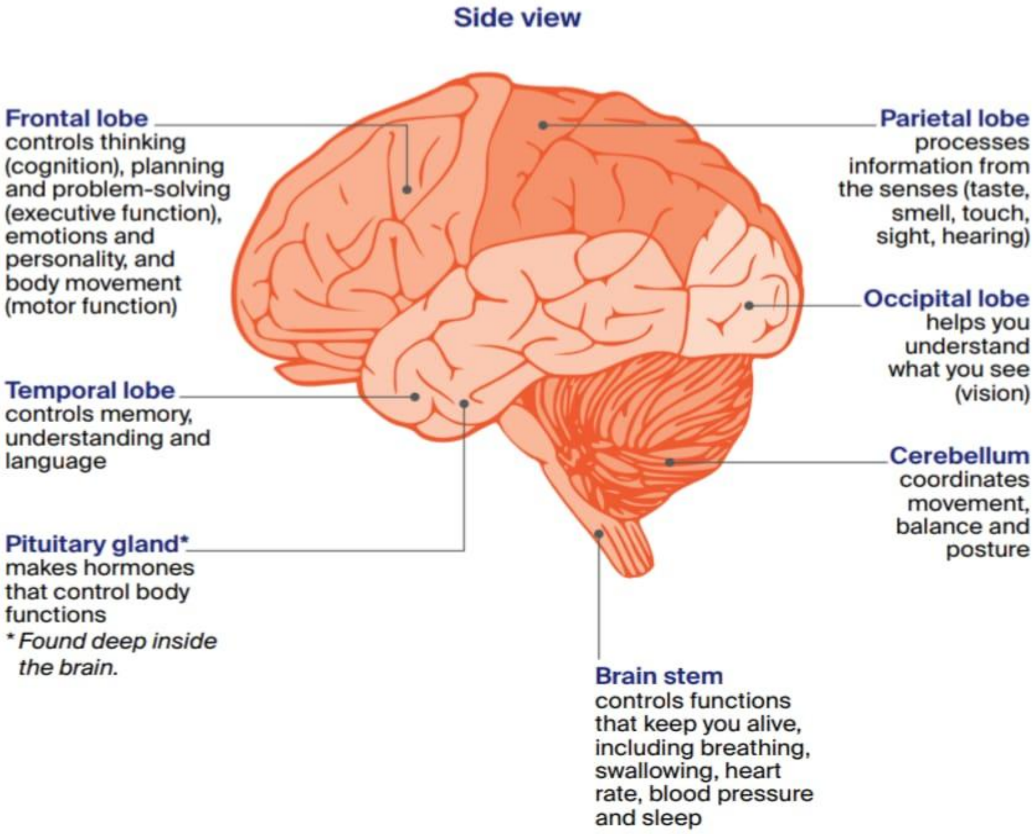


Fig 1.3 Side view of the brain. [1]

The human brain - a highly specialized organ made of highly soft and spongy tissues, is technically called the central processing unit of the human body. Information enters through sensory organs via nerves to this processing unit in form of nerve signals. Our brain only assists us in articulating our words, carrying out our actions, and sharing our thoughts, ideas, and feelings. This brain only helps us to regulate, sustain and control different body functions in vivid environmental conditions. However, under certain conditions, brain cells grow and multiply uncontrollably. This abnormal growth of brain cells leads to an increase in the overall mass of nerve tissues of the brain which increases pressure on neighboring tissues of the brain. Due to this, surrounding brain tissues get shifted and pushed up against the brain skull. An abnormal gain in a mass of tissues is called a tumor. [2]

So, the Brain is the most important part of the human nervous system, and cancer in this part of the body is not only more painful than any other part of the body, but it also degrades the entire human body system to a much greater extent.

The Brain controls the entire functionality of our body because it is a more complex and principal part of the human body. The body gets affected badly if any damage occurs to the brain. The protective skull hides the direct sight of the Brain. The Brain is protected from various injuries by this skull and it also prevents the functionality of the Brain. If any change has been seen in normal behavior and structure, then this shows that a tumor has affected the Brain. The abnormal growth of brain cells is caused by brain tumors. Therefore, these cells affect the human normal routine. In human beings, brain tumor is the most noted cause of tumor cancer deaths. [3]

The estimated cases are 1,958,310 [4] in the US and the number of death cases caused by brain tumors is 18,990 [5] If the tumor has been diagnosed wrong, it may lead to severe results, thus brain tumor diagnosis is one of the most critical and crucial tasks. In a complex way, the cells of our brain are bounded together closely. The structure of the brain is very complicated and delicate internally. The death rate of humans due to brain tumors was high some years before but due to the early diagnosis of brain tumors, this rate is significantly decreased. Due to the accurate brain tumor diagnosis in the early stages, long survival chances for a patient are increased. [2]

1.2.1 The Brain and Nervous System

The brain is a soft mass of supporting tissues and nerve cells that are linked to the spinal cord. Messages are sent throughout the body by nerves in the brain and spinal cord. The brain and spinal cord comprise the central nervous system (CNS). The central nervous system is at the heart of our being. It is in charge of our personality thoughts, memory, intelligence, speech, understanding, and emotions as well as our senses vision, hearing, taste, smell, and touch as well as our basic body functions breathing, heart rate, and blood pressure and how we function in our environment movement, balance, and coordination. Learning about the normal workings of the brain and spine will help you understand the symptoms of brain tumors, how they are diagnosed and how they are treated. [1]

1.3 Brain Tumors Definitions

A brain tumor, known as an intracranial tumor, is an abnormal mass of tissue in which cells grow and multiply uncontrollably, seemingly unchecked by the mechanisms that control normal cells. More than 150 different brain tumors have been documented, but the two main groups of brain tumors are termed **primary** and **metastatic**. [6]

A tumor is an abnormal growth of cells. Cells are the basic building blocks of the body; they form tissues and organs. The body is constantly producing new cells to help us grow, replace worn-out tissue, and heal injuries. Cells normally multiply and die in an orderly fashion, with each new cell replacing one that has died. Cells, on the other hand, can become abnormal and continue to grow. In solid cancers, such as a brain tumors, the abnormal cells form a mass or lump called a tumor. So, it's clear how cancer starts and that is shown in figure 1.4. [1]

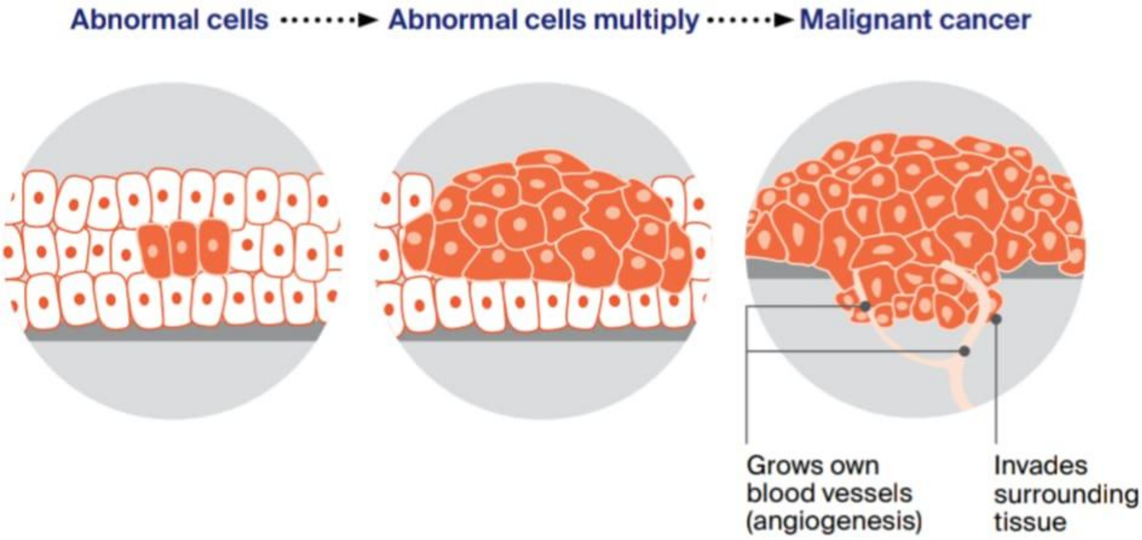


Fig 1.4 Tumor growth stages. [1]

In other terms, early detection and classification of brain tumors are very important in clinical practice. Numerous analysts have proposed outstanding methods for the identification of the type of brain tumors based on different sources of facts. [7] A brain tumor is an uncontrolled boom of tumor cells in our mind due to unsuitable human lifestyles and residing and unbalanced diets. According to the World Health Organization, tumors can be labeled in subsequent organizations:

Grade I Pilocytic or benign, slow-growing plant with well-defined borders. Astrocytoma of grade II is slow-growing and rarely spreads along a well-defined border. Grade III: Anaplastic Astrocytoma, grows faster. Grade IV: Glioblastoma Multiform, the most invasive malignant, spreads to nearby tissues and develops rapidly. [8]

A brain tumor is any intracranial tumor created by abnormal and uncontrolled cell division, normally either found in or around the brain itself or spread from cancers primarily located in other organs (metastatic tumors). Although they can affect any part of the brain, primary (true) brain tumors are most commonly found in the posterior cranial fossa in children and the anterior two-thirds of the cerebral hemispheres in adults [9].

A brain tumor is one of the most terrifying diseases in world. One of the most common causes is the collective behavior of abnormal cells in the brain. Two stages of brain tumors including primary and secondary are reported in the relevant literature. The tumor is small in the primary stage and is referred to as benign in biology. Tumors spread from other parts of the body in the secondary stage, and their size is larger than benign, resulting in the term "malignant" [10]. According to the National Brain Tumor Society, in the USA, approximately 700,000 patients are suffered from brain tumor disease. Of those, 69.8% are benign, whereas the rests 30.2% are malignant. According to the report, the survival rate of the patients is 36% only. At 2020 Approximately 87,000 patients was diagnosed with a brain tumor. In 2023, the estimated number of diagnosed brain tumor patients is 1 million. There will be 79,340 adults diagnosed over the age of 40.

Figure 1.5 shows the types of tumors which divided into primary and metastatic brain tumor [1].

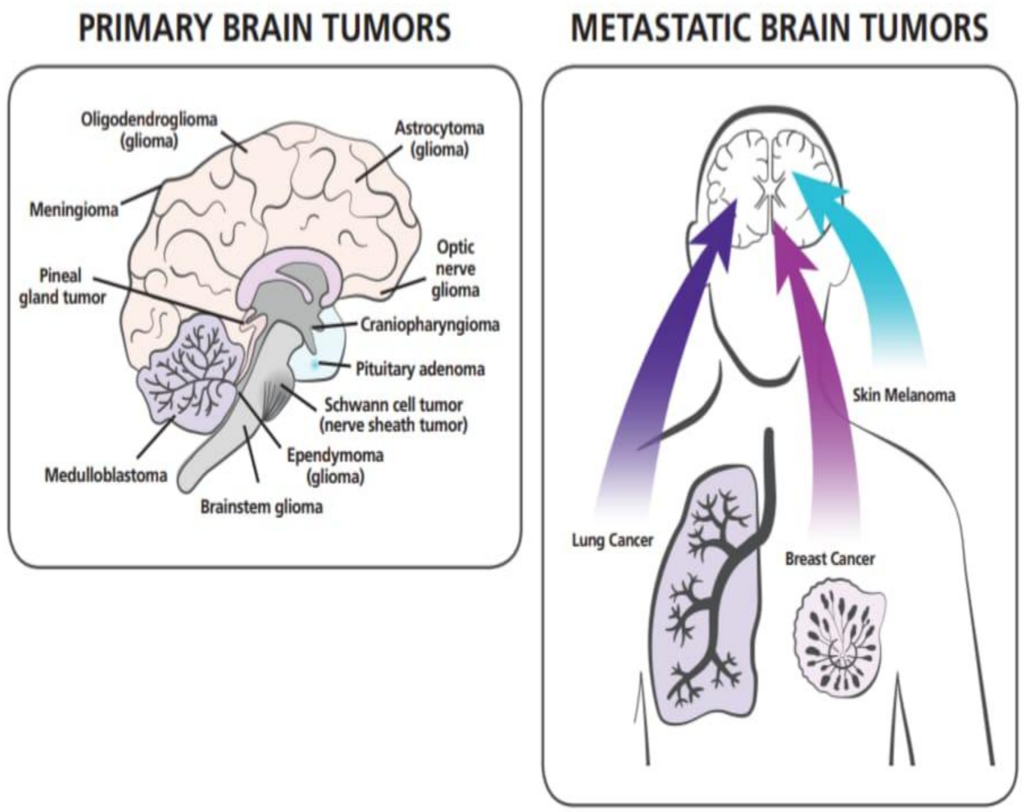


Fig 1.5 Types of tumors. [1]

There are two types of brain tumors: benign and malignant as shown in table1.1. The benign tumor does not spread to surrounding tissues and is usually not life-threatening. A malignant tumor, on the other hand, spreads to other tissues and is thus harmful. [11]

Table 1.1 Types of tumors. [11]

BENIGN TUMORS	MALIGNANT TUMORS
• Slow growing. • Distinct borders. • Rarely spread. • Can usually be removed.	• Usually rapid growing. • Invade brain tissue. • Life-threatening. • Difficult to remove.

Brain tumors, whether cancerous or benign, press against the brain's nerve network, causing unnatural triggers throughout the spine.

Brain tumor has been classified by WHO (World Health Organization) into 120 types. Cell origin and behavior of the cell (aggressive and non-aggressive behavior) are the major classifications defined by WHO.

Figure 1.6 showing the progression of a low-grade tumor to a high-grade glioblastoma multiform. [12]

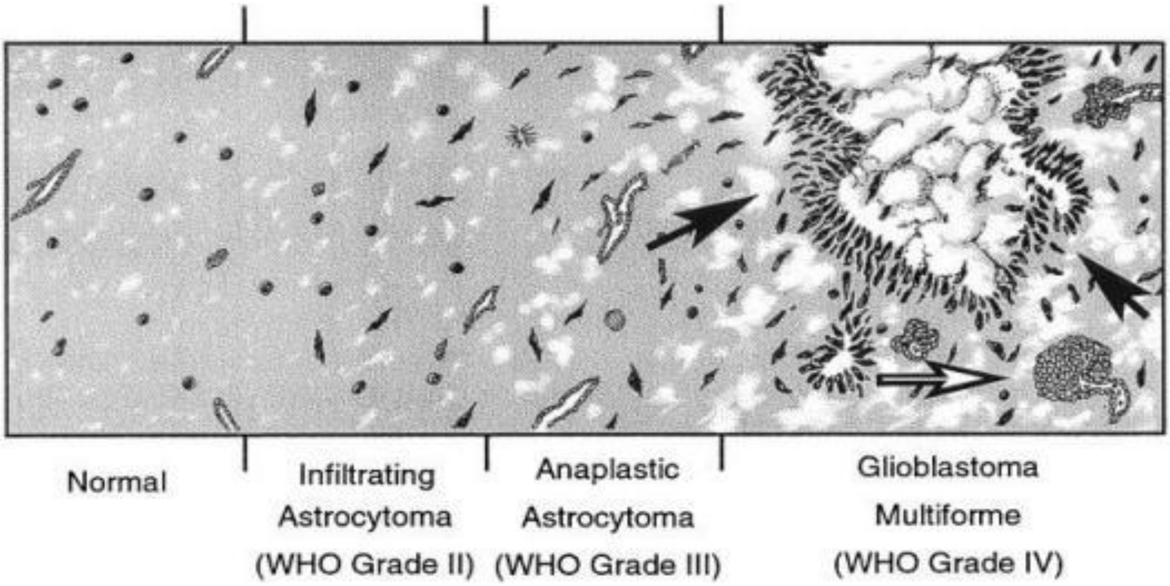


Fig 1.6 Schematic diagram showing the progression of a low-grade tumor to a high-grade glioblastoma multiform. [12]

For the treatment of brain tumors, different techniques are used in clinics. In the benign stage, radiotherapy is beneficial, and the patient can live without surgery. The cancerous stage, on the other hand, is harmful and can be treated with chemotherapy and radiotherapy. As a result, benign tumors typically spread more slowly than malignant tumors. However, in either case, diagnosis is critical, and expert radiologists are required. Recent imaging technology has demonstrated tremendous success in the diagnosis and detection of dangerous human diseases such as brain tumors [13].

We can summarize the types of tumors according to what is stated in the (WHO) in the table 1.2:

Table 1.2 The types of tumors according to WHO. [1]

Grade		Characteristics	Tumor Types
Low Grade	WHO Grade I	• Least malignant (benign) • Possibly curable via surgery alone • Non-infiltrative • Long-term survival • Slow growing	• Pilocytic astrocytoma • Craniopharyngioma • Gangliocytoma • Ganglioglioma
	WHO Grade II	• Relatively slow growing • Somewhat infiltrative • It May recurs as a higher grade	• Diffuse Astrocytoma • Pineocytoma • Pure oligodendroglioma
	WHO Grade III	• Malignant • Infiltrative • Tend to recur as higher grade	• Anaplastic astrocytoma • Anaplastic ependymoma • Anaplastic oligodendroglioma
High Grade	WHO Grade IV	• Most malignant • Raid growth, aggressive • Widely infiltrative • Rapid recurrence • Necrosis prone	• Gliobastoma multiforme (GBM) • Pineoblastoma • Medulloblastoma • Ependym

1.4 Magnetic Resonance Imaging (MRI)

Many diagnostic imaging methods, including Computed Tomography (CT), Positron Emission Tomography (PET), and Magnetic Resonance Imaging (MRI) may be used for the early diagnosis of brain tumors. MRI is green in the utility of brain tumor diagnosis and identification relative to other imaging approaches due to high soft tissue assessment, and high spatial judgment.

This technique is not limited to detecting tumors inside the brain but can scan the whole internal structure of the human body to detect any tumor.

However, MRI scans are more useful than CT images in terms of tumor texture and shape. The size, shape, and location of the detective tissues can be easily computed using MRI. These techniques have a few flaws, such as long computational times and high costs [14].

(MRI) is a noninvasive medical test used to help doctors diagnose and treat medical conditions? MRI creates detailed images of organs, soft tissues, bone, and virtually all other internal body structures by using a powerful magnetic field, radio frequency pulses, and a computer. The images can then be viewed on a computer monitor, electronically transmitted, printed, or copied to a CD (compact disc). Does not use ionizing radiation (x-rays). Detailed MR images allow physicians to evaluate various parts of the body and determine the presence of certain diseases.

MRI is less dangerous because it does not expose living cells to toxic radiation. Following early detection of abnormality using brain MRI, patients typically undergo a biopsy to determine the form and classification of the tumor. Biopsy findings for detecting brain tumors are regarded as an absolute test in this regard. Various computer-aided diagnostic solutions have been proposed to improve the accuracy of brain tumor diagnosis, whether benign or malignant [15].

1.5 Computer-Aided Diagnosis (CAD)

Computer-aided diagnosis (CAD) has emerged as a major area of study in medical imaging and diagnostic radiology.

(CAD) system may be useful for radiologists' second opinions in clinics.

CAD is becoming more widely used in the detection and differentiation of many different types of abnormalities in medical images obtained from various examinations using various imaging modalities. Indeed, CAD has emerged as a major research topic in medical imaging and diagnostic radiology. Although early attempts at computerized medical image analysis were made in the 1960s, serious and systematic research on CAD began in the 1980s with a fundamental shift in the concept of utilizing computer output, from computer-aided diagnosis to computer-assisted diagnosis.

A simple CAD system consists of a few key sequential steps, such as preprocessing original MRI scans, feature extraction from preprocessed MRI scans, feature reduction, and finally classification using a supervised learning algorithm [16].

1.6 Image Processing

For the analysis of brain functionalities, the medical imaging processes provide guide doctors and researchers.

An image is a method of transferring information, and it contains a wealth of useful information. Understanding the image and extracting information from the image to accomplish some tasks is an important area of application in digital image technology, and image segmentation is the first step in understanding the image. In practice, it is frequently not interested in all areas of the image, but only in those with similar characteristics.

Image segmentation is one of the most active research areas in image processing and computer vision. It is also a critical foundation for image recognition. It divides an input image into a number of the same nature of the class based on certain criteria to extract the area that people are interested in. It also serves as the foundation for image analysis and the understanding of image feature extraction and recognition [17].

With the advancement in technologies of image processing, we can refine the images to such clarity that we can easily diagnose a brain tumor. Segmentation is a digital image processing technique that allows us to segment or partition a digital image into multiple segments of pixels - essentially, superpixels of images.

Talking about superpixels of images. The brain region which is detected with the tumor can be easily separated from the surrounding healthy tissues of the brain. A difference can be easily made by assigning different labels to pixels while segmenting. Labeling is done to represent, how pixels with the same label share a common feature which helps us to collectively cover the whole required image of the affected area. Also, proper size and shape, color, texture, and intensity are attained with the help of segmentation. [1]

1.7 Segmentation

The process of dividing an image into regions with similar properties such as grey level, color, texture, brightness, and contrast is known as segmentation. Segmentation's role is to subdivide the objects in an image; in the case of medical image segmentation, the goal is to:

- Study anatomical structure
- Locate the Region of Interest (tumor, lesion, and other abnormalities).
- Measure tissue volume to measure the growth of the tumor (also decrease in size of the tumor with treatment). Help in treatment planning before radiation therapy; in radiation dose calculation.
- Automatic segmentation of medical images is a difficult task because medical images are complex and rarely contain a simple linear feature. Further, the output of the segmentation algorithm is affected due to the partial volume effect, Intensity inhomogeneity, presence of artifacts, and closeness in the gray level of different soft tissue.

Image segmentation plays a critical role in all advanced image analysis applications, a key purpose of segmentation is to divide an image into regions and objects that correspond to real-world objects or areas, and the extent of subdivision depends on the requirements of a specific application. Image thresholding is the most popular segmentation approach due to its intuitive residence and easy implementation. Threshold selection performs a vital function for efficient segmentation results. Some strategies sharpen the histogram peaks in the image enhancement stage as a good way to facilitate edge detection. The most important downside of this approach is the problem of splitting the items from the historical past the item and historical past are of the identical intensity distribution or texture as in MRI scans [18].

Image segmentation is the partition of 2D MRI images into various segments by capturing the RGB (Red, Green and Blue) details in the image. With the detail of RGB in the image, we can specifically target the part of the image that segments it. First, the image is set with a threshold value and specific RGB values of each segment are segmented in the images. For example, the MR images will be segmented like the outer covering part and the brain part and finally the tumor position is segmented as in Figure 1.7.

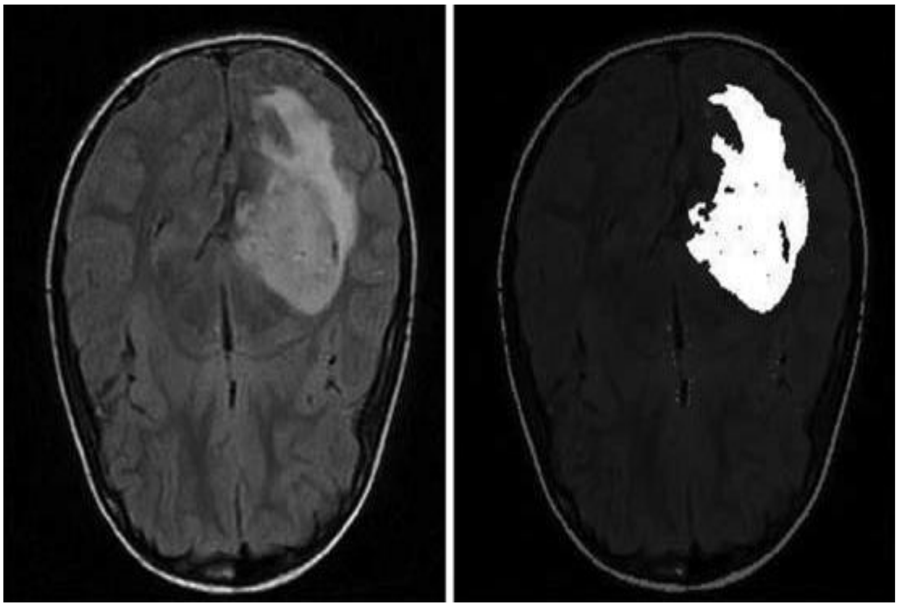


Fig 1.7 Before and after segmentation. [18]

This thesis is organized in five chapters as follows:

Chapter 1: explain an introduction to the brain, shows brain tumor definitions and types, MRI, CAD system, image processing and segmentation.

Chapter 2: shows the theoretical background, history of Deep Learning, types of Deep Learning, Deep learning architecture, Convolutional Networks, Convolution Layer, Subsampling Layer, Image Classification, and Medical Image Analysis.

Chapter 3: shows a proposed system for CNN model, its architecture, and finally showing the experimental dataset.

Chapter 4: explain the results we got it and the high accuracy of the two methods we used on CNN model, and finally we show a comparison of our accuracy results with results from other researches.

Chapter 5: Presents the conclusions obtained from these studies, and the recommendation for future work**.**

Chapter 2

Theoretical Background

2.1 Introduction

The human brain is an amazing organ that controls how inputs from hearing, sight, smell, touch, and taste are processed. The brain keeps track of feelings, encounters, memories, and even dreams. Even the most powerful supercomputers cannot solve all the problems that the brain does. On the basis of this, scientists have fantasized about building brain-like intelligent devices. Later researchers developed self-driving automobiles, automatic illness detection microscopes, and robots to aid humans in their daily chores. These innovations still needed human assistance with some computing tasks. In order to handle more complicated issues faster than the human brain, researchers are working to create a machine that can learn on its own. These prerequisites open the door to deep learning (DL), the most active branch of artificial intelligence [19].

2.2 Neurons

Neurons are the smallest building block of the human brain. Over 10,000 neurons with more than 6,000 connections to other neurons are found in very small, wheat-sized regions of the brain. The neurons in the brain capture the information the brain receives, convey it to other neurons for processing, and then send the finished product to other cells. The neurons' dendrites are an antenna-like structure that serves as the input receiver. The inputs are divided into strengthened and weakened classes based on how frequently they are used. The degree to which the input is related to the neuron's output is estimated by the connection strength. The connection strength is used to weight the input signals, which are then added collectively in the cell body. The estimated total manifests as a new signal that travels up the cell's axon to the target neurons [20].

By focusing on the functional knowledge of the neurons present in the human brain in 1943 and produced an artificial model that was computer-based.

Similar to biological neurons, the artificial neuron takes inputs x_1, x_2, x_3,... x_n, and each input is multiplied by a specific weight w_1, w_2,...w_n; the resulting sum is then thought of as the neuron's logit

$$z = \sum_{i}^{n} 0^{w_j x_i} \qquad (2.1)$$

The bias is a constant that some logistic model or logit models may contain. In order to produce the required output, $y = f(z)$, the logit is finally sent via the function f [21].

2.3 Deep Learning

Deep learning is a well-established and potent machine learning method that is used in many applications to address a variety of challenging problems that become complex and demand extremely high levels of accuracy and sensitivity, especially in the medical industry. In general, brain tumors are among the most prevalent and aggressive cancers, and when they are detected at a more advanced stage, the prognosis is quite poor. Accordingly, grading brain tumors is a crucial step to take when the tumor has been found in order to develop a successful treatment strategy. [22]

Deep learning approach activates a computer model with many processing layers that represent the data at different degrees of abstraction. Deep learning has quickly grown across practically all industries in recent years, particularly in the fields of bioinformatics, medical imaging, and image analysis. Deep learning has consequently fundamentally altered and enhanced detection strategies, prognosis, and diagnosis in numerous healthcare domains, including pathology, brain tumors, lung cancer, abdomen, heart, and retina. Consider a variety of deep learning applications.

Because of its outstanding performance in image analysis domains like object recognition, image classification, and semantic segmentation, deep learning-based approaches and methodologies are gaining popularity in brain tumor segmentation research. The most recent accomplishment of deep learning technology is the automatic segmentation of brain tumors using multiple-model MRI data. [23]

2.4 History of Deep Learning

Deep learning is easy to comprehend in the perspective of history, we note a few significant trends:

Deep learning has a long and rich history, but it has also gone by numerous names, reflecting many philosophical stances, and its popularity has grown and waned. As training data volumes have grown, deep learning has become more practical. As computer infrastructure (including hardware and software) for deep learning has advanced, deep learning models have gotten bigger over time, deep learning has more accurately and efficiently handled increasingly complex applications.

A computer model centered on the human neural system was created by Warren McCulloch and Walter Pitts in the early 1940s, which marked the beginning of the history of deep learning. They used math and algorithms, dubbed "threshold logic," to mimic the way people think. Further development of machine learning, deep learning uses algorithms to process data and create abstractions. Different algorithms are used to process data, identify objects, and understand human speech. The previous layer's output serves as the following layer's input. It uses "threshold logic" to simulate how humans think. Further development of machine learning, deep learning uses algorithms to process data and create abstractions. Different algorithms are used to process data, identify objects, and understand human speech. The previous layer's output serves as the following layer's input.

The Backpropagation Model was created by Henry J. Kelley in 1960, and Stuart Dreyfus expanded on it in 1962. Backpropagation's early iterations were ineffective and awkward. Following this, in 1965, Alexey Grigoryevich Ivakhnenko proposed the data handling methodology utilizing polynomial activation functions, and Valentin Grigorevich Lapa proposed cybernetics and forecasting techniques. The top feature selected statistically is manually transmitted to the following layer [24].

The first convolutional neural networks with several pooling and convolutional layers were created by Kunihiko Fukushima. Neocognitron, a multilayered, hierarchical artificial neural network architecture that can detect visual patterns, was created by him later in 1979. As it employs cutting-edge learning techniques and connections from the top down, the Neocognitron is regarded as the best model at the time. It includes the Selective Attention Model, which can distinguish between different patterns. With the aid of the idea of inference, the developed Neocognitron is capable of identifying unknown and missing information.

Seppo Linnainmaa created a backpropagation FORTRAN code in the late 1970s. Backpropagation can produce "interesting" distribution representations, according to a 1985 study by Williams and Hinton. At Bell Labs in 1989, Yann LeCun used backpropagation and convolutional neural networks to read "handwritten" digits for the first time. Later, many overly enthusiastic researchers overestimated the capabilities of artificial intelligence. In particular, Dana Cortes and Vladimir Vapnik proposed the support vector machine, a model to map and detect related data, in 1995. For recurrent neural networks, Sepp Hochreiter and Juergen Schmidhuber proposed Long Short-Term Memory (LSTM) in 1997.

As a result of the advancement of graphics processing units (GPU), the new era for deep learning began in 1999. The Vanishing Gradient Problem, which opens the door for the growth of extended short-term memory, is discovered in the year 2000. ImageNet, which can handle more than 14 million tagged photos, was built by AI scientist Fei-Fei Li. A convolutional neural network named AlexNet won numerous international contests in 2011 and 2012. The Cat Experiment, a project from Google Brain, was introduced in 2012 and addresses the drawbacks of unsupervised learning. Deep Learning is currently necessary for the development of artificial intelligence and the handling of large amounts of data [25].

2.5 Types of Deep Learning Networks

Depending on the methodologies and architectures utilized for a certain application, such as synthesis, classification, or recognition, the deep learning network is divided into three types [26]. They are categorized as:

1. Unsupervised deep learning network.
2. Supervised deep learning network.
3. Hybrid deep learning networks.

When a target class is not clearly defined, an unsupervised deep learning network captures higher-order correlation data for synthesis. In supervised deep network learning, discriminative capability for pattern classification is provided by depicting the distributions of classes used in the observable data. Deep networks with discrimination are another name for it. A hybrid deep neural network makes use of both generating and discriminative elements. In addition, homogeneous convolution neural network (CNN) classifier convergence is used to form a hybrid deep neural network model. In order to produce an output of one for the anticipated class and zero for all other classes, CNN classifiers are taught to do so. [27]

2.6 Deep Learning Architecture

The most popular deep learning techniques are covered in this section on deep learning architecture. Deep learning depends significantly on representation. The classic approach involves extracting input features from raw data and feeding them to machine learning algorithms. Identifying the pattern, it depends on the practitioner's experience and subject knowledge. The lengthy and laborious parts of the engineering process involve creating, analyzing, choosing, and evaluating the required characteristics. Contrarily, the necessary features are learned directly from the data without any human involvement and help uncover dormant relationships among data that could otherwise be concealed or undiscovered [28].

Figure 2.1 shows the architecture of deep learning:

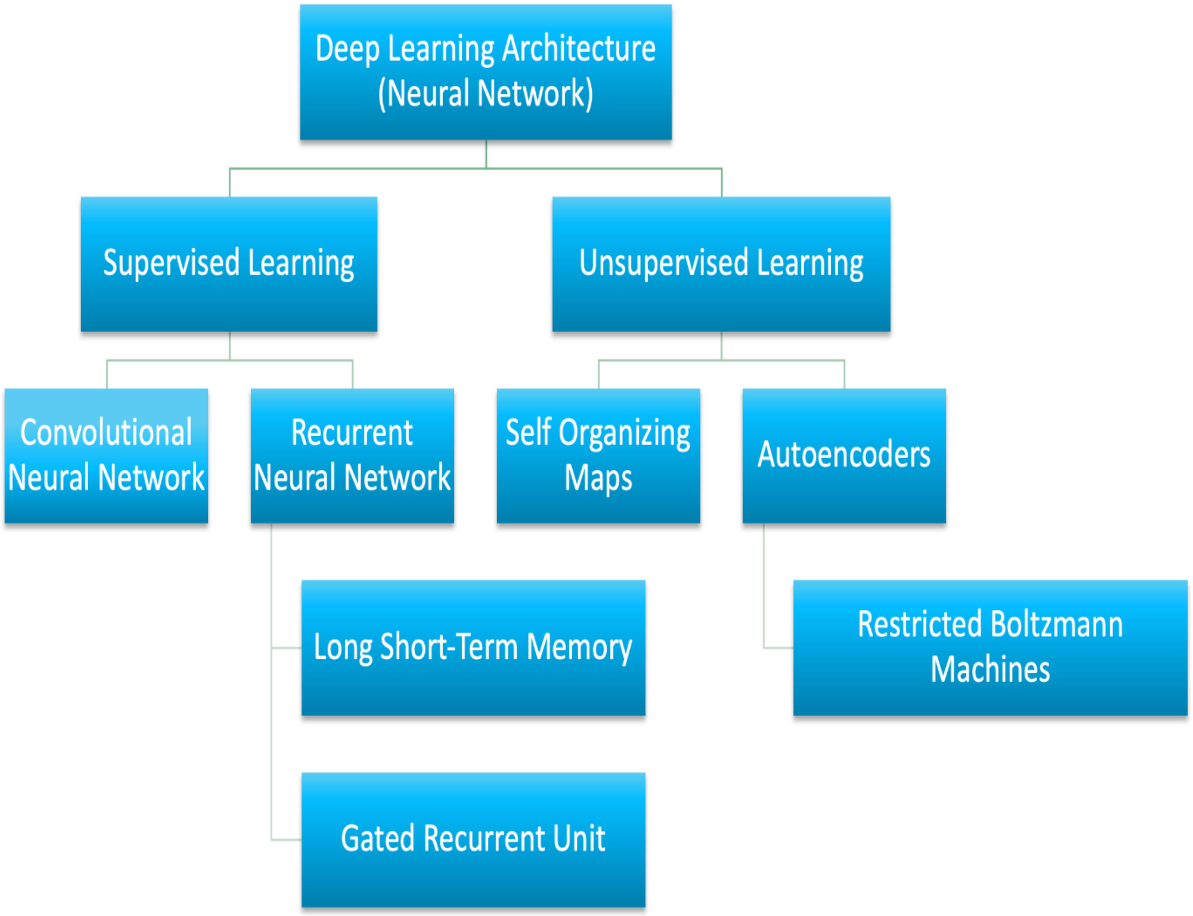


Fig 2.1 Deep learning architecture. [29]

2.7 Concepts of Convolutional Neural Network

In contrast to other networks with FC (fully connected) layers, the Convolutional Neural Network (CNN), also known as ConvNet, is a type of Artificial Neural Network (ANN) that has a deep feed-forward architecture and amazing generalizing abilities. It can learn highly abstracted features of objects, particularly spatial data, and can identify them more effectively.

A deep CNN model is made up of a limited number of processing layers that can learn different input data features at different levels of abstraction. The deeper layers learn and extract the low-level features, whereas the initiatory layers learn and extract the high-level features (with less abstraction) (with higher abstraction) [30]. Figure 2.2 depicts the fundamental conceptual model of CNN, with succeeding sections describing the various types of layers. [31]

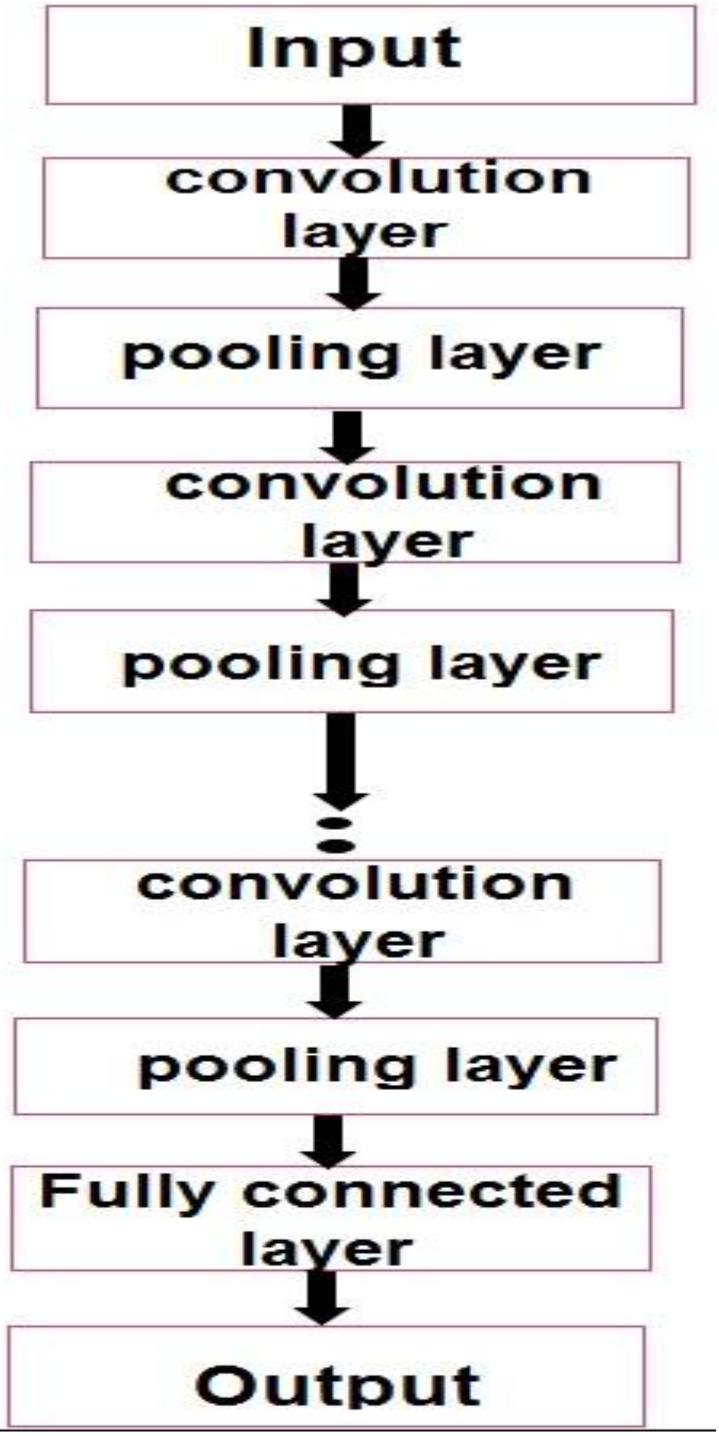


Fig 2.2 Conceptual model of CNN. [31]

2.8 The Convolution Operation

Convolution is an operation on two functions of a real-valued argument in its broadest sense. We begin by giving examples of two functions that we might use to illustrate the definition of convolution.

Let's say we are using a laser sensor to locate a spacecraft. One output, x (t), representing the position of the spacecraft at time t, is provided by our laser sensor. Both x and t are real values, meaning that we can always receive a different signal from the laser sensor.

Let's say our laser sensor is a little noisy now. We want to average many observations to get a less noisy estimate of the spaceship's position. We will want this to be a weighted average that gives more weight to recent measures because, of course, more recent measurements are more pertinent. A weighting function called w (α), where is the age of the measurement, can be used to do this. When we perform such a weighted average operation at each instant, we create a new function s that provides a smoothed estimate of the spaceship's position: [32]

$$S\,(\mathrm{t}) \;=\; \int x(\alpha)\omega(\mathrm{t}\;-\;\alpha)\,\mathrm{d}\alpha \qquad (2.2)$$

Convolution is the name of this operation. Typically, an asterisk is used to indicate the convolution operation:

$$S(\mathrm{t}) = (x * \omega)(t) \qquad (2.3)$$

In our illustration, must be a legitimate probability density function in order for the result to be a weighted average. Additionally, must be zero for all objections, otherwise, it will ostensibly peek into the future, which is beyond our capacity. These restrictions, however, only apply to our case. Convolution can be used for more than just taking weighted averages; it is generally specified for any functions for which the aforementioned integral is defined.

In the language of convolutional networks, the first argument to the convolution (in this case, the function$x$) is frequently referred to as the input, while the second argument (in this case, the function ω) is sometimes referred to as the kernel. The output is occasionally known as the feature map.

Convolution Neural Network (CNN) has a deep feed-forward architecture and a remarkable capacity to generalize better than networks with completely connected layers.

According to, CNN is the idea of hierarchical feature detectors with biological inspiration. It can efficiently detect objects and learn extremely abstract attributes. The following are some of the significant justifications for why CNN is preferred to other traditional methods. The idea of employing weight sharing, which significantly reduces the number of parameters that need training and improves generalization, is the primary motivation for using CNN. Fewer parameters provide for a smoother training process and prevent overfitting. Second, both the feature extraction stage and the classification stage involve the learning process. Thirdly, compared to utilizing CNN, using general models of an artificial neural network (ANN) is significantly more complex to create big networks. Due to their outstanding performance, CNNs are widely used in many fields, including image classification object detection, face detection, speech recognition, vehicle recognition, diabetic retinopathy, and recognition of facial expressions, among others. [32]

So, how does the convolution operation tack place?

Before we delve any further, let's first comprehend the CNN input format. CNN uses a multi-channeled picture as its input rather than the vector format used by other traditional neural networks (e.g. for

RGB image as in figure 2.3, it is 3 channeled, and for Gray-Scale image, it is single channeled). [31]

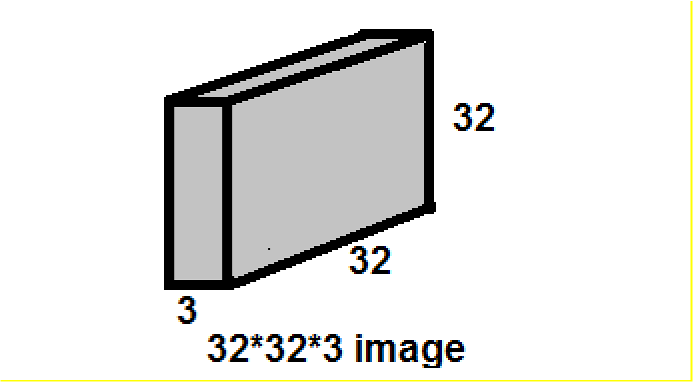


Fig 2.3 Example of an RGB image. [31]

Take a look at Figures 2.4 and 2.5 to see a grayscale image of 4 × 4 dimensions and a 2 x 2 kernel with randomly initialized weights to better understand the convolution procedure.

1	0	-2	1
-1	0	1	2
0	2	1	0
1	0	0	1

Fig 2.4 A 4 x 4 Gray-Scale image.

0	1
-1	2

Fig 2.5 A kernel of size 2 x 2.

In the convolution operation, we now take the 2 x 2 kernel and move it across the entire 4 x 4 image both horizontally and vertically. Along the way, we multiply the relevant values of the kernel and the input picture to obtain the dot product between them. Along the way, we add all values to produce one scaler value in the output feature map. The kernel keeps sliding in this manner until it can no longer [31].

Convolution layers' main benefits are:

- Sparse Connectivity: In contrast to CNN, where only a small number of weights are present between two layers, fully connected neural networks connect every neuron in one layer to every neuron in the layer above it. It is memory efficient because we only need a small number of connections or weights and a little amount of memory to store them. Additionally, computing costs for the dot (.) operation are lower than for matrix multiplication.
- Weight Sharing: In CNN, all weights are applied to each pixel of the input matrix rather than having specific weights for two neurons in adjacent layers. One set of weights for all inputs can be learned rather than learning fresh weights for each neuron, which greatly lowers training time and other expenses [31].

2.9 General Model of Convolution Neural Network

Typical Model Multiple hidden layers are present along with a single input and output layer in the conventional ANN model. A specific neuron uses an input vector X to generate an output vector Y by applying a function F, as shown below and given by. [32]

$$Y = F(X, W) \tag{2.4}$$

Where W stands for the weight vector, which symbolizes how strongly neurons in two adjacent layers are connected. The weight vector that was created can now be utilized to classify images. The classification of images based on pixels has been extensively studied in the literature. Contextual information, such as the image's shape, yield better results or outperforms, but. CNN is a model that is gaining popularity because of its ability to classify data based on context. The general CNN model is shown in figure 2.6 below. [33]

A standard CNN model consists of four parts, including:

- Convolution layer
- Pooling layer
- Activation function
- Fully connected layer.

The functionality of each component is demonstrated later.

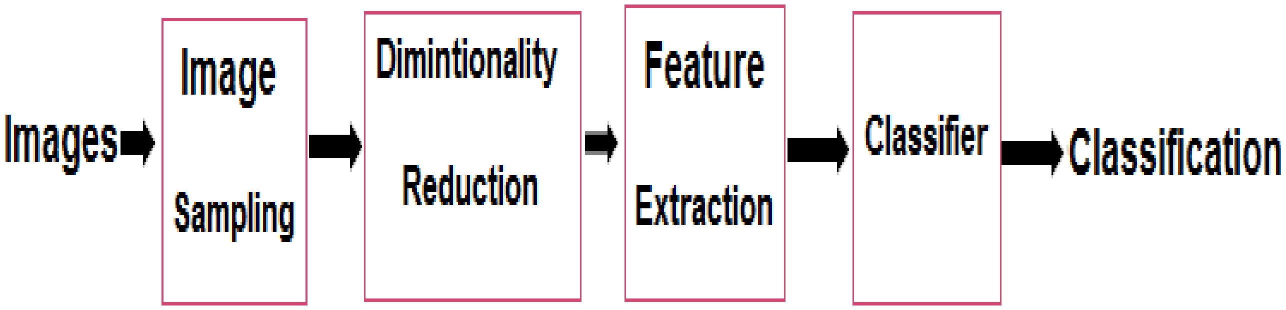


Fig 2.6 Elementary constituents of CNN. [33]

2.10 Architectures of Convolution Neural Network

CNN has developed and implemented a number of architectures, the following sections provide brief explanations of those architecture:

2.10.1 VGGNet

VGG (Visual Geometry Group) Net is a popular CNN architecture that Simonyan and Zisserman introduced in 2014. The authors presented a total of six different CNN configurations, the most successful of which are the VGGNet-16 (configuration D) and VGGNet-19 (configuration E). Figure 2.7 depicts the VGGNet-16 architecture. [31]

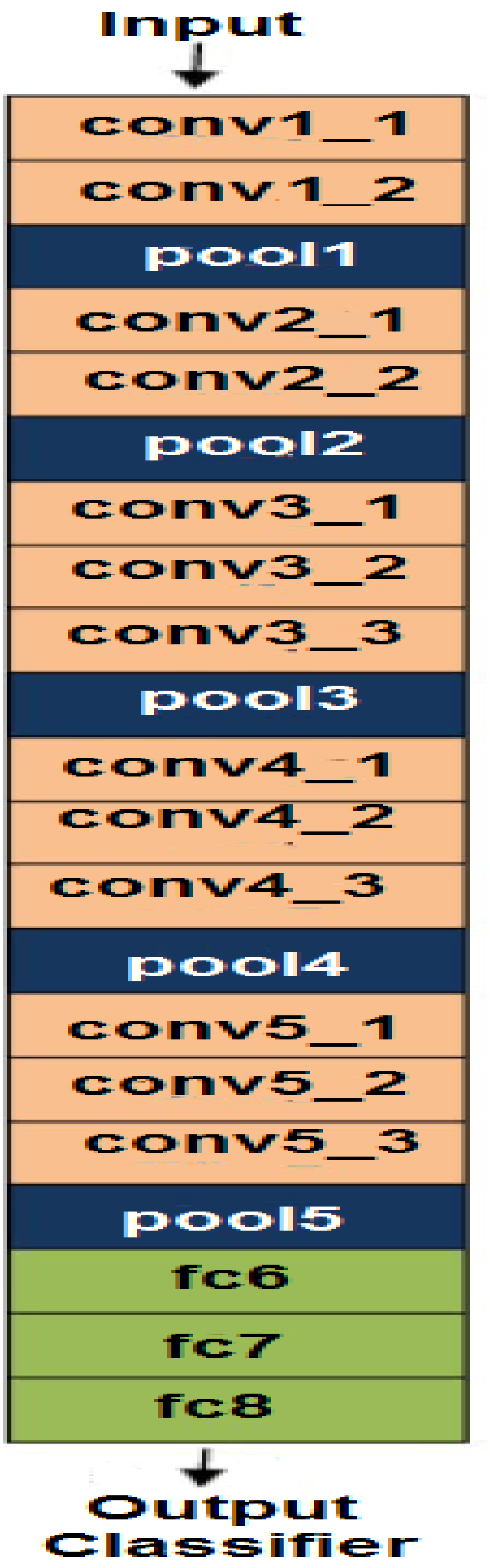


Fig 2.7 The architecture of VGGNet. [31]

- VGGNet's popularity stems from its architectural simplicity and use of small-sized filters for convolutional operation.
- It demonstrates that a stack of 3 x 3 sized filters has the same effective receptive field as larger sized filters in convolution (e.g., two layers of 3 x 3 sized filters have the same effective receptive field as 5 x 5 filters in convolution, 7 x 7 filters with three layers of 3 x 3 sized filters, and so on). Most importantly, using small-sized filters reduces the number of network parameters.
- The ILSVRC dataset was used to design and train the VGGNet.
- It is a much deeper network than AlexNet.
- After each convolutional and fully connected layer, it used a rectified linear unit (ReLU) non-linearity activation function.
- It also employs several regularization techniques, such as dropout and data augmentation, to avoid over-fitting. [31]

The following types are the most popular architectures used in CNNs:

- LeNet Architecture
- AlexNet Architecture
- ZFNet
- GoogleNet Architecture
- ResNet
- DenseNet

2.11 Image Classification

Because of various capabilities such as weight sharing, different levels of feature extraction such as classifiers, and so on, CNN has achieved higher classification accuracy than other methods, particularly in the case of large-scale datasets. The first breakthrough in image classification occurred in 2012, with the development of AlexNet, which won the ILSVRC challenge that year. Following that, several improvements to the CNN model have been made by researchers over time**,** making CNN the first choice for image classification problems. [34]

2.12 Medical Image Analysis

With the advancement of CNN-based image analysis, CNN has quickly proven to be a cutting-edge foundation, achieving enhanced performances in disease diagnosis by processing medical images such as MRI, X-rays, and so on. CNN-based models can now successfully diagnose a wide range of health issues, including breast cancer, pneumonia, brain tumors, diabetes, Parkinson's disease, and many others. [31]

Chapter 3

Proposed System

3.1 Introduction

The work was applied through the system, where two methods were used in order to increase the accuracy of the model's work and reach a high rate of efficiency, in other words to obtain more than one method of work by obtaining varying percentages of accuracy when applying two methods to the same type of data set. Two different size of dataset were used and trained the model on them. Then the results were recorded in each method so that we could make a comparison between each method and see how we get the highest efficiency and from which method?

In the first method, all the datasets were worked on and entered into the model in one stage, and the datasets were large in size.

The second method, Instead of entering all the datasets on the network at once, the dataset was divided into 3 classes and the model was trained on them, that is, as if the model had been created and the data trained on it, repeated 3 times.

All of this is to improve the efficiency of the model and obtain several results until the final result of accuracy is reached. It is expected that this will reduce the model's running time. Despite dividing the dataset into 3 classes and training the model on them 3 times, it makes the work faster, improves efficiency, and produces a better result of accuracy. This is what was expected from the model initially.

These two methods are based on CNN that will be discussed in detail in this chapter.

3.2 Experimental Dataset

For the Performance Evaluation of the proposed model, we used two different types of the dataset containing 3517 images both types are magnetic resonance imaging (MRI) and splitting the dataset by 80 to 20 in terms of training to testing images. As it is shown in table 3.1.

The first type is a small dataset called "Brain MRI images for brain tumor detection" [35] (According to their name on the sites on which they are located) divided into two sections, the first section contains 98 images that do not have a brain tumor called (no), and the second section contains 155 images with a brain tumor called (yes). Total number of this dataset =253 images.

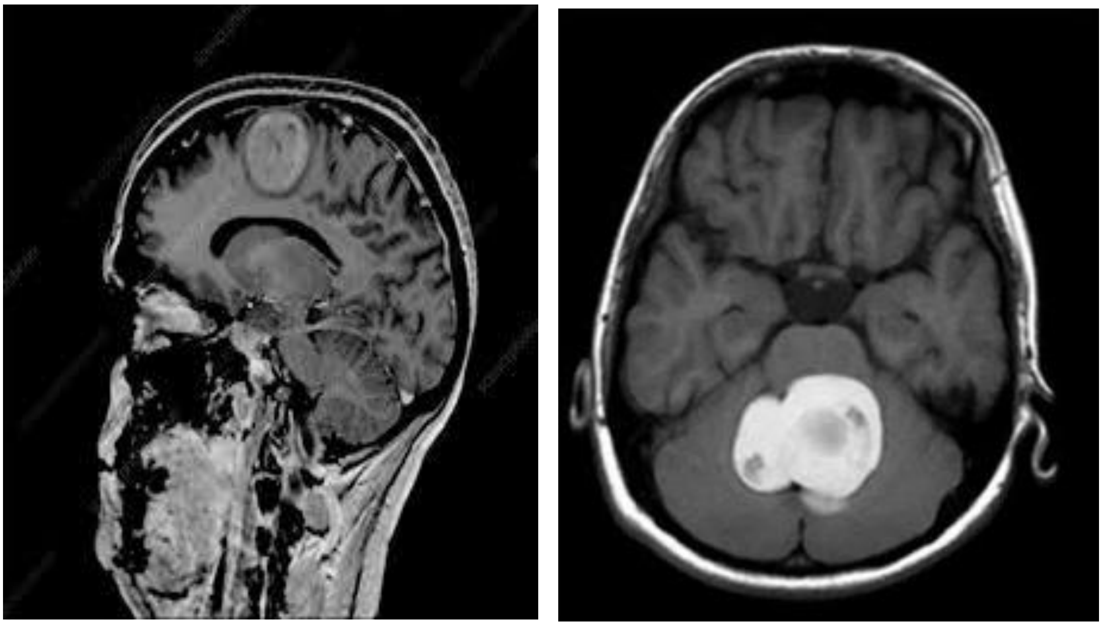
The second type is a large dataset called "Brain Tumor Classification (MRI)" [36] (According to their name on the sites on which they are located) this containing 3264 MRI images divided into 4 classes:

Glioma tumor (926 images), Meningioma tumor (937 images), no tumor (500 images), and Pituitary tumor (901 images).

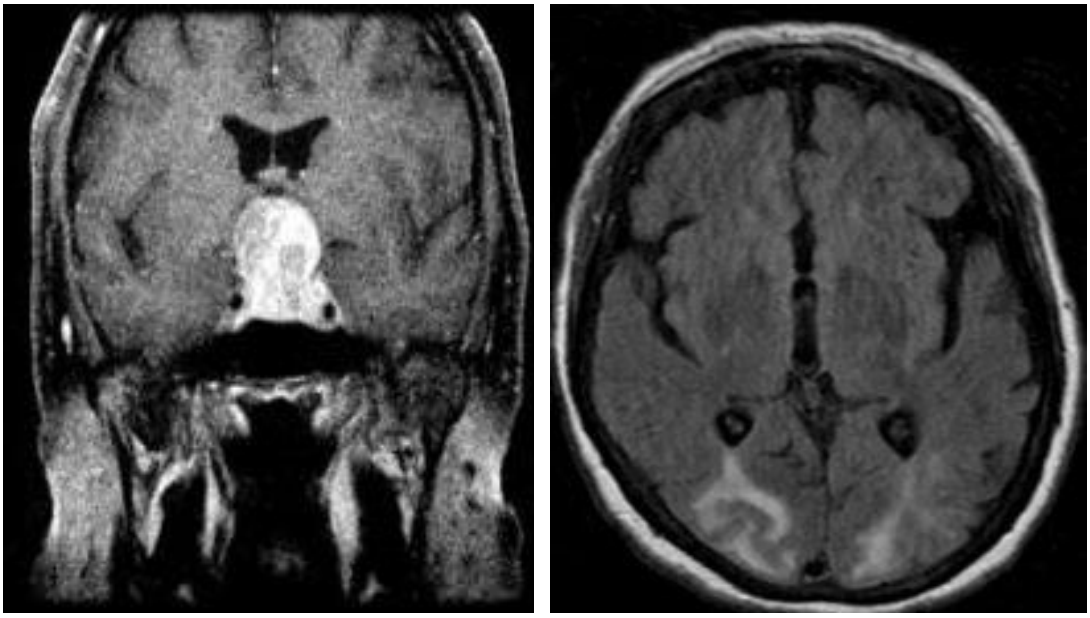
Table 3.1 Types of dataset.

" Brain MRI images for brain tumor detection " (253 images)		" Brain Tumor Classification (MRI)" (3264 images)			
Yes =155 images.	No = 98 images.	Glioma tumor = 926 images.	Meningioma tumor = 937 images.	Pituitary tumor = 901 images.	No tumor = 500 images.

Here we will display samples of data set images for each type glioma tumor, meningioma tumor, pituitary tumor and no tumor, as shown in Figure 3.1.



A: Glioma tumor **B: Meningioma tumor**



C: pituitary tumor **D: No tumor**

Fig 3.1 Samples images of dataset.

3.3 CNN Model

As mentioned previously, it was tested on many models until a model was settled on that worked well on the existing datasets, until a high percentage of accuracy was obtained.

Let's talk more about the CNN model:

In the first method on CNN model, all of the dataset was entered into the network and their number was about 3517 images. This is a large group of images that was diverse and contained many types of tumors so that the model can be trained well on them, but in return it gave a low percentage of accuracy and took a long time and was very slow.

When describing the second method on CNN model, we find that the images were divided into 3 classes of different types, and based on each type of tumor present in these images, the division was done accordingly, and the second method was repeated twice:

Each type of tumor was different in the number of images, but they were entered into the network with an equal number of images "465 images" for 3 types of tumor, and "465" for no tumor type repeated with each tumor and this is first time.

The second time, by entering a different number of images (According to the number present in each type in the dataset).

Each time, a higher accuracy rate was obtained, especially with the equal number of images included in each of the 3 classes.

3.3.1 Dataset Pre-processing

Many datasets were tried, some of which did not work well, some were not compatible with the code, and others were not arranged, not divided, and did not contain different types of tumors. Even obtaining a suitable dataset that is divided into different types of tumors and their size is large, and this is a good feature until it works successfully with the CNN model, and other small-sized data are classified only as to whether they contain tumors or not, and there are two types so that there are differences when training the model on datasets of different sizes. The Dataset is also compatible with the code after making some modifications, as it changes the dimensions of the images entered into the system to 128*128, after their dimensions were large, some of which reached 495*619. The images in both datasets are not RGP, but in grayscale, and are of JPEG type.

The image data is also normalized to the range [0, 1]. When working with image data, this is fairly frequent, as it allows the model to train more effectively. In addition, the integer labels are converted to one-hot encoded labels.

3.4 CNN Architecture

Before we get started on the coding, let's look at the overall structure of the model we're proposing. The model has a structure comparable to VGG-16, however, it has fewer layers and a significantly lower input image size, and thus far fewer trainable parameters. Two convolutional blocks are followed by a fully connected layer and an output layer in the model.

And we will discuss a simple explanation of each layer as shown in figure 3.2.

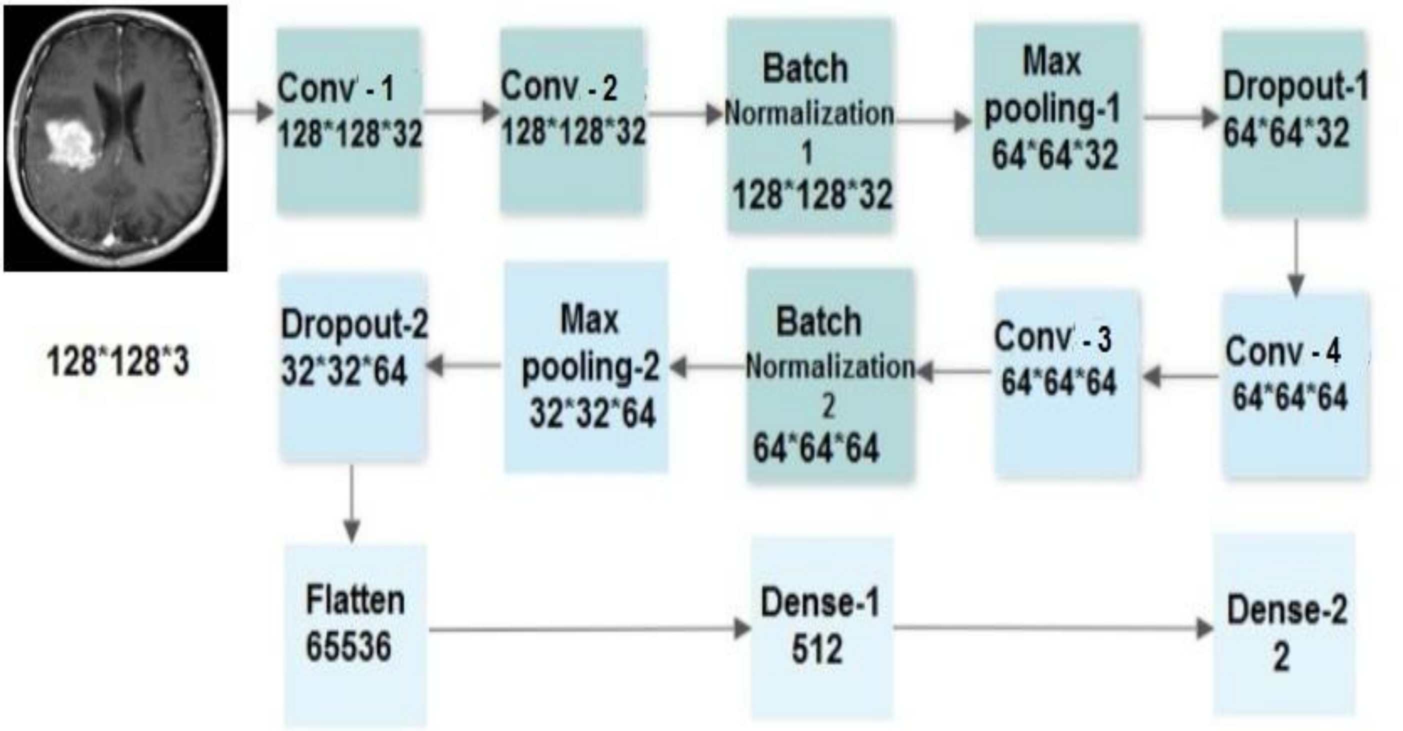


Fig 3.2 Block diagram of the proposed method.

The architecture of CNN model shown in figure 3.3 below, which illustrate the layers of the model starting from the input image until it ends with the output image, passing through Convolution Layer , Pooling layer , flatten and dense layer.

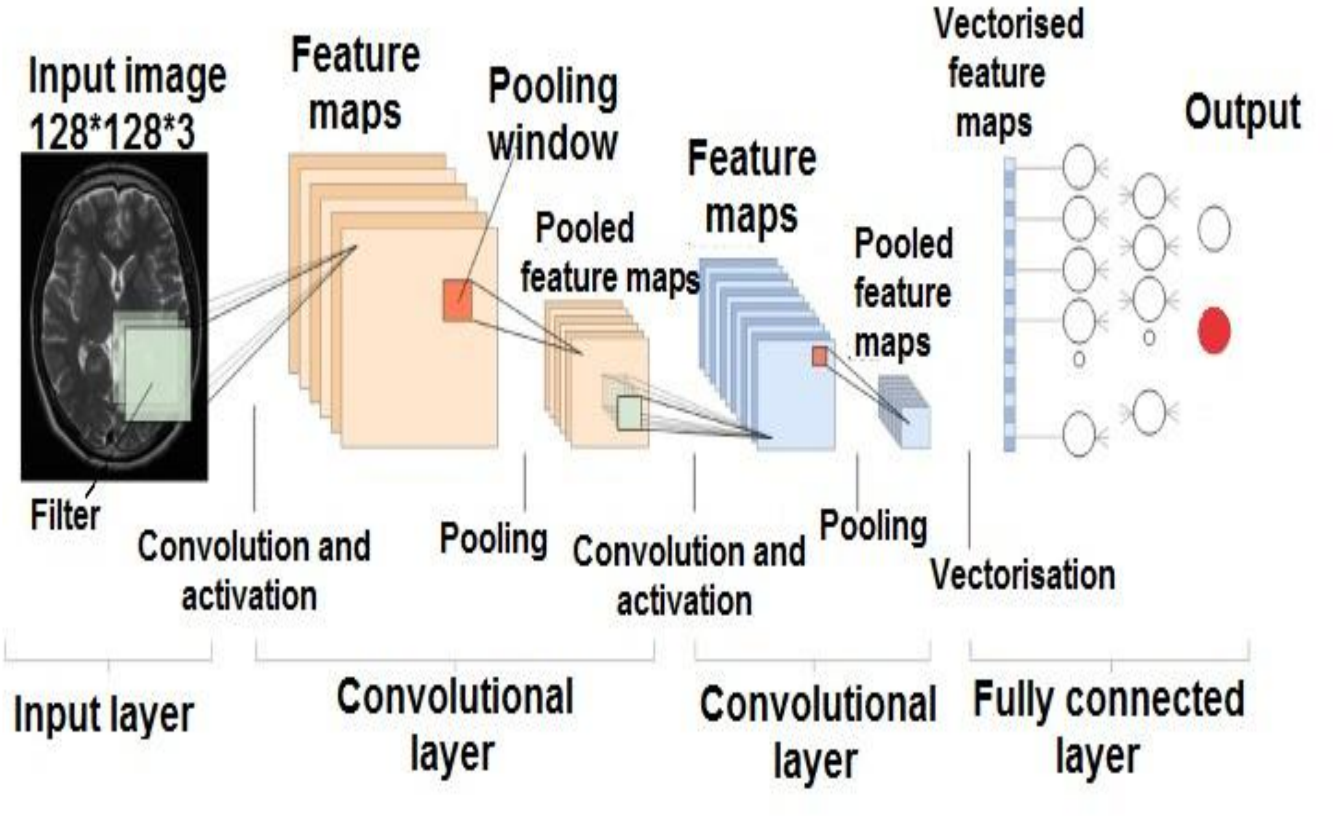


Fig 3.3 CNN architecture.

3.4.1 Convolutional Layer

The model uses two convolutional layers, the first of which is utilized to extract the various attributes from the input photos. The convolutional mathematical action between the input image and a particular size filter is carried out by this layer. The dot product between the filter and the areas of the input image that match the filter's size is calculated by swiping the filter over the input image. This layer outputs feature maps from a dimension h*w*d input. This layer has the following mathematical definition:

$$\psi_k^i = REL(\psi \beta_k^i + \sum_{j=1}^{n^{i-1}} \omega_{kj}^i \times X_j^{i-1}) \tag{3.1}$$

Where (ψ_k^i) is the output of a convolutional layer, (β_k^i) is the bias term, (ω_{kj}^i) is the convolutional layer's weight, (X_j^{i-1}) is the input term, and Rel (.) is the non-linearity ReLU activation function.

The result, referred to as a feature map, gives us details about the image, such as its edges and corners. The input format for the MRI image in our model is 128*128*3 (The code converts the input grayscale images into color images), and thereafter, the feature map is given to various layers so that we can learn about numerous other properties of the input picture.

Begin with the first convolutional layer in the first convolutional block. The Conv2D () function was used, which takes many input arguments to construct a convolutional layer. First, we specified that the layer would have 32 filters. Each filter's kernel size is 2 (which is interpreted as 2*2).

The default behavior has no padding, and the spatial size of the convolutional layer output will be somewhat lower than the input size. Except for the output layer, we utilized a ReLU activation function in all layers of the network.

We must specify the shape of the input for the first convolutional layer, but this is not required for subsequent layers because the shape of the input is automatically computed based on the shape of the output from previous layers, so we have two convolutional layers with 32 filters each, and then we follow that with a max pooling layer with a window size of (2*2) so the output shape from this first convolution block is (64*64*32). The second convolutional block is substantially identical to the first, with the distinction that each convolutional layer now has 64 filters rather than 32.

3.4.2 Pooling Layer

Following the creation of the convolutional layer, the pooling layer is created. Convolution and pooling layers are used in tandem. Pooling operations are classified into two types: maximum pooling and average pooling. Max pooling is used in this case.

The MaxPooling2D () class is used to generate each pooling layer in a CNN, which simply conducts the Max pooling operation in a two-dimensional space.

The pool size was determined using MaxPooling2D and is
(2, 2) as mentioned previously. It is given mathematically as follows:

$$\psi_k^i(\max) = pool_{\max}(REL(\mathrm{X}), REL(\mathrm{X}) \in \psi_k^i) \qquad (3.2)$$

Important parameters in MaxPooling2D:

- Pool size: The pooling window's size. The default value is (2, 2). This accepts either an integer or a tuple. If we use an integer, the same window length will be used for both dimensions.
- Strides: The number of steps (pixels) the pooling window moves over the feature map for each pooling step. A tuple is required for the strides along the height and breadth. We can use an integer if the height and width are the same. The default is none, which takes the value of pool_size.

- Padding: There are two possibilities for padding "valid" or "same". "Valid" signifies that there is no padding. "Same" causes padding with zeros to ensure that the pooled feature map is the same size as the input.

3.4.3 Activation Functions (ReLU)

We utilized a ReLU activation function in all layers of the network. Except the last one as mentioned before.

ReLU is mathematically represented as follows:

$$REL(\mathrm{X}) = \max(0, \mathrm{X}) \tag{3.3}$$

3.4.4 Fully Connected (FC) Layer

Before we create the classifier's fully connected layers, we initially flatten class the two-dimensional activation maps produced by the last convolutional layer (which has a spatial form of 32*32 with 64 channels). This is performed by invoking the flatten () method, which generates a 1-dimensional vector with a length of 65536. Because our dataset has two classes, we add a densely connected layer with 512 neurons and a completely connected output layer with two neurons. We've also included a thorough schematic of the completely connected layers to minimize any confusion.

The ultimate output of CNN, as depicted in Figure 3.4, is produced by the FC layer, which receives input from the final convolutional or pooling layer, which is composed of a series of measurements (feature maps). These measures are processed to build a vector, which is then supplied into the FC layer.

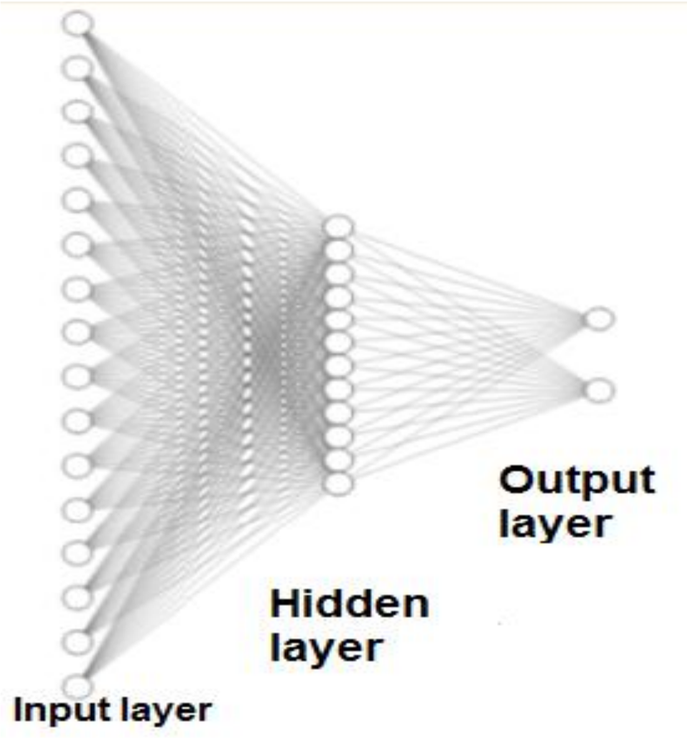


Fig 3.4 The architecture of Fully Connected Layers.

3.4.4.1 Dropout

Dropout is a specific type of layer that removes a percentage of neurons at random throughout the training process. Dropout is typically employed after the max pooling layer in convolutional layers and has the effect of deleting a percentage of neurons in the feature maps. When utilized after a fully connected layer, a percentage of the neurons in that layer are dropped.

3.4.4.2 Batch Normalization

Batch normalization is a technique for training very deep neural networks that standardizes the inputs to a layer for each mini-batch. This has the effect of stabilizing the learning process and dramatically reducing the number of training epochs required to train deep networks.

Here, we divide each dimension by its standard deviations to normalize the data sample's dimensions (which come from the train and test datasets).

3.4.5 Model Compiling

The model is next compiled, where we define the optimizer type, loss function, and any additional metrics we want logged during training. We utilize a cross-entropy loss function, which is the usual loss function for classification problems, and Adamax as the optimizer type. Because our labels are one-hot encoded, we employ binary_crossentropy specially. Finally, we add accuracy as a new statistic to track throughout training.

3.4.6 Model Training

By dividing the code of the existing dataset into training data and test data in a ratio of 80 to 20, the images were chosen randomly and swapped between them, and the average was obtained to calculate the efficiency.

The average accuracy we reached is 98.4 % for the aforementioned model.

3.4.7 Code Information

Many codes were tried and some layers were added to them and modified until the code was ready (see Appendix A).

The proposed model was designed using python programming on Kaggle online platform for easy access to online GPU, This is useful as it allows for the availability of large work spaces.

The Kaggle API and CLI tool provide easy ways to interact with Notebooks on Kaggle. The commands available enable both searching for and downloading published Notebooks and their metadata as well as workflows for creating and running Notebooks using computational resources on Kaggle.

Kaggle provides free access to NVIDIA TESLA P100 GPUs. These GPUs are useful for training deep learning models, you can use up to a quota limit per week of GPU. The quota resets weekly and is 30 hours or sometimes higher depending on demand and resources.

As a final summary of what was designed in the CNN model and what was presented in this chapter:

A CNN For the following scenario, the following layers were used: Two types of datasets were used, both of which contain a huge number of grayscale images. A CNN was developed that should be capable of accurately classifying these images.

Table 3.2 CNN model layers.

CNN layers	Size	No. of layers
Input layer	(128*128*3)	1
Convolution	(128*128*32)	2
Convolution		
Batch normalization	(128*128*32)	1
Max pooling	(64*64*32)	1
Convolution	(64*64*64)	2
Convolution		
Batch normalization	(64*64*64)	1
Max pooling	(32*32*64)	1
Dropout-1	(64*64*32)	2
Dropout-2	(32*32*64)	
Flatten	65536	1
Dense	512	2
Dense	2	

This model was changed several times by adding some layers, changing their values, and recording the resulting value. By observing the changes occurring in the model, the values and number of layers mentioned here were settled.

Chapter 4

Results and Discussion

4.1 Introduction

In this chapter, we will display all the methods, tables, pictures, and accuracy rates that we have achieved through the model presented.

We will also present some of the problems we encountered while working and how they were all overcome and solved.

We will discuss in detail the explanation of the model and how it operates during training and testing on Dataset.

We will show all the modifications we made to the system, the additions to the number of layers, and changing the ratios and types. We will know the extent of their impact on the system and how to access what was used and designed in the system.

Finally, we will show how we evaluated the proposed model.

4.2 Results

By applied two different size of MRI datasets (the first is large dataset called "Brain Tumor Classification (MRI) 3264 images" and the second is small called "Brain MRI images for brain tumor detection 253 images") in order to increase the size of the data and thus increase the accuracy and efficiency of the model by applying two methods to the CNN model.

The first method is to apply all the images on the network together. The network was trained on a large and different size of dataset consisting of 3517 images divided into a group of images that have tumors and others that do not have tumors using 80 to 20 training testing ratio. We recorded the results and obtained an accuracy rate of 94.6 %.

The second method is to divide the images into 3 classes and enter them into the network, each group separately, that is, as if we had repeated the network 3 times until efficiency increased. Although the images were divided into 3 classes, it is expected to improve efficiency, reduce the model’s working time, and speed up the overall time. The accuracy of the model increases .

The accuracy rate in detecting this tumor has increased to 98.4 %, and we will explain them in details.

As we mentioned before the proposed method was designed using python programming on Kaggle online platform, API and CLI tool provide easy ways to interact with Notebooks on Kaggle.

4.2.1 The First Method of Model

All datasets were entered, Brain Tumor Classification (MRI) in addition to Brain MRI images for brain tumor detection datasets, and their number was 3517 images, and the number of trained images entered into the system shown in the table 4.1, all dataset was entered and the training data was randomly selected from it (at a ratio of 80 to 20), as well as the testing data.

Table 4.1 The first method results.

Type	**All dataset**
Contain	Brain Tumor Classification (MRI) (3264 images) + Brain MRI images for brain tumor detection (253 images)
No. of data	3517 images
Training data (80%)	2814 images
Testing data (20%)	703 images
Accuracy	**94.6 %**
Precision	95 %
Recall	98 %
F1 score	96 %

4.2.2 The Second Method of Model

The problem of low accuracy from the previous method was solved by dividing the large dataset into 3 classes, each class represents a type of tumor present in the dataset, in addition to the type of no tumor. Applying the CNN model to each class separately as if entering it into the same model 3 times. It was expected to obtain higher accuracy in less time and increase the efficiency and speed of the model’s work. Discussing the explanation in detail below:

In Table 4.2 we show the part of testing the model on Dataset Through it, we see that all the values of the tumors that the model predicts are almost correct.

Table 4.2 The second method results.

Type	Glioma tumor + No tumor	Meningioma tumor + No tumor	Pituitary tumor + No tumor	Total
No. of data	465+465	465+465	465+465	930
Training data (80%)	744 images	744 images	744 images	-
Testing data (20%)	186 images	186 images	186 images	-
Accuracy	**98.9 %**	**98.4 %**	**97.8 %**	**98.4%**
Recall	99 %	99 %	98 %	98.6%
Precision	100 %	99 %	99.3 %	99.4%
F1 score	99 %	99 %	98.6 %	98.9%
Average accuracy of this method = 98.4 %.				

So, the accuracy of the second model = 98.4 %. (That is a very high rate of accuracy).

4.3 Model Evaluation

Four statistical indices are calculated and used to evaluate the performance of the proposed classification system based on the generated confusion matrix, namely:

True positive (TP): the person has the disease and the test is positive.

False positive (FP): the person does not have the disease and the test is positive.

False negative (FN): the person has the disease and the test is negative.

True negative (TN): the person does not have the disease and the test is negative.

$$\text{Accuracy} = (\text{TP} + \text{TN})/\,(\text{TP} + \text{FP} + \text{TN} + \text{FN}) \quad (4.1)$$

$$\text{Recall or Sensitivity} = \text{TP}/\,(\text{TP} + \text{FN}) \quad (4.2)$$

Recall: measures the percentage of relevant data points that were correctly identified by the model.

$$\text{Specificity} = \text{TN}/\,(\text{TN} + \text{FP}) \quad (4.3)$$

Specificity: the ability of a test to correctly identify people without the disease.

$$\text{Precision} = \text{TP}/\,(\text{TP} + \text{FP}) \quad (4.4)$$

Precision: measures the percentage of predictions made by the model that are correct.

$$\text{F1 score} = 2 * (\text{Precision} * \text{Recall}/\,\text{Precision} + \text{Recall}\,) \quad (4 \cdot 5)$$

A confusion matrix is a table that is used to assess the performance of a classification model. It displays the model's correct and wrong predictions in relation to the actual results. The matrix is often expressed in tabular form, with at least four components produced based on model predictions and actual findings.

Figure 4.1 shows the confusion matrix of the first method showing the high values of true positive and true negative with low values of false positive and false negative.

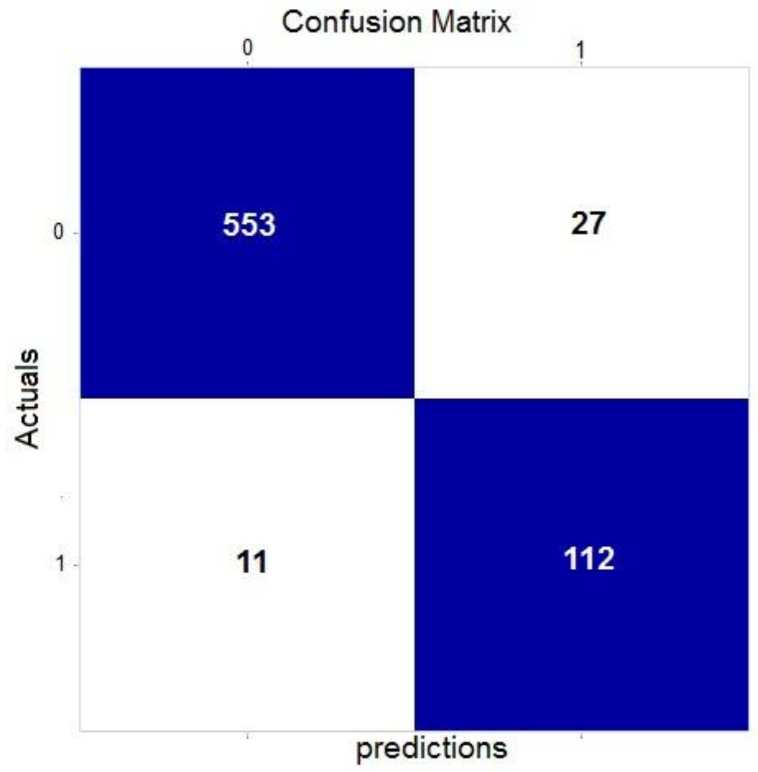


Fig 4.1 First method confusion matrix.

Figures 4.2, 4.3, and 4.4 showing the second method confusion matrix of dataset classes showing the high values of true positive and true negative with low values of false positive and false negative.

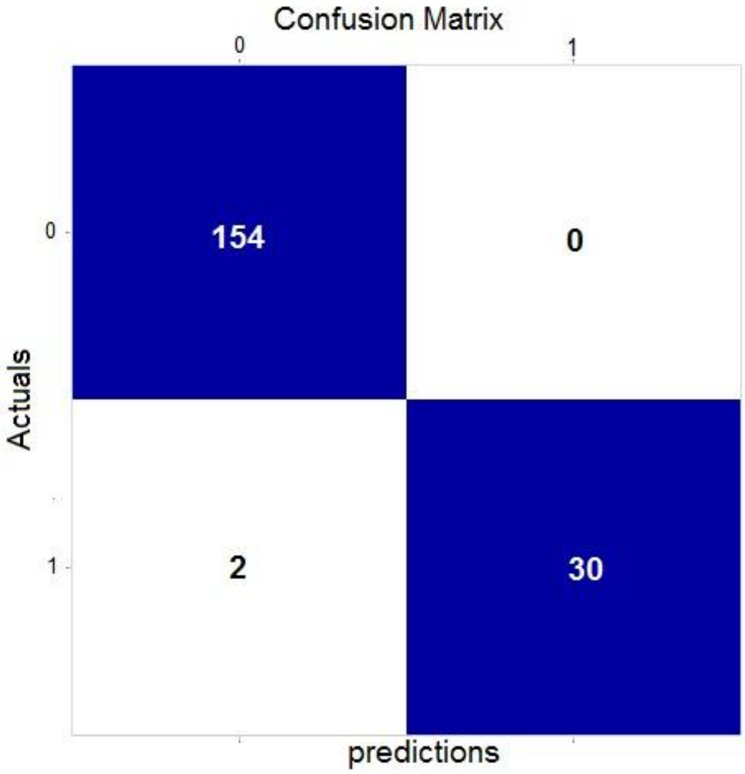


Fig 4.1 Confusion matrix of glioma tumor.

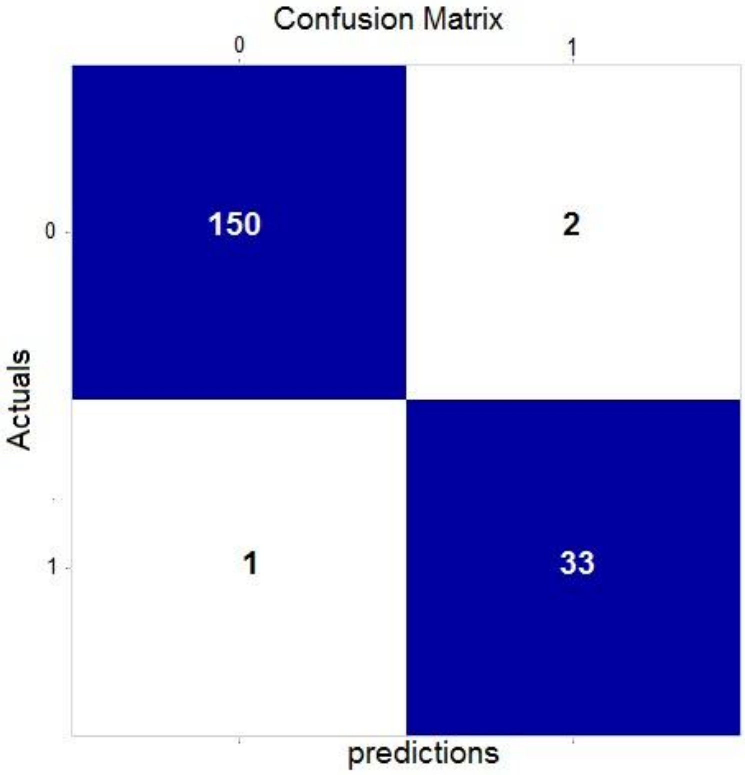


Fig 4.2 Confusion matrix of meningioma tumor.

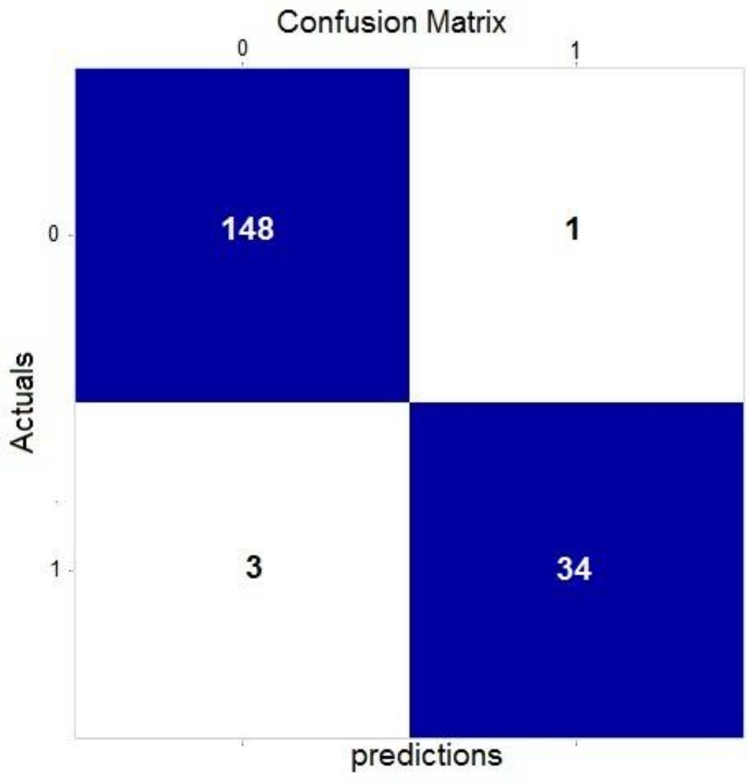


Fig 4.3 Confusion matrix of pituitary tumor.

4.3.1 Trial and error methods:

After creating the CNN model, we tried several methods to obtain the best accuracy, including:

Only "Brain Tumor Classification (MRI)" datasets entered the system, and their number was 3264 images, and the number of trained images entered into the system shown in the table 4.3, all dataset was entered and the training data was randomly selected from it (at a ratio of 80 to 20), as well as the testing data.

The epochs values were =30 and the batch size values were =40 (These were the best values on which the model was trained, and we obtained the highest accuracy from them.), the accuracy rates we obtained were as follows:

Table 4.3 CNN model results on Brain Tumor Classification (MRI) dataset but not unified images.

Type	**Glioma tumor + No tumor**	**Meningioma tumor + No tumor**	**Pituitary tumor + No tumor**
No. of data	926+500=1426	937+500=1437	901+500=1401
Training data (80%)	1141 images	1150 images	1121 images
Testing data (20%)	285 images	287 images	280 images
Accuracy	**99.3 %**	**98.9 %**	**99.3 %**
Precision	99.5 %	99.6 %	99.6 %
Recall	99.5 %	99.2 %	99.6 %
F1 score	99.5 %	99.4 %	99.6 %
Average accuracy of this method = 99.2 %.			

It is very high accuracy but its input data is not unified in number.

Only Brain MRI images for brain tumor detection dataset were entered "253 images", as they are classified into only two types, one with a tumor "155 images" and the other without a tumor"98 images".
The epochs values were =30 and the batch size values were =40 (These were the best values on which the model was trained, and we obtained the highest accuracy from them.), the accuracy rate was = 85%. As it is shown in table 4.4.

Table 4.4 CNN model results on Brain MRI images for brain tumor detection dataset only.

Type	Brain MRI images for brain tumor detection
No. of images	253 images
Training dataset (80 %)	202
Testing data (20%)	51
Accuracy	85 %

Some values have been modified in the code as follow:

When you change ReLU activation function to Tanh, it affected efficiency and the model's accuracy was reduced to 66%.

When changing the last layer from softmax to ReLU, it affected efficiency and the model's accuracy was reduced to 69% and the curve of model losses was also affected and became inaccurate, thus, it affects the accuracy of the model.

Work was also done to change values of epochs and trying many random values as (10, 40, 50, 80, 100) and batch size also as (30, 40, 60, 80, 100).

But, the highest accuracy of the model and its best efficiency were obtained at the values of epoch=30 and batch size=40.

The kernels size of Activation Function has been changed but the values we explained above had priority.

The table 4.5 clearly shows a summary of some of the trial and error methods in the previous paragraph:

Table 4.5 Some changes values and its effects.

Elements	High result	Low result
Tanh	80 %	69%
ReLU	98.4%	94.6%
Epochs	99.4 % at epoch = 30	85.8 % at epoch = 50
Batch size	98.4 % at batch size = 40	85.8 % at batch size = 60

4.4 Model Comparison

We show a comparison of our accuracy results with results from other researches in table 4.6.

Table 4.6 The Proposed Technique versus Previous Techniques.

No.	Ref.	Year	Accuracy	Model used	Dataset used
[37]	Belaid, Ouiza Nait et al.	2020	96.1%	VGG16 model	Brain Tumor Classification (MRI)
[38]	Kesav, Nivea et al.	2021	98.21 %	CNN model	Brain Tumor Classification (MRI)
[39]	More, Rajshree B. et al	2021	97.87 %	CNN model	Brain Tumor Classification (MRI)
[40]	Minarno, Agus Eko, et al.	2021	96 %	CNN model	Brain Tumor Classification (MRI)
[41]	Amin, Javeria, et al.	2022	98.2 % 99 %	CNN model RNN, LSTM, GRU models	1. Brain Tumor Classification (MRI) 2. Brates2020 dataset.
[42]	Rahman, Takowa, et al.	2023	98.12%	PDCNN model	Brain Tumor Classification (MRI)
[43]	Younis, Ayesha, et al.	2022	98.5% 96%	VGG16 model CNN model	Brain MRI images for brain tumor detection.
	Proposed method		**98.4 %**	**CNN model**	**1. Brain Tumor Classification (MRI)** **2. Brain MRI images for brain tumor detection.**

4.5 Data Availability

From the Kaggle website, the dataset "Brain Tumor Classification (MRI)" was downloaded. The above dataset is split into four groups: glioma, meningioma, no tumor, and pituitary tumor. (https://www.kaggle.com/sartajbhuvaji/brain-tumor Classification-mri/metadata, ankita kadam, prajakta bhumkar, sameer dedge, and swati kanchan). The"Brain MRI images for the identification of brain tumors" dataset which seems subdivided into two sections called (no and yes) has been downloaded from (Akshitmadan, https://www.kaggle.com/akshitmadan/tumor-classification-using-keras-for-beginners/data

Chapter 5

Conclusion and Future Work

5.1 Conclusion

In this research, two methods were used by applying deep learning technology to MRI images, using the CNN model. We used two types of the dataset, one of them is large, numbering 3264, divided into 4 classes, and containing 3 different types of tumors and one without tumor, and the other is small in size, numbering 253 images, 98 of them without tumors and 155 images with tumors.

The first method is to apply the CNN model to all the datasets (small dataset and large dataset) are called "Brain MRI images for brain tumor detection".

There are 3517 images in total, and we recorded the results and reached an accuracy of **94.6 %.**

In the second method, we applied the CNN model to each class of the large-sized dataset (second dataset) is called "Brain Tumor Classification (MRI)", separately, and we recorded the results and obtained an accuracy of **98.4 %.**

From these two methods, it is clear that the accuracy increased when we divided the data and tested the proposed model on each type separately. Which is an improvement compared to the first method of the CNN model.

We have made a comparison with some other research papers, and this result Outperformances all other methods.

5.2 Future Work

- We will use a new and different type of dataset that contains a larger number images of brain tumors.
- We will apply this techniques on other tumors on human body.
- Using well-designed a new 3 (Attention-Convolutional-LSTM) 3ACL deep learning model based approaches to perform well in the classification of brain tumors.
- 3D MR images were used directly in the 3ACL model without transforming the 3D MR images into 2D data.

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Appendix A

The proposed system algorithm

This appendix consisting of python code of our proposed system:

1. Import Statements:

```
import os

import keras

from keras.models import Sequential

from keras.layers import Conv2D, MaxPooling2D, Flatten, Dense, Dropout,
BatchNormalization

from PIL import Image

import numpy as np

import pandas as pd

import matplotlib.pyplot as plt

plt.style.use('dark_background')

from sklearn.model_selection import train_test_split

from sklearn.preprocessing import OneHotEncoder
```

2. One Hot Encoding the Target Classes:

```
encoder = OneHotEncoder()

encoder.fit([[0], [1]])

# 0 - Tumor

# 1 – Normal
```

3. Creating 3 Important Lists:

a) data list for storing image data in numpy array form
b) paths list for storing paths of all images
c) result list for storing one hot encoded form of target class whether normal or tumor

```
# This cell updates result list for images with tumor

data = []

paths = []
```

```
 result = []
 for r, d, f in os.walk(r'../input/dataset-five'):
   for file in f:
 if '.jpg' in file:
paths.append(os.path.join(r, file))
 for path in paths:
 img = Image.open(path)
 img = img.resize((128,128))
 img = np.array(img)
 if(img.shape == (128,128,3)):
 data.append(np.array(img))
 result.append(encoder.transform([[0]]).toarray())
 # This cell updates result list for images without tumor
 paths = []
 for r, d, f in os.walk(r"../input/brain-mri-images-for-brain-tumor-detection"):
  for file in f:
  if '.jpg' in file:
   paths.append(os.path.join(r, file))
 for path in paths:
  img = Image.open(path)
  img = img.resize((128,128))
  img = np.array(img)
  if(img.shape == (128,128,3)):
   data.append(np.array(img))
   result.append(encoder.transform([[1]]).toarray())
 data = np.array(data)
```

```
data.shape

result = np.array(result)

result = result.reshape(3542,2)
```

4. Splitting the Data into Training & Testing:

```
x_train,x_test,y_train,y_test = train_test_split(data, result, test_size=0.2,
shuffle=True, random_state=0)
```

5. Model Building:

```
model = Sequential()

model.add(Conv2D(32, kernel_size=(2, 2), input_shape=(128, 128, 3), padding =
'Same'))

model.add(Conv2D(32, kernel_size=(2, 2),  activation ='relu', padding = 'Same'))

model.add(BatchNormalization())

model.add(MaxPooling2D(pool_size=(2, 2)))

model.add(Dropout(0.25))

model.add(Conv2D(64, kernel_size = (2,2), activation ='relu', padding = 'Same'))

model.add(Conv2D(64, kernel_size = (2,2), activation ='relu', padding = 'Same'))

model.add(BatchNormalization())

model.add(MaxPooling2D(pool_size=(2,2), strides=(2,2)))

model.add(Dropout(0.25))

model.add(Flatten())

model.add(Dense(512, activation='relu'))

model.add(Dropout(0.5))

model.add(Dense(2, activation='softmax'))

model.compile(loss = "binary_crossentropy", optimizer='Adamax',
metrics=['accuracy'])

print(model.summary())

y_train.shape

history = model.fit(x_train, y_train, epochs = 10, batch_size = 10, verbose =
0,validation_data = (x_test, y_test))
```

6. Plotting Losses:

```
plt.plot(history.history['loss'])

plt.plot(history.history['val_loss'])

plt.title('Model Loss')

plt.ylabel('Loss')
```

```
plt.xlabel('Epoch')
plt.legend(['Test', 'Validation'], loc='upper right')
plt.show()
x_test.shape
labels =["Yes",  # index 0
 "No",      # index 1
   ]
y_hat = model.predict(x_test)
y_hat = model.predict_classes(x_test)
# Plot a random sample of 10 test images, their predicted labels and         ground truth
figure = plt.figure(figsize=(20, 8))
for i, index in enumerate(np.random.choice(x_test.shape[0],        size=15,
replace=False)):
ax = figure.add_subplot(3, 5, i + 1, xticks=[], yticks=[])
# Display each image
ax.imshow(np.squeeze(x_test[index]))
predict_index = np.argmax(y_hat[index])
true_index = np.argmax(y_test[index])
# Set the title for each image
ax.set_title("{} ({})".format(labels[predict_index],
                          labels[true_index]),
                          color=("green" if predict_index == true_index   else "red"))
plt.show()
# Get the predictions
y_pred = model.predict_classes(x_test)
# Calculate the confusion matrix
conf_matrix = confusion_matrix(y_true=y_test[:,1], y_pred=y_hat)
# Print the confusion matrix using Matplotlib
fig, ax = plt.subplots(figsize=(7.5, 7.5))
ax.matshow(conf_matrix, cmap=plt.cm.Blues, alpha=0.3)
for i in range(conf_matrix.shape[0]):
```

```
for j in range(conf_matrix.shape[1]):
 ax.text(x=j, y=i,s=conf_matrix[i, j], va='center', ha='center',       size='x-large')
plt.xlabel('Predictions', fontsize=18)
plt.ylabel('Actuals', fontsize=18)
plt.title('Confusion Matrix', fontsize=18)
plt.show()
```

7. Checking the Model:

```
def names(number):
 if number==0:
   return 'Its a Tumor'
else:
   return 'No, Its not a tumor'
from matplotlib.pyplot import imshow
img = Image.open(r"../input/dataset-five/Testing/no_tumor/image(1).jpg")
x = np.array(img.resize((128,128)))
x = x.reshape(1,128,128,3)
res = model.predict_on_batch(x)
classification = np.where(res == np.amax(res))[1][0]
imshow(img)
print(str(res[0][classification]*100) + '% Confidence This Is A ' +
names(classification))
from matplotlib.pyplot import imshow
img=Image.open(r"../input/dataset-     five/Testing/pituitary_tumor/image(15).jpg")
x = np.array(img.resize((128,128)))
x = x.reshape(1,128,128,3)
res = model.predict_on_batch(x)
classification = np.where(res == np.amax(res))[1][0]
imshow(img)
print(str(res[0][classification]*100) + '% Confidence This Is A ' +
names(classification))
```

الملخص

ورم المخ هو نمو غير متحكم به لخلايا المخ يحدث في سرطان المخ إذا لم يتم اكتشافه في مرحلة مبكرة. يعد الكشف المبكر عن ورم المخ أمرًا بالغ الأهمية لتخطيط العلاج وبقاء المريض على قيد الحياة. تأتي أورام المخ في مجموعة متنوعة من الأشكال والأحجام والخصائص والعلاجات. نتيجة لذلك ، يعد الكشف اليدوي عن ورم المخ أمرًا صعبًا ويستغرق وقتًا طويلاً وعرضة للخطأ. ونتيجة لذلك ، فإن التشخيص الآلي عالي الدقة بمساعدة الكمبيوتر (CAD) مطلوب حاليًا. و يعد استخدام تقنيات معالجة الصور في التصوير بالرنين المغناطيسي (MRI) مهمة صعبة ولكنها مهمة لمجموعة متنوعة من تطبيقات التحليل الطبي. نظرًا لأن كل طريقة من طرق تصوير المخ توفر تفاصيل فريدة ومهمة حول كل جزء من أجزاء الورم ، فإن هذه الرسالة تستخدم تقنية التعلم العميق ، وخاصة نموذج الشبكة العصبية التلافيفية (CNN) ، للكشف المبكر عن أورام المخ والتشخيص السريع نظرًا لأهمية ذلك المرض وتزايد عدد المصابين به سنويا مما يساعد على خفض معدل الوفيات.

وذلك عن طريق تطبيق هذه التقنية على صور التصوير بالرنين المغناطيسي وتم التطبيق على نوعين مختلفين من الصور (النوع اللأول داتا كبيرة الحجم عبارة عن ٣٢٦٤ صورة والنوع الثانى داتا صغيرة الحجم تتكون من ٢٥٣ صورة) لكى نزيد من عدد الصور وبالتالى نزيد من دقة وكفاءة الموديل من خلال تطبيق طريقتين بنموذج CNN.

الطريقة الاولى هى تطبيق كافة الصور الموجوده على الشبكة معا حيث تم تدريب الشبكة على مجموعة صور كبيرة ومختلفة تتكون من ٣٥١٧ صورة مقسمة لمجموعة صور بها أورام واخرى ليس بها أورام وهما عبارة عن ٣٥١٧ صورة وقمنا بتسجيل النتائج حيث حصلنا على نسبة دقة ٩٤,٦ ٪ .

والطريقة الثانية تم تقسيم الصور الى ٣ مجموعات ودخولها على الشبكة كل مجموعه على حدى اى كأننا قمنا بتكرار الشبكة ٣ مرات حتى تزداد الكفاءة ، وعلى الرغم من انه تم تقسيم الصور على ٣ مجموعات الا انه من المتوقع ان يحسن الكفاءة ويقلل زمن عمل الموديل ويسرع الوقت الكلى ويزيد دقة الموديل.

حيث تم زيادة معدل الدقة في الكشف عن هذا الورم إلى ٩٨,٤٪.

جامعة بنها
كلية الهندسة ببنها
قسم الهندسة الكهربية

نظام الكشف بمساعدة الحاسب المعتمد على التعلم العميق للكشف المبكر لأورام المخ

إعداد

المهندسة/ إيرينى مجدى عبد الملاك فانوس

درجة الماجستير في العلوم الهندسية في الهندسة الكهربية

تحت اشراف

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بنها (٢٠٢٤)