**DEVELOPMENT OF A WEB-BASED BRAIN TUMOUR CLASSIFIER USING DEEP LEARNING**

**BY**

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# ABSTRACT

Early detection of brain tumours is critical to enhancing diagnostic accuracy in treatments as well as patient survival. Recently, deep learning algorithms have become one of the most successful types of machine learning, making it possible to categorise magnetic resonance images of the brain to determine particular tumour types under investigation. In this project, a web application was built and implemented to classify brain tumours from MRI scans. Combining modern image processing techniques with computer vision and advanced pattern analysis enables the diagnosis of brain tumours with more sensitivity, greater specificity, and lower costs than ever before. The MRI brain tumour scans obtained from Kaggle were used to train and validate four pre-trained convolutional neural networks; AlexNet, ResNet152, MobileNetV2, and Xception. The hyperparameters of the classifiers were tuned to obtain optimal results in terms of accuracy and sensitivity. On the average, the classification accuracy of the networks are AlexNet (64.1%), ResNet152V2 (92.7%), MobileNetV2 (91.76%), and Xception (91.5%). The sensitivity, a measure of how well the classifier correctly identified the class of the tumour, ranged from 0.53 to 0.91, with ResNet152V2 performing best. The optimal classifiers were thus implemented with Python in the web application accordingly. Given the shortage of radiologists in places with limited resources, utilising deep learning technology to detect brain malignancies can save time and effort and speed up the detection process. The developed web application can deliver precise findings while maintaining modularity, adaptability, and scalability. The web application is a practical diagnostic tool for medical practitioners.

**Keywords:** Brain Tumour; Deep Learning; Convolutional Neural Networks

# CHAPTER ONE

# INTRODUCTION

## 1.1 Background of Study

A patient’s chance of survival and the effectiveness of their treatment depend heavily on the early detection of brain tumours. Brain tumours consist of tissue that develops abnormally owing to uncontrolled cell division and serves no purpose within the brain. Tumours may cause oedema, which causes abnormal neurological symptoms such as seizures and behavioural changes and increases the size and pressure of the brain. Brain tumour classification is a diagnostic component that categorises aberrant images as malignant or benign tumours. Cancerous tumours are malignant tumours. While benign tumours are not malignant, the cells they contain can multiply and travel to other body areas. They either can't spread, can only grow slowly, or both [1].

In recent years, deep learning algorithms have emerged as one of the essential forms of machine learning, making it possible to modify magnetic resonance scans of the brain to classify the type of tumour under inspection. Frequently utilized networks in deep learning for categorization in computer vision applications are convolutional neural networks (CNN) [2]. This project aims to achieve a web-based solution for brain tumour diagnosis using CNN architectures. The report will give detailed representations of these architectures employed in a web application with its implementation.

## 1.2 Significance of Study

The clinical intent of diagnosing brain tumours is correctly identifying and locating tumour tissues using accurate diagnostic information from Magnetic Resonance (MR) images. An accurate clinical diagnosis should result in prompt and effective medical care.  As the approaches of artificial intelligence attain the highest performance levels in different aspects, the area of brain tumour diagnostics has embraced several current deep learning techniques [1]. Deep learning combined with brain tumour surgery will lead to a better and more efficient treatment [3]. This project aims to develop a deep learning architecture that will help classify brain tumours using two-dimensional MR images.

## 1.3 Problem Statement

It is difficult to diagnose brain tumours in their early stages since there is no reliable measurement of tumours, and there are different tumour forms, sizes, locations, and appearances in the brain [4]. Medical imaging methods are now employed for clinical analysis and medical research to analyse the visual portrayal of the body’s interior. However, there is a global shortage of competent radiologists who can correctly classify these visual representations. Deep learning has the potential to have a significant influence on the brain tumour care, potentially advancing neurosurgical treatment [3].

## 1.4 Aim and Objectives

### 1.4.1 aim

The project aims to design and implement a web application for brain tumour classification.

### 1.4.2 Objectives

The objectives of the project are:

1. to curate different types of brain MRI scans from an existing benchmark database;
2. to pre-process and augment the curated brain MRI scans for analysis;
3. to develop classification models based on pre-trained convolutional neural networks;
4. to evaluate the performance of the developed classification models; and
5. to implement and test the models in a web application for practical use.

## 1.5 Methodology

The methodology includes:

1. The acquisition of a suitable brain tumour MRI benchmark dataset that would have sufficient images, balanced in at least four classes, for tumour classification,
2. The selection of four different Convolutional Neural Network architectures which would give accurate results which would be used on a cross-platform web application,
3. Building each of the selected CNN architectures with Python on the Jupyter interface on Visual Studio Code using the TensorFlow library,
4. Training and testing the models created to determine the most efficient,
5. Developing the web application with the Streamlit library and integrating the model into the application.
6. Test the web application.

## 1.6 Scope of Study

An ideal web-based brain tumour classifier is intended to be developed that neurosurgeons and other healthcare professionals can use. Due to the combination of advanced image processing techniques with computer vision and advanced pattern analysis, it is possible to identify brain tumours with higher sensitivity, specificity, and lower costs than ever before. The application should be able to deliver accurate results with modularity, flexibility, and scalability.

## 1.7 Limitation of Study

Training deep learning models requires vast quantities of precise data. The precision and quality of the data are essential for developing algorithms that accurately depict the clinical context. Even with good classification, standard administrative or medical data in the project work has limitations. For supervised machine learning methods, which take a lot of time and work, this data may need to be sufficiently labelled and evaluated. The availability of enormous amounts of correctly labelled data may be a substantial hurdle to deep learning in neurosurgery since supervised machine learning algorithms' analytical accuracy is only as good as the data given [3].

## 1.8 Project Organization

The following is the organisational structure of the report.

Chapter One highlights the background, relevance, scope, objectives, and limitations in classifying brain cancers using Convolutional Neural Networks.

Chapter Two contains the project’s literature review. It briefly overviews brain tumour diagnosis and reviews past work on brain tumour classification.

Chapter Three highlights the neural network system design in detail. It explains the suggested CNN model and defines the dataset used for training and testing the performance of the different types of CNNs employed.

Chapter Four treats the application implementation, testing, the software development process, and comparison of model performances.

Chapter Five highlights the project’s achievements, recommendations, and main conclusions.

# CHAPTER TWO

# LITERATURE REVIEW

## 2.1 Chapter Introduction

In medical diagnostics, the accuracy and robustness of prediction models are critical since the results directly impact a patient’s treatment. There are over 120 distinct forms of brain tumours, and because of the wide range of tumour types and shapes, manual diagnosis of brain tumours consumes time and is imprecise. The correct clinical diagnosis should result in quick and effective medical treatment [5]. This chapter examines some present ways of diagnosing and classifying brain tumours and some critical issues of brain tumour diagnosis.

### 2.1.1 Brain Tumour Diagnosis

In recent years, delicate processing and medical tomography experts have significantly improved the detection of brain tumours. Medical specialists have relied on the ease of computation and monitoring to detect diagnostic approaches in clinical practice, and both completely automated and semi-automatic systems are offered. Figure 2.1 depicts the three phases of brain tumour diagnosis: tumour detection, segmentation, and classification. (The tumour identification phase is not shown since CAD assumes the tumour is already present in the gathered data) [1].

Diagram

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Figure 2.1 A flowchart of brain tumours diagnosis using a generic computer-assisted diagnosis system [1]

Using MRI image databases, detection is the process of determining if a tumor is present or absent. The outcome from the tumor detection approach is an image from an MRI that has labels indicating whether it is normal or abnormal. Various approaches, including K-Nearest Neighbour, Support Vector Machines, and Artificial Neural Networks, may be used to identify brain tumours using MR images.   An extensive standard database serves as a baseline for training the classifier and determining the ideal strategy for feature extraction and detection [1].

To better understand, characterise, and visualise data, it is necessary to divide an MR image into smaller regions of interest (ROI). Segmentation is used to improve the significance and ease of interpretation of MR images regarding tumour location and boundaries by altering their representation. Segmentation distinguishes tumour-associated tissues like oedema and necrosis from normal tissues like white and grey matter. Image discontinuities and similarities serve as the foundation for tumour segmentation algorithms. The segmentation method works by dividing an MR image into sections according to differences in intensity. Setting criteria for dividing the sections can help, for example, those near the margins and corners or similarities in intensity [1].

The practice of categorizing input characteristics into distinct subgroups is known as classification. For classification, selection and extraction of characteristics are essential, especially for the classification of brain tumors, which needs a large number of MR images from a varied patient population and serves as a basis for training. The main objective of brain tumor categorization is to identify whether a tumor is malignant or benign using MRI images. Additionally, supervised methods, like Support Vector Machine and Convolutional Neural Network, can be used to classify brain tumors. Unsupervised methods include Fuzzy C-Means and Self-Organizing maps [2].

### 2.1.2 The Intracranial Tumour

Brain tumors are abnormal cell groupings that develop within the brain's tissues and are occasionally referred to as intracranial tumors in some contexts. Brain tumours are classified as primary or metastatic when they have a lesion or neoplasia. Primary tumours develop from the brain’s tissues and its surrounding tissues. The initial brain tumour is classed as benign or malignant based on its location. A metastatic brain tumour has spread to the brain and other organs via the circulatory system (such as the breast or lungs). Its features might be classed as malignant or cancerous. Gliomas and central nervous system lymphomas are the most prevalent primary brain tumors in adults, with gliomas making up more than 80% of malignant tumors [6], [7].

As ‘previously stated, brain tumours are classified as either slow-growing or aggressive. A benign (slow-growing) tumour does not infiltrate nearby tissues, whereas a malignant (aggressive) tumour spreads from its primary location to a secondary site. WHO divided brain tumours into four categories: I, II, III, and IV. Tumours of grades I and II are less malignant and have a better prognosis than those of grades III and grades IV, which are more invasive and have a poor prognosis [8]. In this sense, the following is a breakdown of brain tumour grades: ’

1. **Grade I:** Unlike other tumours, these develop slowly and spread slowly. These can nearly entirely be eliminated by surgical procedures in certain persons and are linked to an enhanced chance of survival. Grade 1 pilocytic astrocytoma is a tumour of this kind.
2. **Grade II:** This type of tumour grows more slowly but can travel to other body parts and develop into a much more severe tumour. Even after surgery, these tumours may reappear. When it comes to cancer, oligodendrogliomas are among the most common.
3. **Grade III** tumours develop more rapidly and have the potential to spread to nearby tissues than tumours of the same grade in the body. Postoperative radiation or chemotherapy is required for malignancies such as these. An anaplastic astrocytoma is an example of this type of tumour.
4. **Grade IV:** These types of cancer are the most deadly and spread quickly. They may exploit blood vessels to speed up their growth. Tumours of this kind include glioblastoma multiforme [8].

Figure 2.2 depicts how the World Health Organization (WHO) divided the cytological features of brain tumours based on microscopic analysis into four categories (Grade I – Grade IV).

Diagram

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Figure 2.2 Grades of Brain Tumour by the World Health Organization (WHO) [7]

### 2.1.3 Brain Magnetic Resonance Imaging

In neurology, MRI is utilised to evaluate the intricate aspects of the brain as well as all various cranial structures. It enables the visualisation of the anatomy in coronal, sagittal, and axial planes. The three unique anatomies of the human brain are portrayed in Figure 2.3 and Figure 2.4, with Figure 2.4 exhibiting these planes of the brain as obtained by magnetic resonance imaging [7].

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Figure 2.3 (a) Axial plane, (b) Coronal plane and (c) Sagittal Plane of the Brain Image [7]

A close-up of the back and the back of a coin

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Figure 2.4 MRI Brain Observations of (a) Axial Plane, (b) Sagittal Plane, and (c) Coronal Plane [7]

Due to its low radiation and good contrast, MRI is superior to the majority of scanning methods. It has the following characteristics:

1. MRI can detect blood flow and cryptic vascular dysfunctions.
2. It can identify neurological disorders.
3. MR imaging is accomplished without the use of ionising radiation.
4. Brain-related ailments, including Alzheimer’s, dementia, and Parkinson’s, may also be treated using MRI [7].

The fundamental feature of MRI is that it exposes the brain to a magnetic force and electrifies the hydrogen atoms within the body by producing a radio frequency pulse; once the radio frequency is turned off, the hydrogen nuclei store energy and release it in the form of an electronic signal. Atoms relax when they release their accumulated energy and revert to their original condition. Relaxation time is defined as time spent relaxing. Based on relaxation time, brain tissues may be classified: as longitudinal (T1) and transverse relaxation time  (T2)  [7].

Three ‘MRI sequences are available, as shown in Figure 2.5: Fluid Attenuated Inversion Recovery (Flair), T1-weighted, and T2-weighted. The most common MRI sequences are T1-weighted and T2-weighted scans. T1- weighted pictures have a short Time to Echo (TE) and Repetition Time (RT), while T2- weighted images have a longer TE and RT. The time between transmitting a radio signal and getting an echo signal is called the Time to Echo. The gap between two subsequent pulse sequences on the same image slice is called repetition time (RT). The T1 and T2 properties of tissues primarily govern the brightness and contrast of tissues. The TE and RT periods of flare sequences are relatively lengthy. These intervals, TE and RT, are crucial for finding anomalies in brain imaging [7]. ’

A group of coins

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Figure 2.5 (a) T1- weighted, (b) T2-weighted and (C) Flair [7]

### 2.1.4 Artificial Intelligence for Brain Tumour Diagnosis

A branch of computer science known as artificial intelligence (AI) aims to give computers the capacity to learn, reason, and resolve problems when confronted with a variety of data kinds. New and ground-breaking technology in neurosurgery has transformed the treatment of acute and long-term conditions [3].

Due to the intricacy and sophistication of the method in neurosurgery, the discipline of brain tumour surgery is an excellent starting point for future Implementation. Figure 2.6 shows the major components that constitute Artificial Intelligence [3].

Diagram

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Figure 2.6 Major Components of Artificial Intelligence [3]

1. **Machine Learning**

Machine learning (ML) has gotten much attention in contemporary computing, and one of the areas of concentration is the medical sector. The process of training and analysing algorithms to find patterns in data, execute tasks, or make predictions is known as machine learning. Sophisticated methods such as image reconstruction, image de-noising, registration, and skull stripping have facilitated brain imaging and improved the collected data. The field of brain tumour diagnostics has used many of these ML approaches. For instance, supervised machine learning may be used to identify patterns in expected outputs by giving a collection of clearly labelled inputs, which requires the labelling of training data prior to its presentation to the algorithm. When a patient’s ethnicity, age, stage or co-morbidities upon diagnosis are included in an algorithm for glioblastomas (GBMs), the method may be used to calculate the patient’s survival time. Eventually, the algorithm can predict a patient’s life expectancy based on the patterns and tendencies it has seen in past cases. Compared with traditional programming, this technique employs an algorithm to get the desired outcome rather than a collection of rules. Just input and output are given in machine learning, and via trial, the computer "observes" the important trends and patterns [3], [1].

It is also possible to use unsupervised machine learning, in which the data is examined without labels, resulting in similarity and grouping of data to find trends and patterns. With the use of AI technology, scientists may identify clusters and patterns linked to particular glioblastoma grades, or they may compile GBM individuals who had extraordinarily good outcomes and then identify the patterns shared by these people. Finally, a reminder Reward and punishment are used in ML to fine-tune algorithms so that they are more likely to succeed in achieving their desired outcomes while penalising behaviours that could otherwise derail their progress. Afterwards, the system learns the optimal way to deal with a given issue. Therefore, machine learning has enabled doctors, engineers, and computer scientists to collaborate on developing semi-automatic and, eventually, completely automatic tumour diagnosis systems with improved accuracy and reduced processing time [3].

1. **Deep Learning**

Deep learning (DL) architecture has recently been named the criterion in machine learning. Furthermore, it has steadily emerged as the most widely used heuristic algorithm in machine learning, achieving outstanding results on various challenging cognitive tasks that match or exceed human ability. As a subgroup of machine learning, shown in Figure 2.7, the human brain’s information processing pathways influence deep learning. Deep learning uses enormous amounts of data to connect input to specific identifiers rather than relying on rules developed by humans. Each artificial neural network layer in deep learning (DL) offers a distinct data analysis. Pre-processing, extraction of features, classification, intelligent feature selection, and training are the sequential processes in standard ML approaches [9].

The choice of features significantly influences how well machine learning algorithms function. An inaccurate class distinction may be the result of a small feature set. For many applications, deep learning approaches can optimise the training of feature sets, unlike conventional ML approaches. Figure 2.8 shows how DL enables simultaneous learning and categorisation. Because of the enormous growth and innovation of the significant data sector in recent years, DL has become an increasingly popular kind of ML approach. It is still rising due to creative performance for various ML tasks. It has aided in the growth of other learning disciplines, such as image super-resolution,  image recognition, and object identification [9].

Diagram

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Figure 2.7 Deep Learning Family [9]

Diagram

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Figure 2.8 Difference between Traditional Machine Learning and Deep Learning [9]

In some cases, machine intelligence is comparable to or superior to human knowledge, suggesting that DL may be used to address the following conditions:

1. when no human specialists are available;
2. in which people cannot explain judgments created with their knowledge (language understanding, speech recognition, and medical choices);
3. in which the issue solution evolves (price prediction, stock preference, tracking, and weather prediction);
4. when solutions must be adapted depending on circumstances (personalisation, biometrics); and
5. the enormity of the issue surpasses our poor cognitive skills (matching Facebook advertisements, calculating website rankings, and sentiment analysis) [9].

### 2.1.5 Convolutional Neural Networks

The most well-known and often used deep learning method is the convolutional neural network (CNN). CNNs, like any other neural network, draw their structure from neurons in animals’ and humans’ brains. CNN models the complex sequence of neurons that comprise a cat’s visual cortex. CNN has a huge advantage over its predecessors in identifying key traits without human interaction. CNNs have been extensively used in several disciplines, including computer vision, audio processing, and facial recognition [9].

Goodfellow et al. [10] noted three significant advantages of CNN: similar representations, parameter sharing, and sparse interactions. Unlike traditional fully connected networks, CNN uses local connections and shared weights to fully use 2D input-data formats such as image signals. This approach uses a very small set of variables, streamlining and speeding up network training. The visual cortex has identical cells. Interestingly, the cells only detect tiny portions instead of detecting the entire image.  A typical CNN, similar to a multi-layer perceptron (MLP), has numerous convolutional layers followed by subsampling (pooling) levels and FC layers as final layers [9]. Figure 2.9 depicts a CNN architecture for image classification.

Chart

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Figure 2.9 Classification of Images Using a CNN Architecture [9]

In a ‘convolutional neural network, each layer’s input x is organised in three parameters: height, width, and depth, or m × m × r, where the width (m) matches the height (m). The term “channel number” is frequently used to refer to depth (r). In an RGB image, for example, the depth is three. Multiple kernels (filters) are accessible within every convolutional layer and have three dimensions (n× n × q), similar to the input image; however, ‘n’ must be fewer than m, and q must be equal to or less than r. Additionally, the local interconnections, which have similar qualities, are based on the kernels (bias ‘bk’ and weight ‘Wk’) for creating ‘k’ feature maps ‘hk’ with a size of (m - n - 1) and are convolved with input as previously mentioned. Like MLP, the convolution layer uses Equation 2.1 to build a dot product between its weights and inputs, but the inputs are lower than the initial picture size. Adding nonlinear behaviour or an activation function to the convolutional layer’s output results in the following outcome [9]: ’

*2.1*

The feature map of each subsampling layer is then down sampled. Consequently, the network parameters are reduced, accelerating the learning process and handling the overfitting issue. The pooling function (such as maximum or average) is applied to a surrounding region of size p × p, where ‘p’ is the kernel size for all feature maps. The FC layers produce the high-level abstraction after receiving the mid-and low-level input, which is equivalent to the last layers of a conventional neural network. The last layer, SVM or SoftMax, is used to get the classification scores. The likelihood of a particular class is represented by each score for an inevitable event [9].

## 2.2 Review of Related Works

Researchers have examined the identification of brain tumours using machine learning techniques in the past, particularly during the last several years. New artificial intelligence and deep learning technologies have significantly influenced medical picture analysis, particularly in cancer detection [11].

In [12], J. Amin et al. suggested a system for categorising and segmenting data brain tumours automatically. An SVM classifier was used to segment the ROI, including the image’s shape, intensity, and texture. This characterises the various stages of malignant or non-cancerous images. The recommended approach was evaluated on the Local, Harvard, and Rider datasets. The recommended method also included an accuracy metric and an area under the curve. The outcomes demonstrate the efficacy of the suggested approach.

In [13], S. Deepak and P.M. Ameer have focused on glioma, meningioma,  and pituitary tumours as the core focus of their research. In order to classify brain tumours, several factors must be considered, including shape and size, which have a high degree of variability; different types of tumours look similar, and finally, there is no consensus on how to classify brain tumours. This made it challenging to classify brain tumours. Typical machine learning algorithms will have difficulty handling this task because of its unique characteristics. Even with a smaller data set than previous models, the suggested method could reach greater accuracy by utilising transfer learning. The model proposed here uses an existing GoogLeNet with slight adjustments to categorize various kinds of tumors at the SoftMax level. Multiclass SVM produced an accuracy of 92.3%. In comparison, the CNN-based GoogLeNet model enhanced this to 97.8%.

Ryo Ito et al. [14] give a method for semi-supervised learning to classify brain tumours using magnetic resonance images. The proposed approach outperforms the current Deep Neural Network (DNN)- and registration-based approaches. To determine the actual label of a latent picture, it used the Expectation Maximisation (EM) approach. According to a study, the actual label of an unlabelled picture may be determined if its probability distribution is known. This probabilistic model was trained using both the EM and DNN models. In this stage, the erroneous label is locatedlabel is located from the potential picture. The Internet Brain Segmentation Repository (IBSR) provides access to human MR datasets and marmoset MRI datasets. Both datasets have proved the method’s effectiveness.

M. Mittal et al. [15] presented a hybridisation of the Stationary Wavelet Transform (SWT) with the Growing Convolution Neural Network (GCNN) In enhancing CNN's precision for classifying and segmenting tumours. SWT has been used for extracting features because, compared to the Fourier technique, it yields superior results for discontinuous data. After extraction of features, the model was trained using GCNN. After extracting features, segmentation was carried out using the Random Forest Classifier. The suggested technique outperforms the standard Convolutional Neural Network (CNN) in terms of Peak Signal-to-Noise Ratio (PSNR) and Sparse Switchable Normalization (SSN), with a 2 per cent improvement in both metrics.

The supervised approach suggested by S.T. Kebir and S. Mekaoui [16] to detect abnormalities in the brain using magnetic resonance imaging was employed by N.B. Bahadure et al. [17]. The method was divided into three basic steps: The first step is creating a CNN model for deep learning. Then, using the k-means technique, the MRI images of the brain were divided. Finally, as previously stated, the newly built CNN model categorises brain components into normal or abnormal classes. The segmented and extracted regions are depicted in Figure 2.10.

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Figure 2.10 Segmented and area extracted result of brain MR image. (a) Original image. (b) Enhanced image. (c) Skull-stripped image. (d) Wavelet transpose image(e) Intense segmented image. (f) Inverse intense image. (g) Grey matter. (h) White matter. (i) CSF, (j) Dice overlap image, (k) Eroded image, (l) Area extracted image [16]

Muhammed Talo et al. [18] suggested "Deep transfer learning," as they refer to it, is an automated method for classifying both healthy and unhealthy MRI images of the brain. An already-trained CNN model named ResNet34 was used to carry out the categorization. The dataset's size has been increased through the use of data augmentation techniques. The MR database from Harvard Medical School was used to illustrate the efficacy of this method. Other anomalies, such as those linked to autism, stroke, Parkinson's, and Alzheimer's disease, among others, can be discovered using this approach.

In [19], Differential Evolution (DE), also known as Adaptive Differential Evolution with Lévy Distribution, is an evolutionary method utilized to develop a unique strategy. It was developed by O. Tarkhaneh and H. Shen et al. During the multi-level thresholding process. DE was employed to keep the balance between exploration and exploitation in balance with one. The multi-level thresholding approach was applied to segment brain magnetic resonance imaging (MRI) pictures.

Thaha et al. [20] suggested a segmentation deep learning method that makes use of convolutional neural networks (CNNs). This method employs three tiny kernels, each three times smaller than the preceding one, for the deep architecture of the CNN model. The pre-processing of images includes the use of intensity normalisation and data augmentation. This approach was assessed using the Heterogeneous Brain Tumor Image Segmentation Benchmark (BRATS) 2013 and BRATS 2015 datasets. The architecture of the model is shown in Figure 2.11.

Diagram

Description automatically generated*Figure 2.11 Central-point-Enhanced CNN Architecture [20]*

K. Kamnitsas et al. proposed an automated brain lesion segmentation approach in [21] based on machine learning. This strategy uses a dual-route design with two key parts. A 3D CNN is used for extraordinarily accurate soft segmentation, and a 3D Conditional Random Fields (CRF) is used for post-processing the labels generated during soft segmentation. Complex classification labels are effectively delivered by the 3D CRF, and false positives are eliminated. The system’s performance was assessed using two independent benchmark datasets: BRATS 2015 and ISLES 2015. In [22], an innovative strategy was provided for tumour sectioning based on the Cuckoo Search Algorithm (CA), developed by V. Rajinikanth et al. to section MRI images of the tumour. Tsallis entropy-monitored multi-level thresholding is the preferred method when applied to brain imaging. Later, image filtering was carried out to get a smooth outside image. Once stripped of its cranium, the morphological image function was applied to the picture; the regularized level set strategy, was utilized to accomplish the segmentation.

S. Damodharan et al. [23] showed an effective method for segmenting brain tumors from MR images by combining the segmented sick tissues, extracting the essential properties, and then classifying the resulting data with a CNN model. The implementation of the k-nearest neighbour classifier and the Bayesian Classifier was used to make the comparative analysis. The values of True Positives (TP), False Positives (FP), False Negatives, True Negatives, Sensitivity, Specificity, and accuracy were calculated using the input MRI picture and the testing dataset. The values are presented in Table 2.1.

The suggested NN-based tumour classification approach significantly outperformed the existing algorithms in terms of performance. The results showed the accuracy of Bayesian and NN-based classification, and cancer identification from brain MRI images was confirmed, with both techniques having an accuracy of about 80%.

Table 2.1 Detection accuracy of the Bayesian Classifier in training and testing dataset [23]

|  |  |  |  |
| --- | --- | --- | --- |
| **Input MRI Dataset** | | | |
| **Evaluation Measures** | **K-NN Classification** | **Neural Network** | **Bayesian Classification** |
| **True Negative (TN)** | 3 | 3 | 2 |
| **True Positive (TP)** | 2 | 1 | 1 |
| **False Negative (FN)** | 1 | 2 | 2 |
| **False Positive (FP)** | 0 | 0 | 1 |
| **Specificity** | 0.6 | 0.75 | 0.67 |
| **Sensitivity** | 1 | 1 | 0.67 |
| **Accuracy** | 0.67 | 0.83 | 0.67 |

M. Alfonse and A.-B.M. Salem [24] have proposed a Support Vector Machine-based automated process for brain tumour segmentation and classification using magnetic resonance images. Following image segmentation using adaptive thresholding, features were extracted using the Fast Fourier Transform (FFT). Afterwards, feature selection was made using Minimal Redundancy Maximum Relevance techniques. Then the brain images are classified as abnormal or normal according to the criteria. The accuracy of this approach is said to be 98.9%. E. Abdel-Maksoud et al. [25] demonstrate using an integrated strategy that includes K-means clustering and Fuzzy C-means (FCM). This method clusters pictures using an integrated FCM algorithm and K-means, then segments the clustered image using the level set contouring approach after de-noising the images with a median filter and a Neural interface extractor. Segmentation is 100 per cent accurate. Figure 2.12 depicts the significant steps of the proposed framework as it was applied to three benchmark data sets.

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Figure 2.12 The main stages of the proposed framework applied to three benchmark data sets [25]

X. Zhao [26] proposes a novel approach for segmenting brain tumour images by merging Conditional Random Fields with Fully Connected Convolutional Neural Networks. CRFs are used to forecast the structure and are a subset of the sequence modeling family. With the use of image patches, an FCNN model and a CRF-RNN as Recurrent Neural Networks (RNN)  were trained. They then used image slices to fine-tune both models. Voting-based fusion was utilised to generate and segment 2D image slices from coronal,  sagittal and axial perspectives. This approach was evaluated using datasets from the previous years: BRATS 2013, BRATS 2015, and BRATS 2016.

W. Zhang presented in [27] a method for segmenting isointense stages of infant brain tissues from T1, T2, and fractional anisotropy (FA) images using a Deep Convolutional Neural Network (DCNN) and multi-modality images. The outcomes of the two most popular approaches, Random Forrest (RF) and Support Vector Machine (SVM), as well as the two most popular segmentation techniques, Majority Voting (MV) and Coupled Level Set (CLS) were to be compared. The result shows that CNN outperforms the four other rivals in terms of performance.

By using Deep Convolutional Neural Networks, an automated approach for segmenting brain tumors was created M. Havaei et al. [28], who used a two-phase training approach and studied cascade architecture. Additionally, in [17], an automated brain tumour segmentation approach using magnetic resonance imaging (MRI) was suggested. Regarding feature extraction, this approach employed the Berkeley wavelet transform (BWT), followed by the support vector machine (SVM) to classify the data. Accuracy is said to be 96.5 per cent, specificity is 94.2 per cent, and sensitivity was claimed to be 97.72 per cent with this technique.

## 2.3 Chapter Summary

Artificial intelligence can fundamentally alter how brain tumour patients are treated soon. Computer-aided strategies for identifying brain cancers have been generated by combining MR images to detect brain tumours, their segmentation, and their classification, which is faster and more accurate than human techniques. Many of the critical issues and efforts in the field of brain tumour diagnostics were covered in great depth in this chapter.

# CHAPTER THREE

# SYSTEM ANALYSIS AND DESIGN

## 3.1 Chapter Introduction

In brain tumour classification, essential characteristics can be gleaned from the combination of images to determine the class of a new image under inspection. The Convolutional Neural Network (CNN) is a simplified and trustworthy classification technique that can analyse an image and determine the relevance of various elements and objects in the image [29]. This chapter will provide extensive information on the method and system utilised to determine the type of brain tumour present by evaluating the data.

## 3.2 Process Overview

This section examines the individual modules involved in implementing the brain tumour web application, discussed in subsequent sections. Figure 3.1 illustrates the system’s general process- flow.

Diagram

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Figure 3.1 Process Flow for Web-Based Brain Tumour Classifier

1. **Data Acquisition**: The dataset was obtained from Kaggle, a respected platform for data science that offers high-quality data for solving real-world issues and doing different machine learning tasks; this benefited the model’s training and execution.
2. **Building the CNN models and training the model**: Convolutional Neural Networks are constructed of layers that, when applied correctly, provide the best classification results. The implemented models were constructed using Python with the Jupyter Notebook interface and integrated with the TensorFlow, a machine learning and artificial intelligence framework.
3. **Evaluation of the model**: The models were evaluated to determine the accuracy with which they identify brain cancers from input MR images. In addition, specific metrics were investigated to see if the model is optimal.
4. **Developing the web application and integrating models**: A web application was developed using the Streamlit library to make the model available to end-users.
5. **Implementation of web application**: The application’s functionality was evaluated to see if it delivers precise results.

## 3.3 Design Requirements

This section outlines the design criteria and guidelines used during the project’s development and implementation.

### 3.3.1 Functional Requirements

The following comprises the services rendered by the web application, reactions to user inputs, and other behavioural patterns:

1. The application will support uploading multiple image formats (e.g., JPG, JPEG, or PNG).
2. Users should be able to upload images on both mobile devices and laptops.
3. Allow users to register and log in.
4. The application should allow users to save prediction results and view the results.
5. Allow users to select their preferred CNN model (network).

### 3.3.2 Non-Functional Requirements

The constraints of the web application are highlighted below.

1. The system must deliver real-time and accurate cancer predictions.
2. The system must give predictions in less than a minute.
3. The information delivered by the system must be easy to comprehend.
4. The system should work on all devices with an internet connection and a web browser.
5. The system should be user-friendly.

## 3.4 System Models

This section discusses the models that comprise the web application’s basic functionality. Understanding the system model is essential for conducting an accurate system analysis of the system’s many properties. This section will also discuss the system’s behavioural models, including the activity diagram, use case model, sequence model, and class diagrams.

### 3.4.1 The Activity Diagram

This model is essential for viewing the web application process to predict the type of brain tumour. Figure 3.2 depicts the data flow diagram of the web application for detecting brain tumours.

Diagram

Description automatically generated

Figure 3.2 Activity Diagram of Brain Tumour Classifier

### 3.4.2 Use Case Model

This model dully captures the rapport between the possible stakeholders and the system. The use case model hauls out from the functionalities of the web-based brain tumour classifier. Figure 3.3 shows the use case model of the brain tumour classifier.

Diagram

Description automatically generated

Figure 3.3 Use Case Model of the Brain Tumour Classifier

### 3.4.3 Sequence Diagram

The sequence diagram depicts the interactive relationship between the various objects of the system. Figure 3.4 shows this interaction through a sequence diagram.

Diagram

Description automatically generated

Figure 3.4 Brain Tumour Classifier Sequence Diagram

## 3.5 Architectural Overview

The brain tumour classifier was created with Streamlit, an open-source app framework that helps to build web apps for data science and machine learning quickly. The convolutional neural networks are the critical components within the system that extract the necessary characteristics utilizing the MR brain pictures, then categorize the type of tumour present in the image under investigation. The individual components within the web application were developed using the Jupyter interface. This section will describe the architecture of these models and other components combined to make up the web application. Figure 3.5 depicts the system’s implementation.

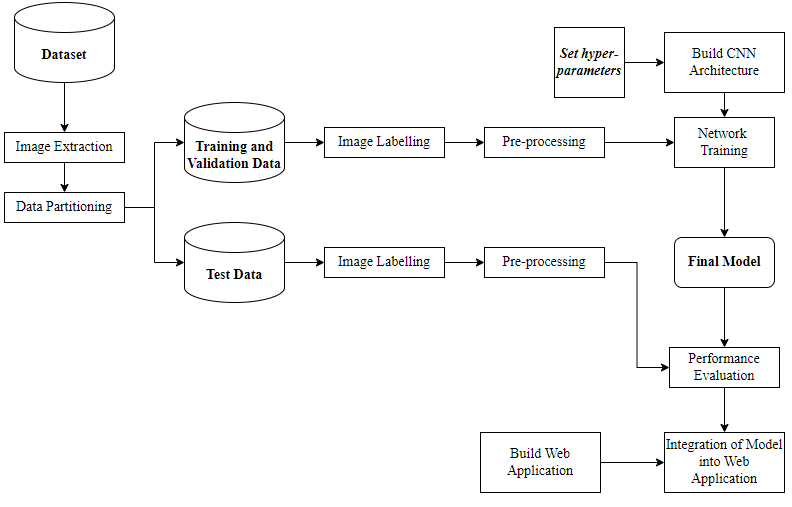


Figure 3. Block Diagram of the System

### 3.5.1 Brain Tumour MRI Dataset

Collecting, storing, and annotating raw data is critical in supervised learning approaches. It is the first and most essential step technique for generating a high-quality dataset. Magnetic resonance imaging (MRI) databases were employed in this study as an input to the created system since MRI can offer detailed information about the brain’s soft tissues[30].

The dataset was obtained from Kaggle and comprised 7022 magnetic resonance imaging images of the human brain divided into four categories: glioma, meningioma, no tumour, and pituitary. The images were then divided into 5712 training images and 1311 testing images. Table 3.1 provides a complete explanation of the dataset per class, and Figure 3.6 shows each image.

Table 3.1 Brain Tumour MRI Dataset

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | **Glioma Images** | **Meningioma Images** | **No Tumour Images** | **Pituitary Images** | **Total** |
| **Training** | 1321 | 1339 | 1595 | 1457 | 5712 (81.3%) |
| **Testing** | 300 | 306 | 405 | 300 | 1311 (18.7%) |
| **Total** | 1621 | 1645 | 2000 | 1757 | 7023 |

Graphical user interface

Description automatically generated with medium confidence

Figure 3.6 Brain MR Images: (a) Glioma, (b) Meningioma, (c) Pituitary, (d) No Tumour

### 3.5.2 Data Pre-processing

Preparing the MRI for the following stage is the aim of the pre-processing stage. Using traditional filtering procedures raises total image resolution and improves image quality [29]. The MR images were resized to 256×256 and 227×227 RBG images and then converted to a NumPy array to allow maximum interoperability with other libraries (Python libraries). The images were then normalised by dividing by 255, which changes the values of numeric columns in the dataset to a standard scale. The images were then attached to their respective classes, i.e., glioma, meningioma, pituitary, and no tumour. An example of the resultant image after pre-processing is shown in Figure 3.7. The implementation code for the networks is provided in Appendix A.

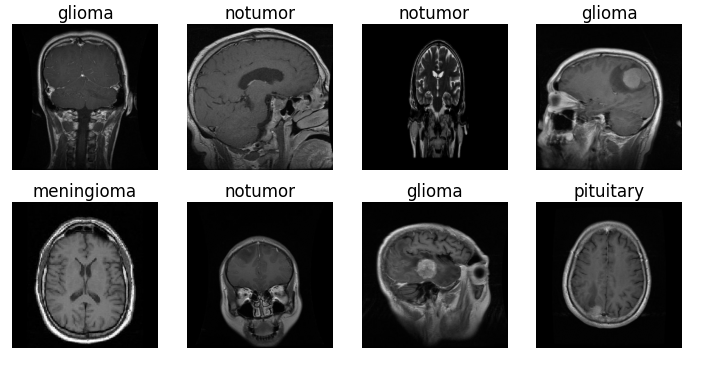


Figure 3.7 Example of Pre-processed Images

Afterwards, a data generator was created, and given the image paths, it yielded the images with the respective labels as a batch.

### 3.5.3 CNN Layers Description

Several layers make up the CNN architecture (or so-called multi-building blocks). Each model has its specific arrangement of layers and certain values that differentiate its performance outcomes. Each layer of the CNNs employed is detailed for each network constructed, and their roles are underlined [9]. A general representation of the CNNs architecture is shown in Figure 3.8.

Diagram

Description automatically generated

Figure 3. Depiction of a basic CNN Architecture [31]

1. The **Convolutional Layer** includes several convolutional filters (kernels). These filters are convolved with the input picture to produce the output feature map. Conv2D is the layer representation.
2. **Pooling Layer**: This layer condenses huge feature maps into smaller ones. Simultaneously, it keeps most of the dominating information (or characteristics) in every stage of the pooling process. The layer representation is *MaxPooling2D*.
3. The **Fully Connected layer** was located after each network’s architecture. Each neuron in this layer is linked to all neurons from the previous layer and serves as the CNN classifier. A *Dense* layer is a traditional fully connected layer in which each input node is linked to each output case (in the systems case; four output nodes) [9].
4. The **Batch Normalization Layer** guarantees that the output activations work correctly. It avoids the vanishing gradient problem, controls the wrong weight initialisation well, and considerably decreases the time required for huge datasets. The layer representation is *BatchNormalization*.
5. **Dropout Layer**: Neurons are lost at random throughout each training session. Dropout uniformly distributes the feature selection power over the whole set of neurons, pushing the model to pick up several distinct traits [9].
6. The **Flatten Layer** transforms the data into a one-dimensional array to feed into the next layer [9].
7. **Activation Functions** determine whether to release a neuron regarding a specific input by producing the relevant output. The implemented activation function is’ ReLU,’ and it transforms the absolute values of the input into positive integers. (The key advantage of ReLU over the others is its lower computing load) [9].
8. **Loss Functions**: Loss functions are used in the output layer of the networks to compute the expected error produced over the dataset. Such error highlights the disparity between the actual and anticipated production [9]. (The *Cross*-*Entropy* or *SoftMax* function was used to create the result within a probability distribution.)

### 3.5.4 CNN Architectures

Four convolutional neural networks were employed: the AlexNet, ResNet152, MobileNetV2, and Xception. Their respective architectures are described as follows.

1. **AlexNet**

The size of the input image is 256×256. The model consists of five convolutional layers, three sub-sampling layers, and the classification layer. The convolutional layers comprise *Conv2D*, *Activation*, *MaxPooling2D*, and *BatchNormalization* layers. The classification layers consist of Flatten, Dense, Activation, Dropout, and BatchNormalization. The output layer has a dense layer of four classes and a SoftMax activation layer. There are a total of 33 layers. The representation of this architecture is shown in Appendix B.

1. **ResNet152V2 (Residual Network)**

The ResNet152V2 model employed is a pre-trained ImageNet model which consists of 152 convolutional layers (564 individual layers). The layers are the ZeroPadding2D, MaxPooling2D, *BatchNormalization*, and Activation (ReLU). The input size is 256×256. The pre-trained model was added to 5 custom layers for the specific training purpose: the Flatten, Dropout, and Dense layers. The representation of this architecture is shown in Figure 3.8.

Diagram

Description automatically generated with medium confidence

Figure 3.9 ResNet152 Architecture

1. **MobileNetV2**

The MobileNetV2 model is a pre-trained ImageNet model which consists of 53 deep layers (154 individual layers). The layers are the *DepthwiseConv2D, Conv2D, ZeroPadding2D, MaxPooling2D, BatchNormalization, Activation* (ReLU), The input size is 256×256. The pre-trained model was added to 5 custom layers for the specific training purpose: the Flatten, Dropout, and Dense layers. The representation of this architecture is shown in Figure 3.9.

Diagram

Description automatically generated

Figure 3.10 MobileNetV2 Architecture

1. **Xception**

The Xception model is a pre-trained ImageNet model which consists of 71 deep layers (132 individual layers). The layers are the *SeparableConv2D, Conv2D, MaxPooling2D, BatchNormalization, and Activation (ReLU)*. The input size is 256×256. The pre-trained model was added to 5 custom layers for the specific training purpose: the Flatten, Dropout, and Dense layers. The representation of this architecture is shown in Figure 3.10.

Diagram

Description automatically generated with medium confidence

Figure 3.11 Xception Architecture

### 3.5.5 Training and Testing

Specific parameters were considered for correct predictions when training to attain an accurate model. The section highlights the functions and specifications of the parameters implemented in each model.

1. **Optimiser**: An optimiser’s function is to alter model weights to maximise a loss function [9]. The Adaptive Moment Estimation (Adam) optimiser was used.
2. **Learning Rate**: This hyperparameter describes how much the model should adjust each time the weights are updated to account for the expected inaccuracy. The adopted learning rate used was 0.0001.
3. **Loss**: The loss is a number that indicates how incorrect the model’s forecast was on a particular example. The loss used was the ‘sparse\_categorical\_crossentropy.’
4. **Metrics**: During the training stage, metrics improve the classification algorithm. The metric used was the ‘sparse\_categorical\_accuracy.’
5. **Batch size** is a gradient descent hyperparameter that regulates the number of training samples to go through before updating the internal parameters of the network. The batch size was set to 512.
6. **Epochs**: The parameter update is conducted once utilizing all of the training data throughout the training period. The number of epochs set was 40.

### 3.5.6 Performance Metrics

To create the best classifier, performance metrics for DL tasks are essential. They were utilized to improve the classification algorithm during the training phase and to assess it during the testing phase [9]. The performance metrics used with their respective formulae and representation are:

1. **Confusion Matrix**: A popular statistic for solving classification challenges is the confusion matrix. For binary and multiclass classification, it can be utilized [32]. Table 3.2 shows an example of a confusion matrix for binary classification.

Table 3.  Binary Classification Confusion Matrix

|  |  |  |  |
| --- | --- | --- | --- |
|  | **PREDICTED** | | |
| **ACTUAL** |  | **Positive** | **Negative** |
| **Positive** | TP | FN |
| **Negative** | FP | TN |

Confusion matrices show the total of expected and observed counts. True Negative and the number of correctly detected negative situations are represented by the output "TN." Similar to that, "TP" stands for True Positive and indicates how many accurately detected positive occurrences there were. False Positive is the acronym representing the number of genuine negative instances that were mistakenly classified as positive. False Negative, or "FN," refers to the amount of good cases that were mistakenly categorized as negative [32].

1. **Accuracy**: one of the most often used categorization criteria is accuracy. It is the proportion of properly predicted classes to all the samples that were examined [32]. The accuracy is calculated with the formula in Equation 3.1.

*3.1*

1. **Precision**: The precision demonstrates how good at forecasting positive values the model is. It is the total number of positive patterns that all anticipated patterns in a positive class correctly predict [32]. The formula for calculating precision is given in Equation 3.2.

*3.2*

1. **Sensitivity (Recall)**: the recall helps measure a model’s strength in predicting positive outcomes. It is the proportion of adequately identified positive patterns [32]. The formula for calculating recall is given in Equation 3.3.

*3.3*

1. **F1-Score**: is the harmonic mean of recall and precision [32]. The formula is given in Equation 3.4.

*3.4*

### 3.5.7 Web Application and Database

The web application receives an MR image uploaded by the user and predicts the type of tumour in the image. The app allows for the use of any of the models employed. The supported image formats are PNG, JPG, and JPEG. The significant functionality implemented in the web application involves:

1. Loading the trained model
2. Resizing the image and converting to RGB format
3. The normalisation of the images, then reshaping.
4. Predict image class and display result.

The database implemented used the sqlite3 library to store information from the web application. The information stored was the user credentials during registration and prediction records after the prediction result was displayed. The code for implementing the web application in conjunction with the database is provided in Appendix C.

### 3.5.8 Additional Dataset for Evaluation

In order to assess the model's performance on fresh data, a second dataset was employed. The dataset, which came from Kaggle as well, included 3264 magnetic resonance imaging (MRI) scans of the human brain that were separated into four groups based on their cancerousness: glioma, meningioma, no tumor, and pituitary. Following that, the photos were split into 394 testing images and 2870 training images.

## 3.6 Chapter Summary

The proposed system successfully demonstrates an unique method for identifying and categorizing brain tumors using MRI data. The absence of solid tumour classification patents restricts the system’s performance comparison. Nonetheless, this technique would undoubtedly aid researchers and clinicians in understanding their patients’ tumour states.

# CHAPTER FOUR

# RESULTS AND DISCUSSION

## 4.1 Chapter Introduction

This chapter presents and discusses the project findings concerning the project’s objective, which is to design and implement a web application for brain tumour classification. The degree to which the web application provides accurate predictions and the influence of varying the exact training settings used to generate the various CNNs is highlighted.

## 4.2 Results

The highest accuracy (that also gave the correct prediction) was achieved with the following parameters:

1. ‘Adam’ optimiser with a learning rate of 0.0001,
2. A batch size of 256 with 20 epochs and,
3. Input image size of 227×227 for AlexNet and 256×256 for MobileNet, ResNet, and Xception.

The variations in the batch size, epochs, and image sizes significantly affected the accuracy and loss of the respective convolutional neural networks that were observed and recorded.

### 4.2.1 Overall Evaluation Metrics

The evaluation metrics are highlighted for their respective classes and networks used.

Table 4.1 Evaluation Metrics for Glioma Class

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Network** | *AlexNet* | *ResNet152V2* | *MobileNetV2* | *Xception* |
| **Accuracy (%)** | 64.1 | 92.7 | 91.76 | 91.5 |
| **Loss** | 1.350 | 0.198 | 0.238 | 0.237 |
| **Precision (%)** | 68.00 | 87.00 | 91.00 | 94.00 |
| **Recall (%)** | 12.00 | 89.00 | 90.00 | 84.00 |
| **F1-Score (%)** | 20.00 | 88.00 | 90.00 | 89.00 |

Table 4.2 Evaluation Metrics for Meningioma Class

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Network** | *AlexNet* | *ResNet152V2* | *MobileNetV2* | *Xception* |
| **Accuracy (%)** | 64.1 | 92.7 | 91.76 | 91.5 |
| **Loss** | 1.350 | 0.198 | 0.238 | 0.237 |
| **Precision (%)** | 81.00 | 89.00 | 88.00 | 82.00 |
| **Recall (%)** | 7.00 | 72.00 | 78.00 | 81.00 |
| **F1-Score (%)** | 13.00 | 79.00 | 83.00 | 82.00 |

Table 4.3 Evaluation Metrics for Pituitary Class

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Network** | *AlexNet* | *ResNet152V2* | *MobileNetV2* | *Xception* |
| **Accuracy (%)** | 64.1 | 92.7 | 91.76 | 91.5 |
| **Loss** | 1.350 | 0.198 | 0.238 | 0.237 |
| **Precision (%)** | 33.00 | 89.00 | 91.00 | 92.00 |
| **Recall (%)** | 100.00 | 99.00 | 98.00 | 96.00 |
| **F1-Score (%)** | 50.00 | 94.00 | 94.00 | 94.00 |

Table 4.4 Evaluation Metrics for No tumour Class

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Network** | *AlexNet* | *ResNet152V2* | *MobileNetV2* | *Xception* |
| **Accuracy (%)** | 64.1 | 92.7 | 91.76 | 91.5 |
| **Loss** | 1.350 | 0.198 | 0.238 | 0.237 |
| **Precision (%)** | 74.00 | 95.00 | 93.00 | 93.00 |
| **Recall (%)** | 62.00 | 99.00 | 99.00 | 99.00 |
| **F1-Score (%)** | 67.00 | 97.00 | 96.00 | 96.00 |

### 4.2.2 Accuracy and Loss for Different Batch Size and Epochs

Using the Adam optimiser with a learning rate of 0.0001, the variations considered were for batch size and epoch of; 128 and 10, 256 and 20, and 512 and 40, respectively. (The evaluations are for input size 227×227 for AlexNet and 256×256 for the other Networks.

Table 4.5 Accuracy and Loss for Batch size = 128 and Epochs = 10

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Network** | *AlexNet* | *ResNet152V2* | *MobileNetV2* | *Xception* |
| **Test Accuracy (%)** | 47.6 | 92.4 | 89.78 | 91.22 |
| **Test Loss** | 1.830 | 0.210 | 0.262 | 0.250 |

Table 4.6 Accuracy and Loss for Batch size = 256 and Epochs = 20

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Network** | *AlexNet* | *ResNet152V2* | *MobileNetV2* | *Xception* |
| **Test Accuracy (%)** | 64.1 | 92.7 | 91.76 | 91.5 |
| **Test Loss** | 1.350 | 0.198 | 0.238 | 0.237 |

Table 4.7 Accuracy and Loss for Batch size = 512 and Epochs = 40

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Network** | *AlexNet* | *ResNet152V2* | *MobileNetV2* | *Xception* |
| **Test Accuracy (%)** | 41.5 | 90.62 | 88.56 | 90.77 |
| **Test Loss** | 1.91 | 0.250 | 0.326 | 0.275 |

### 4.2.3 Accuracy and Loss for Different Image Input Size

The size of the input image to the network also affects the network’s performance. The input sizes considered were 96×96, 128×128, and 256×256. The previous evaluation used an input image size of 256×256, the stipulated image size for AlexNet was fixed at 227×227, so there are no records for the other image sizes.

Table 4.8 Evaluated Metrics for Input Size = 96×96

|  |  |  |  |
| --- | --- | --- | --- |
| **Network** | *ResNet152V2* | *MobileNetV2* | *Xception* |
| **Test Accuracy (%)** | 87.9 | 86.80 | 87.60 |
| **Test Loss** | 0.357 | 0.361 | 0.327 |

Table 4.9 Evaluated Metrics for Input Size = 128×128

|  |  |  |  |
| --- | --- | --- | --- |
| **Network** | *ResNet152V2* | *MobileNetV2* | *Xception* |
| **Test Accuracy (%)** | 88.0 | 91.1 | 86.56 |
| **Test Loss** | 0.316 | 0.256 | 0.371 |

### 4.2.4 Accuracy & Loss Graphs

The link between accuracy and loss can aid in determining a network’s performance. The graphs show the relationships between the training loss, the validation loss, and the training accuracy and validation accuracy. The graphs are shown in Figure 4.1.

Engineering drawing

Description automatically generated with low confidence

Figure 4.1 Accuracy and Loss Graphs for (a) AlexNet, (b) ResNet152V2, (c) MobileNetV2, and (d) Xception

### 4.2.4 Confusion Matrix

The confusion matrices for the networks used are shown below.

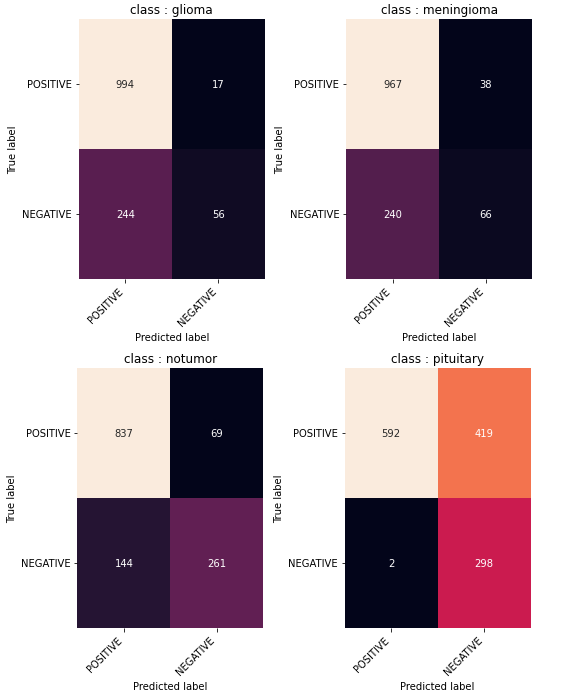


Figure 4. The AlexNet Confusion Matrix for the Four Classes

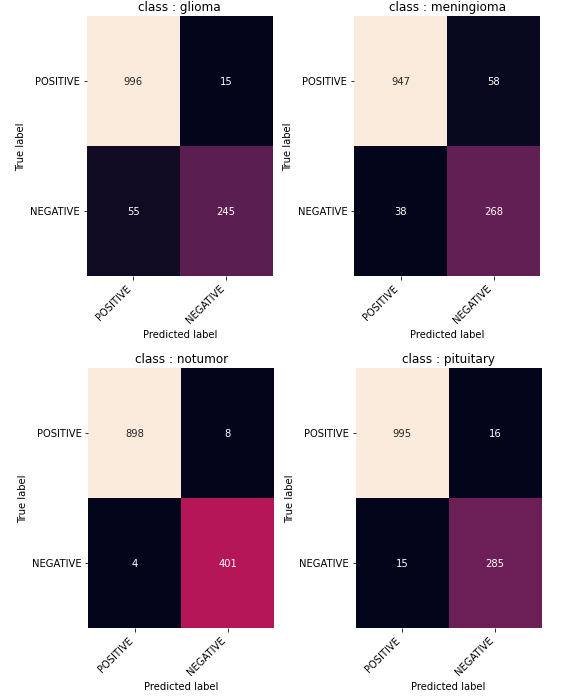


Figure 4. The ResNet152V2 Confusion Matrix for the Four Classes

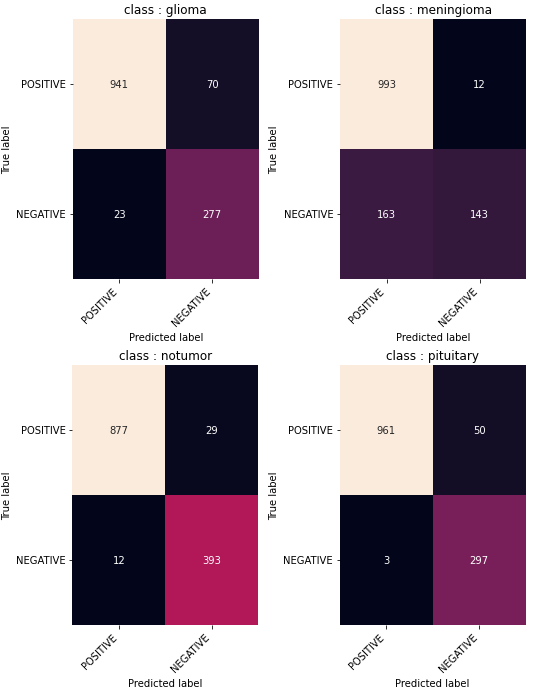


Figure 4. The MobileNetV2 Confusion Matrix for the Four Classes

Chart, treemap chart

Description automatically generated

Figure 4. The Xception Confusion Matrix for the Four Classes

### 4.2.5 Evaluation Metrics on Additional Dataset

The model was tested on a new dataset separate from that used to train and validate. The results are shown in Table 4.10.

Table 4.10 Evaluation Metrics on Additional Dataset

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Network** | *AlexNet* | *ResNet152V2* | *MobileNetV2* | *Xception* |
| **Accuracy (%)** | 26.40 | 80.00 | 65.00 | 68.50 |
| **Loss** | 4.390 | 1.220 | 2.037 | 1.540 |
| **Average Precision (%)** | 24.00 | 75.00 | 69.00 | 77.00 |
| **Average Recall (%)** | 26.00 | 70.00 | 65.00 | 69.00 |
| **Average F1-Score (%)** | 17.00 | 67.00 | 61.00 | 65.00 |

### 4.2.6 Web Application Interface

All the features required for the end-user were provided on a single web page. The functionalities provided by the web application include user registration and login, model selection and upload of MRI image to get a prediction, and record of predictions and display of recorded results. The interfaces for these functionalities are shown in Figure 4.6, Figure 4.7, and Figure 4.8.

Graphical user interface

Description automatically generated with medium confidence

Figure 4.6 User Registration and Login Page

Graphical user interface, application

Description automatically generated

Figure 4.7 Logged in User Page with Classification Functionalities

Graphical user interface, application, Teams

Description automatically generated

Figure 4.8 Previously Saved Prediction from User Input

## 4.3 Discussions

From the above results, it was seen that specific parameters gave rise to a better prediction network which was employed in the web application. The adopted parameters for batch size, epoch number, and input image size were for an image size of 256×256 and a batch size of 256 with 20 epochs. The larger the image size, the more accurate the network trained, leading to a longer training time. The most accurate network was the ResNet152V2 model, with an accuracy of 92.7 %. The relation between the accuracy and the loss can tell how well the model can classify an image. Over-fitting was the fundamental difficulty involved with achieving well-behaved classification for CNN models. When a model excels on training data but fails on test data, it is said to be "over-fitted" (unseen data). A model is ‘Under-Fitted’ when it does not learn sufficiently from its training data. ‘Good-fit’ refers to a model that performs well on training and testing data [9]. The AlexNet network gives under-fitting data as the model did not learn sufficiently from the training data. The other networks had a good fitting, performing well on both test and training data.

Finding proper datasets (MRI scans) is a significant challenge. Other researchers have employed the dataset used for this model to classify brain tumours. Using a comparable dataset, Kiraz in [33] created a Classification Learner App that significantly aided the classification process by testing over 20 models with the corresponding accuracy. The project finished with selecting the Weighted KNN algorithm model of the machine learning algorithm for this project, with high accuracy of 89.8 %, and the testing of this algorithm on a test set, with an estimated accuracy of 91%. In addition, Papageorgiou [34] designed a CNN with three fully interconnected layers of 2048, 256, and 1 node. There was a dropout layer between the first two fully connected layers to eliminate overfitting effects. The model was trained for 75 iterations using the Adam optimiser and a value of 0.001. The validation accuracy of the proposed design was 99.56 per cent. These variations in accuracy show that the model employed is commendable for tumour classification.

## 4.4 Chapter Summary

Training sessions were conducted to demonstrate the system’s effectiveness in performing the tumour detection task. Based on a comparison with other models utilised, it is abundantly clear that the system proposed is exceptional from the others in terms of prediction.

# CHAPTER FIVE

# CONCLUSION

## 5.1 Chapter Introduction

The prevalence of brain tumours has risen rapidly in recent decades, making developing effective methods for detecting them an intriguing project for researchers and experts in related fields. The results showed the effectiveness of the recommended deep learning-based technique in the medical field as well as the effectiveness of the entire system in localization and tumour identification.

## 5.2 Summary

A deep learning-based approach has been developed for detecting brain tumours based on MRI scans. The primary objectives of this research are to precisely identify the tumour within the aberrant MRIs and categorise the images obtained from magnetic resonance imaging (MRI) as normal or abnormal depending on whether or not a brain tumour is present in the patient. In the first phase of the system, feature extraction and classification were handled by CNN. The methodology attained accuracies of 64.1%, 92.7%, 91.76% and 91.5% percent for AlexNet, ResNet152V2, MobileNetV2, and Xception. This classification functionality was then integrated with a web application to give availability to medical practitioners, i.e., radiologists

## 5.3 Recommendations

There are several significant roadblocks to overcome to understand images of brain tumours using deep learning techniques and algorithms. The shortage of big training datasets for deep learning systems is a significant difficulty. Also, the datasets provided should have more classes to give a broader range for classifying MR images. MRIs, CT scanners, and other medical imaging equipment have been deployed in hospitals around the country during the last decade, resulting in a flood of data. Several other sectors make use of image data stored in well-organised digital archives. Other medical specialities, such as pathology and ophthalmology, do not regularly use PACS and CT systems. As noted, the amount of publicly available datasets has steadily increased. It is necessary to utilise advanced text-mining methods, deep-learning approaches, and techniques when automatically providing reports on annotations or updating structured labels. According to the experts, structured labelling reports will be used more frequently in medical research, notably in the study of brain cancers [35].

Text-free and structured reports for network training are projected to become increasingly popular in the future, notably in brain tumour research. Labelling images with tumours takes time and requires a high degree of understanding, both of which are scarce in brain tumour research. Deep learning techniques for tumor segmentation are frequently taught in 3-dimensional networks, which need hard and time-consuming slice-by-slice annotations. One major drawback of deep learning algorithms is their inability to learn well from sparse visual input. Many researchers have only used 2D to train their 3D segmentation algorithms. When using this data to train a deep learning system, additional issues for modeling ambiguity and distortion in the reference standard must be taken into account. This problem still needs to be resolved despite the fact that some researchers have devised methods for explicitly integrating label inconsistency in the loss function. Another data-related problem is the imbalance of classes. By scaling and spinning data, for instance, data preprocessing techniques are employed to create new brain tumor lesions; nevertheless, this might lead to class imbalance [35].

## 5.4 Achievements

Medical imaging technology has recently improved and advanced, giving health professionals more freedom and creativity. These developments promote a variety of medical disciplines, including disease diagnosis, treatment, and rapid clinical application decision-making. Hospitals produce a lot of medical data every day. Systems of expert clinical assistance are essential for healthcare professionals to make the best decisions. Research in medical informatics aids doctors and other professionals in their search for the most palatable options available to use these enormous amounts of data effectively. Effective therapy for brain tumour disorders requires early discovery and available choices. The pathological type of sickness, tumour grade, and stage of the tumor at the time of diagnosis all affect treatment options [36]. This project utilises deep learning to achieve a novel system for empirically evaluating MRI brain scans. The web application, when utilised by radiologists or pathologists, will; give predictions in a relatively short time, account for more than the usual number of classes for categorisation of brain MR images and provide a means of classification through mobile devices (making use of MobileNetV2 network). It would also provide a cheaper means of getting MRI results if Computer-aided Diagnosis is considered a first option.

## 5.5 Conclusion

In regions with inadequate healthcare systems, an analytical framework based on deep learning can be a useful alternative tool. The framework for medical applications based on deep learning demonstrates outstanding results, particularly for early preventive therapy. Given the scarcity of radiologists in areas with limited resources, detecting brain cancers with deep learning technologies can save effort and accelerate the detection process. One of the most important and helpful models which may be utilized in automatic cancer diagnosis is deep CNN, which can categorize hundreds of images per second. Therefore, it is strongly advised that radiologists have an excellent grasp of deep CNN to apply these technologies for therapeutic applications.

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