BRAIN TUMOR DETECTION AND CLASSIFICATION USING CONVOLUTIONAL NEURAL NETWORK (CNN)

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I certify that in my opinion, the thesis submitted by Fakhri lahmood Hameed titled "BRAIN TUMOR DETECTION AND CLASSIFICATION USING CONVOLUTIONAL NEURAL NETWORK (CNN)" is fully adequate in scope and quality as a thesis for the degree of Master of Science.

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ii

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ABSTRACT

M. Sc. Thesis

BRAIN TUMOR DETECTION AND CLASSIFICATION USING CONVOLUTIONAL NEURAL NETWORK (CNN)

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Brain tumor, according to the World Health Organization (WHO) one of the significant causes of death worldwide. Due to its complexity and silent nature, early detection of this disease makes it hard to detect. The associated danger of clinical occurrences, which makes it a severe public health condition globally, is affiliated with chronic brain tumor disease. Even though it is widely accepted that chronic brain tumor disease has significant interactions with magnified hazards of end-stage excretory organ disease, vessel occurrences and all-cause mortality, there is still a lack of comfortable information on individual patients. We will apply the deep learning-based Convolutional Neural Network (CNN) technique for this brain tumor prediction problem which no one has used so far in the research, especially on Image Dataset. The CNN has been a popular method and highly sought-after model classification in today's society. The CNN based expert system works like the human brain with input, neurons, hidden layers and output. For this research, chronic brain tumor images of

healthy and unhealthy images are collected with good lighting conditions to identify all hidden features. The image samples are then passed through different image processing methods such as Grayscale, Complement, Robert, Resize and power Transform. The chronic is then passed through a texture feature extraction algorithm know as Convolutional Neural Network (CNN). The features are Contrast, Correlation, energy, Homogeneity, Entropy, Mean, Standard deviation, Variance, skewness and Kurtosis. After the feature extraction, the data are arranged on a spreadsheet, which serves as a record. Lastly, a convolutional neural network has one hidden layer, 16 input neurons, and two healthy or not outputs. The data are split into train and test datasets with 70% for training, 10% validation and 20% for testing. The detection accuracy was 92.78%, with the execution time of 5.33s only depending on 60 epochs. For the confusion matrix of brain tumor detection and classification, an accuracy of 97.9% was recorded, a precision of 98.3% was accounted with a recall of 98.5%, and an AUC of 99.7% was calculated for this dedicated research work.

ÖZET

Yüksek Lisans Tezi

KONVOLÜSİYONEL SİNİR AĞI (CNN) İLE BEYİN TÜMÖRÜ TESPİTİ VE SINIFLANDIRMASI

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Beyin tümörü, Dünya Sağlık Örgütü'ne (WHO) göre dünya çapında önemli ölüm nedenlerinden biridir. Karmaşıklığı ve sessiz doğası nedeniyle bu hastalığın erken teşhisi, tespit edilmesini zorlaştırmaktadır. Onu küresel olarak ciddi bir halk sağlığı durumu haline getiren klinik oluşumların ilişkili tehlikesi, kronik beyin tümörü hastalığına bağlıdır. Kronik beyin tümörü hastalığının, son dönem boşaltım organı hastalığı, damar oluşumları ve tüm nedenlere bağlı ölümlerin büyütülmüş tehlikeleri ile önemli etkileşimleri olduğu yaygın olarak kabul edilse de, bireysel hastalar hakkında hala rahat bilgi eksikliği vardır. Araştırmada şimdiye kadar kimsenin kullanmadığı bu beyin tümörü tahmin problemi için özellikle Görüntü Veri Kümesi üzerinde derin öğrenme tabanlı Evrişimsel Sinir Ağı (CNN) tekniğini uygulayacağız. CNN, günümüz toplumunda popüler bir yöntem ve çok aranan bir model sınıflandırması olmuştur. CNN tabanlı uzman sistem, girdi, nöronlar, gizli katmanlar ve çıktı ile insan beyni gibi çalışır. Bu araştırma için, sağlıklı ve sağlıksız görüntülerin

kronik beyin tümörü görüntüleri, tüm gizli özellikleri belirlemek için iyi aydınlatma koşullarıyla toplanır. Görüntü örnekleri daha sonra Grayscale, Complement, Robert, Resize ve power Transform gibi farklı görüntü işleme yöntemlerinden geçirilir. Kronik daha sonra Evrişimsel Sinir Ağı (CNN) olarak bilinen bir doku özelliği çıkarma algoritmasından geçirilir. Özellikler Kontrast, Korelasyon, Homojenlik, Entropi, Ortalama, Standart sapma, Varyans, çarpıklık ve Basıklıktır. Özellik çıkarımından sonra veriler, kayıt işlevi gören bir elektronik tablo üzerinde düzenlenir. Son olarak, evrişimli bir sinir ağının bir gizli katmanı, 16 giriş nöronu ve iki sağlıklı veya sağlıklı çıktısı vardır. Veriler %70 eğitim, %10 doğrulama ve %20 test için olmak üzere eğitim ve test veri kümelerine bölünür. Algılama doğruluğu, yalnızca 60 çağa bağlı olarak 5.33 saniyelik yürütme süresi ile %92.78 idi. Beyin tümörü tespiti ve sınıflandırmasının karışıklık matrisi için, %97,9'luk bir doğruluk kaydedildi, %98,3'lük bir kesinlik, %98,5'lik bir geri çağırma ile hesaplandı ve bu özel araştırma çalışması için %99,7'lik bir AUC hesaplandı.

Anahtar Kelimeler : CNN, beyin tümörü, derin öğrenme, segmentasyon, sınıflandırma, tahmin.

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CONTENTS

LIST OF FIGURES

LIST OF TABLES

SYMBOLS AND ABBREVIATIONS INDEX

SYMBOLS

ABBREVIATIONS

ANN   : Artificial Neural Network

BDNF   : Brain-Derived Neurotrophic Factor

CNN   : Convolutional Neural Network

DCNN   : Deep Convolutional Neural network

FC   : Fully-Connected

VCT   : Vessels Coherence Tomogrphy

GPU   : Graphic Processing Unit

GHz   : Giga Hertz

LSTM   : Long Short-Term Memory

QT   : Quantitative Traits

BPE   : Brainl Pigment Epithelium

RNN   : Recurrent Neural Network

SVM   : Support Vector Machine

BT   : Brain Tumor

MRI   : Magnetic Resonance Imaging

PSO   : Particle Swarm Optimization

WHO   : World Health Organization

DVM   : data volume management

TFKCM   : Temper based K-means and modified Fuzzy C-means

DARPA   : Defense Advanced Research Projects Agency

VGG   : Visual Geometry Group

ML   : Machine Learning

AI   : artifical intelegent

<center>**PART 1**</center>

<center>**INTRODUCTION**</center>

1.1. INTRODUCTION

In the 21st century, the software is used effectively in every field. The intensive use of information systems has developed big data and the storage of this big data. On the other hand, the databases created with these big data have directed human beings to research and produce useful information with existing information. Developing statistics and software-based systems using existing information will prevent any mistakes encountered in a profession again and again. They will bring many benefits, such as fast and accurate diagnosis and treatment in medicine. In a sense, just as ore is mined and processed and becomes a useful product for human beings, data mining also uses the data in the existing database and processes them, offering a useful product to human beings. In data mining, this process is done using different techniques such as statistical science and machine learning.

A brain tumor is a serious disease, and if the necessary intervention is not done, it can eliminate functions such as walking and eating that meet the person's basic needs. It can also cause the patient's life to come to an end. In addition, diagnosing brain tumors requires serious expertise and unfortunately, the number of specialists in this sense is low in our country. A surgical intervention that is not a brain tumor but diagnosed with a brain tumor can cause different problems due to its high risks. If there is indeed a brain tumor and if it is not diagnosed and treated, the patient will be adversely affected.

Although Magnetic Resonance MR Spectroscopy has a short history, it is an effective diagnostic method for diagnosing brain tumors. Diagnosis of serious diseases such as brain tumors is not made by a single method. Different techniques are used to confirm the diagnosis.

<center>1</center>

MR Spectroscopy is not a stand-alone method for diagnosing brain tumors but an effective method of diagnosing. We can attribute the effectiveness of MR Spectroscopy in diagnosis to the fact that it can measure the choline (Cho) metabolite because there is a rapid increase in cells in the tumor area. Choline (Cho) metabolite value is high in the region where the number of cells increases rapidly. Creatine (Cr) and N-Acetyl Aspartate (Naa) metabolites are also important in brain tumor diagnosis. In other words, these metabolite values may vary in different diseases, such as cerebral hemorrhage. Detection of the ailment here requires good expertise.

Technological developments are widely used in medicine, as in every field [1]. Today, with the development of this technology, devices and treatment methods used in hospitals are also being developed. Thanks to these methods, which are constantly developed in hardware and software, it is possible to apply diagnosis and treatments [2] professionally. Thus, more effective decisions can be taken in a shorter time in important processes where human life is at stake.

Since it is related to human health in medicine, supporting R&D studies as comprehensively as possible is important. Because human life is too valuable to be measured by material assets [3]. Early diagnosis is of great importance in many treatments. When treatment is delayed, the disease may progress further and be more difficult to treat. In some cases, it can cause irreversible losses. For these reasons, data extraction methods used to assist physicians in diagnosis and treatment are frequently encountered in the literature. Promising results have been obtained in many studies [4,5].

The detection of radiation health risks mostly improved the degree of brain tumors amongst exposed patients, elevated the query of cultural compassion to dissimilar heights of radiation, and concentrated on health risk and grade of damage amongst cultural collections exposed in the US and Israel [6]. The initial radiation studies depended on suitcases of growing degrees of leukemia or other medical situations in persons from dissimilar cultural and ethnic upbringings (e.g., African-American vs. Caucasian; Hispanics vs. Caucasians).

In recent years, a California study likened cultural sets of Hispanics to Caucasians, over levitating the query of ethnic-related compassions to radioactivity and Brain Tumor (BT). Image processing approaches production a significant role in observing tumor situates between radiologists and computers in the analysis and action procedure with data mining. Radiologists increase analytic accuracy from a dissimilar viewpoint in understanding medicinal images with these hybrid techniques [7].

Segmentation of tumors on MR images is very important in diagnosis and treatment. Tumor classification can be made using the volumetric dimensions of the image obtained due to the segmentation. What type of tumor it is, whether it is a progressive or non-progressive tumor, etc. can be obtained. Diagnosis and treatment can be made easier with the data obtained. The segmentation process is usually done manually by experts. These procedures require much time and effort compared to the number of patients. In addition, segmentation can be interpreted differently according to the person performing this operation. It means that the diagnosis and treatment will be made differently by different specialists. However, automatically performing the segmentation process by an algorithm can provide a lot of convenience in this area and increase reliability [8].

1.2. PROBLEM STATEMENT

The cerebrum or tumor growths work as channels to eliminate the byproducts from the blood in various small veins. In specific cases, it deteriorates and mind cancers lose their ability to recognize supplements, which closes in nephropathy of human brain growth. The expanded risk of clinical events, which makes it a serious general ailment worldwide, is partnered with persistent mind growth illness. Despite the fact that it is generally acknowledged that persistent cerebrum sickness forecast has huge connections with amplified perils of end-stage excretory organ illness, vessel events and all-cause mortality, there is as yet an absence of agreeable data on individual patients. A versatile and solid framework is required with the end goal of the robotized constant cerebrum cancer sickness destruction on imbalanced picture-based dataset. The test intrinsic in biomedical data frameworks and mind cancer illnesses discovery from identifying extremely switched sickness growth.

Because of its developing intricacy, this sickness frequently makes serious harm vessels nerves that can be found and recognized. Be that as it may, there is no such mechanized master framework accessible for distinguishing cerebrum growth utilizing profound learning methods. Ordinarily alluded to as a most terrible infection, these kinds of illnesses can be exceptionally harming and baffling to people [8].

1.3. AIM OF STUDY

This research study aimed to design and develop a deep learning-based system, that is, the CNN and supervised learning in developing a system for the detection and prediction of chronic brain tumor diseases classification with a delicate problems such as accuracy and to evaluate the system under all types of input images from imbalanced image dataset and unseen data. The system should give high accuracy of detection and classification using CNN.

The main challenge of chronic brain tumor disease prediction on imbalanced data by convolutional neural network work is to manage image datasets as the medical dataset is not publicly accessible in our country, and the dataset we have used is not big enough. Although the limitation, we managed to solve it by using the convolutional neural network (CNN), a deep learning-based technique, and showed the best outputs in detection and recognition based on a structured deep learning algorithm.

The application will be solely designed and developed for chronic brain tumor disease prediction on imbalanced data by a convolutional neural network, as no one has previously done such a task. The state-of-the-art CNN architecture with GPU will average, consume less time per image. The CNN learning with non-maxima suppression times will be negligible in this application's detection and classification of brain tumors.

1.4. RESEARCH OBJECTIVE

This novel research fulfills the gap of managing the expert system development for detecting and classifying brain tumor disease.

A direct sampling expert system can be considered a type of hybrid disease detection that directly samples the incoming sample of brain image and then uses CNN techniques to extract total information, which is analyzed and managed through features. The research goals in this thesis are all about creating a convolutional neural network architecture that can handle the criteria for early detection and classification of brain tumor. Therefore, this research is experimental in that a model will be designed and then tested through experiments. The design procedure moves forward through ideas of related works, reflections on concepts in the field, and incremental improvement of models through testing. We choose this type of methodology because it is the most common in the field. The focus is on finding a new theoretical concept or architecture and the performance in a particular domain on the Kaggle dataset. This might inherently lead to new models on the way and, at the very least, provide more insight into the field of deep learning on brain tumor disease

1.5. THESIS ORGANIZATION

The letter includes five chapters prepared as follows:

Chapter I: Introduction: problem statement, aim of study, and Research objective.

Chapter II: Literature review, in which several previous studies are presented and explained in detail form.

Chapter III: Methodology and CNN Algorithm, And the Proposed Method.

Chapter IV: Details of the implementation of the experiment and the consequences gained for all planned situations and comparison of results.

Chapter V: Conclusion and Future Work

PART 2

LITERATURE REVIEW

2.1. INTRODUCTION

Since as far back as the 1920s, brain tumor research has gained from a multitude of epidemiological studies conducted across continents investigating the prevalence of open-angle brain tumor as described in [9]. In many earlier studies, brain tumor and ocular hypertension were synonymous and failed to meet certain methodological standards, such as clearly describing the criteria used to define the disease [10]. One of the first studies to be well received as adequately designed and conducted was the Welsh Brain Survey [11]. 92% of the town's eligible population were examined, but only people between the ages of 40 and 75 were included in the study.

In brief, the mechanical disease theory in [13] suggests that when intraocular pressure rises above physiological levels, the pressure gradient across the lamina cribrosa increases, leading to pressure-induced backward bowing of the lamina cribrosa, misalignment of the pores within the connective tissue complex and subsequent deformation and mechanical stress to the brain ganglion cells, their axons and supporting cells as described in [14]. Brain ganglion cells are damaged directly and indirectly by the mechanical stress induced by this raised pressure. This stress has been shown to obstruct both anterograde and retrograde axoplasmic flow of the vessels nerve. The ability of brain ganglion cells to survive and thrive can be seen as a dynamic balance between various factors promoting their continuing existence and other factors encouraging apoptosis and hence extinction, as described in [15].

Obstruction of retrograde axoplasmic flow has been demonstrated to impede the movement of neurotrophic factors, for example, brain-derived neurotrophic factor (BDNF) and its receptor, to the perikaryon of the brain ganglion cell and cause the

accrual of these factors at the level of the lamina cribrosa as explained in [16]. Deprivation of the brain ganglion cell soma of neurotrophic factors is believed to stimulate apoptotic cell death. Raised hydrostatic pressure has also been shown to cause the activation of glial cells, cause changes that may impair their neuro-protective and supportive function, and increase the secretion of neurotoxic substances such as tumor necrosis factor-alpha. Such changes would also promote the apoptotic death of brain ganglion cells. In addition, raised Intraocular Pressure (IOP), can cause the atypical deposition of various forms of extracellular matrix proteins, such as different forms of collagen, elastin, and basement membrane material, which may alter the biomechanical. The possibly biochemical environment of the vessels nerve leads to some of the change's characteristics of brain tumor vessels neuropathy, as stated in [17].

Much of the research into the genetics of brain tumor has involved treating brain tumor as a binary or qualitative trait. This approach poses several problems. The first is the lack of a standard definition for the very heterogeneous disease that is buried beneath the solitary term "brain tumor." The differences in definition between published epidemiological studies as described in [18]. This is further compounded by the different methods of the visual field, vessels disc, and IOP assessment, and criteria used to diagnose brain vessels neuropathy, visual field defects, and "normal" intraocular pressure. This was investigated more formally in a literature review. We demonstrated the importance of having a standard definition for open-angle brain tumor even further by showing the prevalence of open-angle brain tumor in Rotterdam could vary 12 fold (from 0.1 to 1.2%) depending on how a case of open-angle brain tumor was defined; different definitions for the disease having been obtained from other major population-based studies as described in [19].

The second is the prevalence of brain tumor. The prevalence is only around 1-4% in the over 50 population of white Caucasian ancestry, as described in [20]. Though this prevalence is sufficient for a brain tumor to be classified as a common disease, a considerable amount of effort still needs to be expended in order to find a sufficient number of cases for a meaningful genome-wide association study if association methods are to be used. A chronic brain tumor is also a disease of late-onset.

Hence, finding large enough pedigrees for linkage analysis is problematic, as explained in [21]. Rather than studying the disease itself, a method of circumventing some of these issues is to dissect the disease into contributing components in the form of Quantitative Traits (QT). Generally, a quantitative trait or QT could be considered one whose distribution is continuous, for example, blood pressure, as opposed to a discrete trait such as blood group. QTs can be subdivided into three main categories. Metric traits include many traits of clinical importance, such as weight, blood pressure, intraocular pressure, and axial length. These traits can take any numerical value and are measured on a continuous scale.

Meristic traits consist of integers and are measured by counting—for example, egg production and bristle number. Finally, threshold traits are traits that, on the surface, appear to be binary traits but reflect an underlying continuous liability determined by the interaction of both genetic and environmental factors, as stated in [22]. Once a certain threshold is exceeded, the defining trait becomes manifest. This paradigm probably describes the pathogenesis of most common disorders, including brain tumors.

Mircea Gurbina et al. aim to differentiate between a normal brain and abnormal cases [23]. Various brain tumors, like metastatic tumors from bronchial carcinoma, glioblastoma, and sarcoma, have been evaluated using brain magnetic resonance imaging (MRI). MRI is finding and categorizing brain tumors. MRI was performed using various wavelet transforms and helper vector machines, In [24] TA Jemimma et al. Dynamic Basin Angle Projection - Proposal for Advanced Tumor Detection Methods Using CNN. The Watershed procedure precisely fragments the tumor area. The dynamical direction estimate model extracts the structural features of the brain, and the CNN classifies tumor and non-tumor regions from the brain MRI image. A brain imaging abnormality is identified, and the test is effectively performed on the Previous BraTS datasets. The classification success of this method is 91.03%. In [25], Hein Tun Zaw uses a naive Bayesian classification to identify the tumor site that contains all the disseminated cancerous tissue. This study used brain MRI databases, preprocessing, morphological operations, pixel extraction, maximum entropy thresholding, statistical feature extraction, and scoring algorithms based on a Naive

Bayes classifier. This method aims to locate a tumor area on multiple MRI images of the brain and predict the presence of a tumor in the detected area. Compared to other methods, it allows precise detection of tumors in different parts of the brain, including in the central region (at the level of the eyes), which is an important advantage of this method. This method has been tested on 50 MRI images and has a success rate of 81.25% for tumor images and 100% for non-tumor images, with an overall accuracy of 94%, the aim of the system proposed in [26] is to classify images of brain tumors into three subtypes: meningiomas, gliomas, and pituitary glands, using a convolutional neural network (CNN) and a vector machine (VM). The dataset images have been resized to reduce the amount of computation, and salty noise has been added to make the model more robust and the dataset larger. The performance comparison was performed in Python on the Google Colab and Tensorflow platforms.

In [27], Arun Kumar et al. Import MRI images of brain tumors into an online database and develop a machine learning model using a particle swarm optimization (PSO) algorithm for feature selection. Next, the support vector machine (SVM) classifier is used to classify the type of tumor in the current brain.

Adela Kermietal. [28] proposed an autologous method to segment brain tumors using the similarity of the brain in standard analysis and 3D MRI. The photo is pre-processed to remove noise. Symmetry analysis methods are efficient and uncontrollable. With this method, tumor detection takes place automatically. A deformable 3D model based on the corrected geodetic plane is used to determine the shape and volume of the tumor and its corresponding margins. The average calculation time for detecting and segmenting tumors is approximately 5 minutes. The precision and sensitivity obtained were 38.04% and 89.01%, respectively.

V. Anita, S. Murugavalli [29] presented a clear, systematic review method using algorithms. The extraction of the properties and filtering coefficients of the results obtained after applying the discrete wavelet transform using the proposed algorithm and training a self-organizing neural network map was trained by a nearby ANN. The testing procedure was carried out in two stages.

This method is more powerful than traditional classification methods and gives better results than SVM-based classification methods. The results show that this work can be integrated into medical imaging applications for image classification and computer recognition. This study's precision was 85%, and the sensitivity was 100%. Parveen and Iitpalsingh [30] proposed a data mining method to classify magnetic resonance images. Classification is performed in four steps: preprocessing, separation, feature extraction, and classification. The first phase includes skull enhancements and segmentation to increase speed and accuracy. In the segmentation phase, the fuzzy sets method is used. Extraction of photographic features in MRI images is performed using a grayscale array. The final step is to implement data volume management (DVM) for image classification. The final results of this study demonstrated high accuracy and efficiency in classifying magnetic resonance images. The accuracy was determined as 91.24%.

Daniele Ravi et al. propose new processing and size reduction methods to obtain a detailed structural map to determine operating income [31]. This procedure is a two-step process. First, a stochastic neighborhood operation is performed with a semantic segmentation method using a semantic textile forest from which the T distribution flows, and finally, the organization is classified. The accuracy and precision obtained in this study were 81.90% and 80.91%, respectively [32].

Lamia Salemi et al. announced a new algorithm for modeling glioblastoma [32]. The distant region of the tumor is created by applying rapid diffusion mapping based on global pixel information. The new algorithm uses Rapid technology to assess cancer progression over time. This method has an optimized execution time of fewer than 0.5 seconds per frame and does not require extensive training. Glioblastoma exhibits varying shades of gray in effectiveness compared to safe cells. This information is used to divide the brain image into two regions. Glioblastoma regions are then compared with a predictive model based on density levels. The proposed system eliminates tumors in real-time and is used to predict growth with 89.74% accuracy. Mukambika and Uma proposed a stage in which MRI images are processed in four stages [33]. These are the pre-processing, segmentation, pattern extraction, and pattern recognition stages.

These are pretreatment steps, and the skull is extracted from the MRI using the double threshold method. The first method was developed using a nonparametric active contour deformable model for excising brain tumors from brain MRI images. The second method is the K-means clustering method. In addition to segmentation, a two-step decision process is provided. Discrete wavelet transforms, and grayscale matching matrices are applied in the first stage of feature extraction, and a support vector machine (SVM) is used in stages. Classification.

The magnetic resonance imaging dataset of brain tumors is T2-enhanced from multiple patients. It contains 17 images of benign tumors and 24 images of malignant tumors. Level-corrected SVM segmentation and mean K values classify images as normal, benign, or malignant brains with an accuracy of 94.12% and 82.35%, respectively. The established K-Average level is more efficient than segmentation.

K. Sudharani et al. in the case of. In addition to the proposed methods, there are techniques such as histogram, resampling, K-NN algorithm, and distance matrix [34]. First, the histogram shows the number of pixels in a particular image. The image is reduced to 629x839 for proper geometric representation. After adjusting parameter K, use the applied ANN algorithm to classify and determine brain tumors. The Manhattan distance criterion was used for the classification. The dataset used to test the algorithm contains 48 images. All images tested have a rating of 95%.

Razel Ahmed et al. Proposed methods that include image preprocessing, segmentation, feature extraction, SVM classification, and tumor staging using artificial neural networks (ANN) [35]. In this study, the Temper based K-means and modified Fuzzy C-means (TKFCM) algorithm was applied. This hybrid algorithm consists of segmentation, k-means, and fuzzy c-mean.

For feature extraction, primary and secondary statistics are derived based on area features. The SVM then classifies MRI images of the brain as healthy or cancerous. The stage of brain tumors is classified according to the ANN classifier. The proposed method achieved a classification success rate of 97.44%.

2.2. KINDS OF BRAIN TUMOR

Astrocytomas are tumors arising from astrocytes, the star-shaped cells that make up the "glue-like" or supporting tissue of the brain. These tumors are staged on a scale from I to IV, depending on how normal or abnormal the cells appear. There are low-grade astrocytomas and high-grade astrocytomas. Low-grade astrocytomas are usually localized and grow slowly. High-grade astrocytomas grow rapidly and require a different course of treatment [7].

Furthermore, an anaplastic astrocytoma is a Stage III tumor. These rare tumors require more aggressive treatment than benign pilocytic astrocytoma. Anaplastic astrocytomas tend to have tentacle-like projections that grow into the surrounding tissue, making them difficult to remove completely during surgery [8]. Moreover, Gangliogliomas contain both neurons and glial cells. These tumors are very rare in adults. They are typically slow-growing (Stage I) tumors and can usually be treated with surgery alone or radiation therapy [9,10].

2.3. ARTIFICIAL INTELLIGENCE

The term artificial intelligence first appeared in 1956. Artificial intelligence is now widely used to increase the amount of data, the complexity of algorithms and data processing, and the development of data and information technologies. Early research into artificial intelligence in the 1950s focused on problems such as problem-solving and symbolic methods. In the 1960s, the US Department of Defense became interested in these AI processes and began teaching computers to simulate basic human thinking. For example, Defense Advanced Research Projects Agency(DARPA) developed a roadmap for the 1970s. This research has opened up opportunities to complement and enhance the formal and automated thinking inherent in modern computing, such as information systems, decision support, and intelligent sensor systems—human ability. Artificial intelligence is currently being developed to bring many benefits in many fields, such as health, business, and the military.[36]

Recently, artificial intelligence technology has contributed to major advances in medicine. In the future, AI will help clinicians make informed clinical decisions and can replace human thinking in some functional areas of medicine (e.g., radiology). In recent years, the increasing availability of medical data and the rapid adoption of big data analytics have enabled the successful use of artificial intelligence in the healthcare sector [37].

2.3.1. Computer Vision

Computer vision is a branch of artificial intelligence in which objects that can be seen in the outside world are interpreted and understood. Although it has long been associated with artificial intelligence and is considered a sub-branch, it is becoming increasingly important in some fields.

Computer vision was first created in 1966 as a system for describing objects with the Summer Vision Project written by Seymour Papert and Marvin Minsky [38]. The next study was carried out by Kunihiko Fukushima's suggestion of a computer vision system, which took an important place in 1979 [39]. Convolutional Neural Networks (CNN), which have been successfully applied recently, have been developed inspired by Neocognitron [40]. Successful results in deep learning have turned our eyes to computer vision, especially with the brilliant victory of AlexNet, which ESA developed as part of the ImagetNet image recognition competition [41].

For computer vision, there are three basic processes. These are image acquisition, image processing, and image understanding. Computer vision types are image segmentation, object recognition, face recognition, edge recognition, pattern recognition, image classification, and feature processing. Computer vision applications are used in many places in the real world. Examples include facial recognition on Facebook, target recognition in the military, transportation, driverless vehicles used in companies such as Tesla-google, facial recognition technology in security applications, and automatic payment transactions in modern retail stores.

2.3.2. Machine Learning

ML is an area of AI focused on building products that understand information and enhance precision around a period with no software development. In information knowledge, a process is a sequence of actions in numerical handling. Machine learing (ML) uses a lot of data to train algorithms and make choices and forecasts depending on new information. Better algorithms, data processing, accurate decision-making, and prediction. There are four main steps to building a machine learning application (or model). This task is usually performed by a scientist working with a model expert. This simple example may explain the difference between machine learning algorithms, so-called "classic" or "traditional" algorithms, and non-machine learning AI algorithms. Imagine someone who knows nothing about animals. This child cannot distinguish between a cat and a dog. In this thought experiment, imagine someone thinking of a child as an artificial intelligence algorithm and a computer scientist studying the difference between the two [42]. In classical artificial intelligence applications, instead of teaching the baby the difference between cat and dog, we give him a full set of instructions that will enable him to distinguish between cat and dog. These instructions should be prepared in such a way that this ignorant baby should be able to both follow those directions and distinguish between cat and dog mostly correctly. It is obvious how difficult this is for both the baby and the teacher.

On the other hand, as you may have noticed, we don't need to do this to increase the baby's success: If we give the baby lots of pictures of cats and dogs and repeatedly tell which is which, the baby will at some point begin to distinguish the two with high accuracy. This is exactly how ML algorithms work, as the name suggests. Of course, computers, unfortunately, do not come with a learning algorithm in them when they are built. Computer scientists design and adapt the most suitable machine learning algorithm for each problem. Machine learning is essentially built around this logic. We have seen many artificial intelligence applications recently are ML applications. ML is indispensable for most artificial intelligence applications we see in science fiction movies [43]. At this point, although we have largely avoided the conceptual confusion by revealing the difference between the concepts of ML and AI, there is one more step we need to take: Although machine learning is a narrower concept than artificial

intelligence, it still includes many different algorithms, and It is a method field. That's why the concept of "machine learning" still doesn't adequately describe the products of popularization we're talking about. Therefore, by talking about deep learning, a sub-branch of machine learning, we will both avoid broadcast-level conceptual confusion and better understand why artificial intelligence has been so popular for the last ten years. Classification and regression determine which class the new data will be included according to the available training data. In other words, the classes to be obtained as a result of the process in classification are predetermined. In addition, which type of data characteristics are used in machine training as training data? Classification and regression is the most widely used data mining technique. The main difference in classification and regression is that the predicted related variable is categorical or continuous. In recent studies, classification and regression have increasingly converged. The algorithms used for classification techniques and regression techniques are similar. For example, a training data set can be created according to blood values, age, and gender of people with a certain disease. It can also be determined whether the new patient has this disease. A company can create a training data set by looking at how the advertisement of a product affects the sales of the product, the time of the advertisement, the duration of the advertisement, and the visual content. This training data set will inform the company officials how to advertise a new product, thus saving the company from unnecessary advertising costs [44].

2.3.3. Training and Testing Data Selection

From Kaggle website I got data and did training data point is a dataset that symbolizes the data the machine learning prototype will power use to resolve the difficulty. In several instances, the training data is "tagged" to indicate the elements and categories that the model should identify. Additional data are not labeled, and the prototype should remove these features and classify them on its specific [45].

2.3.4. Choosing the Algorithm to Run on the Training Dataset

The algorithm to be used is a series of numerical handling measures. The algorithm varies depending on the type of data (with or without labels), the quantity of data in the training dataset, and the kind of trouble to resolve [45].

2.3.5. Using the Algorithm in Training to Build the Model

Training the algorithm is an iterative process. This process involves running the variables through the algorithm, comparing them with the results produced, adjusting the weights, labels within the algorithm, and rerunning the variables in the algorithm to give a more accurate result [45].

2.3.6. Model application and further development

The final step is to run the model with the new data and improve its accuracy and efficiency over time. This need to select new data based on the problem to be solved.

2.3.7. Supervised Learning

In supervised machine learning, the system is trained with labeled data. Labels classify each data point into one or more groups, such as "X" or "Y". The system learns how this data, called training data, is organized. The information from the training results is used to predict new categories of data or "test" data [46].

2.3.8. Artificial Neural Network (ANN)

Artificial Neural Networks (ANN) belong to the technology of artificial intelligence. ANN is a computer system aimed at realizing the human brain's capabilities without help. When programming these systems, traditional methods are often inadequate. He was inspired by human and animal biological neural networks when designing artificial neural networks. Electrical signals are passed from one neuron to another for neurons in the human brain to transmit information.

The transmitted signal can be stored in the brain (memory). In other words, the memory that a computer uses to store it mimics the brain of a biological system. The purpose is the same, but the mechanism used is different. In short, ANN is considered a computer algorithm for data processing and is designed for one-off events [47].

In recent years, ANNs such as CNNs have become popular when solving various image-related problems. The recent surge of CNNs is likely attributed to the many advances in the field. In 2016, AlexNet beat all current methods in the ImageNet competition, having a top-5 error 10.8 percentage points lower than the runner-up [47]. After this, a new architecture for CNN won the yearly competition. CNN has excelled at image-related tasks through countless publications and competitions, especially classification. These models are becoming deeper thanks to concepts such as the ReLU, batch normalization, skip connections, and more. More depth allows for more complex internal representations.

Therefore, the advancement of GPUs has also been important to handle the increasing load of training larger and larger models. In medicine, tasks such as brain tumor diagnosis rely on a health professional's classification. The work may include manually segmenting parts of the image or finding specific patterns in the picture that indicate symptoms. These are tasks CNNs have been shown to handle quite well. Unlike many existing methods, including traditional ANNs, CNNs have very few design decisions or assumptions made by humans. As CNNs are their feature extractors, one avoids the need for most human assumptions, which might be the hardest part of designing a model in complex cases. The model will create its feature extractors and classifier based on the dataset. This means making the dataset representative of the domain it should handle is important, as mentioned in [47]. Large datasets with variation covering the whole domain is ideal. There are often large amounts of data in the medical field, image evaluation can be quite complex, and objectivity is desired. These are aspects suited for CNNs. However, it should be noted that though a large amount of data exist, it can be hard to gain permission to use it. With lower amounts of data, ANN can still handle some tasks

2.4. IDENTIFICATION OF RESEARCH

A big focus in the review was finding papers on detecting brain tumors with deep learning methods. Furthermore, to compare approaches, the search also focused on documents using the most extensive public dataset on brain tumor from the Kaggle repository. Therefore, two search strings were used: One for relevant works conducted on the Dataset and one for classifying healthy versus brain tumor cases in more general terms.

The search domain was Google Scholar. This is a search engine used for searching scientific papers from multiple sources. Google Scholar also has features such as finding documents that have cited a specific article. A similar approach was used in the preliminary studies, though outside of any formal protocol. In the early stages of the project, the objective was to understand what works when detecting glaucoma by exploring approaches in the domain. Google Scholar was used, but also suggestions from fellow students and professors. Two tables containing groups of terms were assembled to come up with search strings. Each group includes words that are synonymous or have a similar meaning semantically. In review, the author in [47] found great results in classifying brain tumor with 2D convolution with a VGG architecture. The author suggests a new way to do 3D convolution that outperforms other traditional methods in their domain. Finally, the author presents a visualization technique for CNNs is covered. In all of these works, exciting aspects that can be used in the papers will be highlighted. This includes methods, architectural choices, performance studies, and tools

Table 2.1. Summary table for show previous study work.

Source	Dataset	Techniques	Performance
[58]	BRATS 2015 BRATS-MICCAI	Multi-level thresholding with level-set segmentation	JI 81.94%, DSC 89.91%
[59]	https://radiopaedia.org	K-means and FCM	ACC 56.4 %
[60]	BRATS	Patch based k-means with FCM	SI 91%
[61]	BRATS 2012	Random	DSC 91%
[62]	collected by authors	Bi-secting	ACC 83.05%
[63]	BRATS	Force Clustering	-
[64]	BRATS 2017	Random	DSC 62.5%

PART 3

METHODOLOGY

3.1. INTRODUCTION

I used CNNs algorithm and did pre-processing is commonly used to reduce image contrast, undesired noise, and brightness. The image is transformed to grayscale, black and white, histogram equalization, and thresholding for the pre-processing component. Using a developed GUI on MATLAB software, so The simplest method is to use data augmentation and add specified instances to the training dataset, and used meadin filter in Convolution layer and one hidden layer, 16 input neurons also Hyperparameters are boundaries whose values control the algorithm training in terms of learning experience and decide the upsides of model boundaries that a learning calculation winds up learning for final decision making based on set parameters for testing the samples. The prefix 'hyper_' recommends that they are 'high level' boundaries that control the educational experience and the model boundaries that outcome from it, so The collecting of raw data is a difficult task in this research. Working with raw data is also difficult since it has numerous repeating rows and aberrant numbers that do not reflect reality. As a result, raw data must be filtered and transformed into a dataset that can be used for the researcher's purposes. Similarly, duplicate rows are removed from our data. To reflect better outcomes on the sets, synthetic values have been introduced.

3.2. METHODOLOGY OVERVIEW

Brain tumor disease detection depends on extracting features from chronic pictures. The many phases would be depicted on a flowchart, allowing a better understanding of the procedures. This approach will cover a research gap in which a separate model has been built for each chronic image of the disease. The motivation is that training, implementing, and maintaining an expert system for brain tumor disease in large

19

networks, especially deep learning techniques, might quickly become problematic. This study focuses on a more recent benchmark dataset that has recently been available to researchers. On MATLAB R2019b, the Kaggle Dataset [48] will be used with a convolutional neural network. This convolutional neural network will be the same size and number of layers as the previous one. Their threshold formula will be used, but it will be modified by adding a parameter. This parameter is subjected to optimization. Some specifics, such as the choice of activation function and optimization algorithm, are unique to this work. In addition, this research will use deep learning to forecast the accuracy of feature selection parameters using a feature selection mechanism. This research will allow for a more accurate evaluation of convolutional neural network method accuracy on smaller feature subsets and a more balanced comparison of illness detection and classification for brain tumors using a more sophisticated deep learning method.

This thesis aims to detect and classify brain tumor using CNN to aid in the time-efficient diagnosis process. It does so in a semi-supervised fashion using a two-step approach. The model first trains what they call the feature extractor of the model on 2D slices of the brain tumor scans, and then in a second step, trains the classification part of the model using the already learned features on full brain tumor scans. While CNN is computationally demanding, they don't require physical contact and is friendly compared to active devices. Deep learning-based approaches rely on tracking the natural user movements without requiring users to wear or hold any sensor for series classification, this research also presents a method for comparison patterns to improve their robustness to the classification of provided comparison instances.
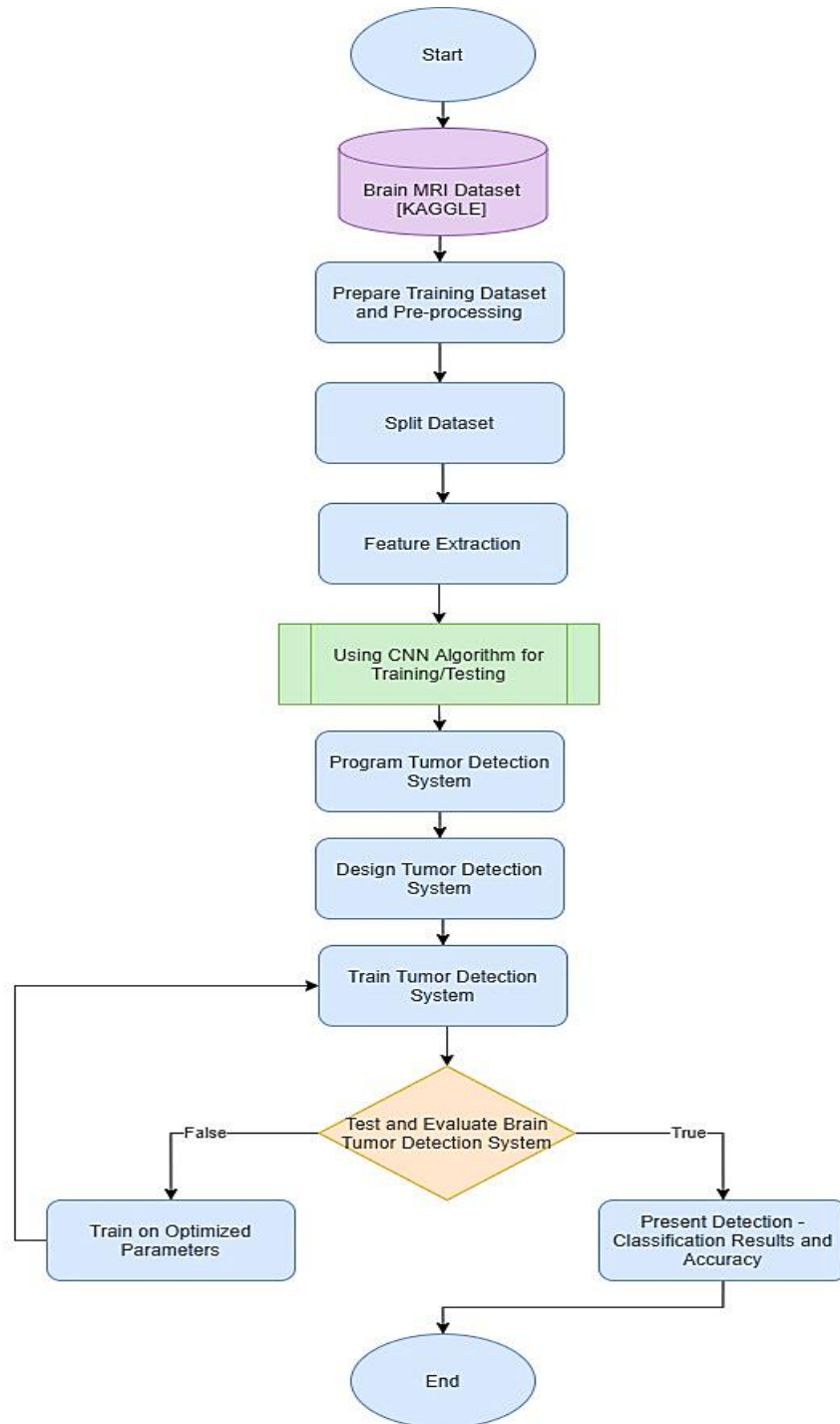
Figure 3.1. Flowchart shows an overall approach being followed.

3.3. DATASET DETAILS

Kaggle Dataset is concerned with the method and format in which data is often collected from the Kaggle repository.

The data can be in either.JPEG or.PNG format. The performance of networks with identical architecture will be compared to isolate the training component. These are the pre-trained model, the network with only the last layer retrained using machine learning and the network with only the last layer retrained using machine learning. Their performances are presented depending on the level of occlusion applied to the instance they had to classify. Having a high cluttering factor also allows a large portion of the self-interference signal to remain and not be canceled.

Finally, the cluttering factor is determined by canceling the self-interference signal and the analyzing time's minimum allowable speed. Many devices with minimal processing power require deep learning classification, necessitating a ranging system with a low computational cost. There are some low-cost ways to estimate a wireless channel's impulse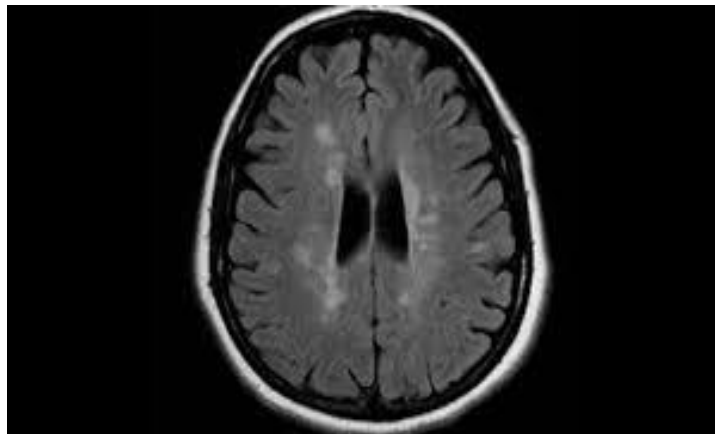 response. The dataset can be accessed from the link: https://www.kaggle.com/navoneel/brain-mri-images-for-brain-tumor-detection

Figure 3.2. A sample of brain image being acquired from Kaggle

3.4. CONVOLUTIONAL NEURAL NETWORK (CNN)

Since this closely corresponds to the time required for a brain input to arrive, the Convolutional neural network (CNN) has been working. As a result, this procedure should rely on feedforward data processing. Cascade. The conclusion was that additional recurrent processing was needed in handling occlusion in the brain when it was discovered that the identical recognition selective response only appeared around 200ms following input.

Deep learning researchers found that when recurrent networks were trained to do comparison recognition of specified examples, they outperformed feedforward networks. This thesis is built on the foundation of the study described above, by experimenting with the use of recurrent models to recognize provided comparisons. Hyperparameters are boundaries whose values control the algorithm training in terms of learning experience and decide the upsides of model boundaries that a learning calculation winds up learning for final decision making based on set parameters for testing the samples. The prefix 'hyper_' recommends that they are 'high level' boundaries that control the educational experience and the model boundaries that outcome from it.

The CNN is based on the neural network technique, and the fundamental feedforward architecture was chosen for imaging. Aside from one original network pre-trained on the Image network and utilized as a control, five other models were constructed. Recurrent and feedforward connections, on the other hand, would imply a larger search space, but these do not appear to be especially relevant. One explanation for this peculiar discovery could be that the recurrent layers provide too much search space, allowing the models to overestimate their computational search areas and lose whatever benefit they might have. Looking back at the training evaluation can be beneficial; nevertheless, fewer training losses are still associated with better testing performance does not allow any conclusions to be drawn.

The CNN aims to understand better how the models' training differed and what impact this would have had on the observed outcome. The training loss was exhibited alongside the image networks' performance, for example, around 90% visibility. This occlusion was picked since it was in the region where the networks' performance changed the most. The researchers demonstrated that not all image networks could accommodate the supplemented data equally well. It can be seen that imaging networks, rather than feedforward networks, deliver superior information. The plot also illustrates that two-layer retrained networks can achieve lower training losses than a single-layer retrained model. When comparing the left red plot to the right blue plot, it's clear that networks with lower training loss can achieve superior results in that region. There are numerous strategies to address this deficit.

The simplest method is to use data augmentation and add specified instances to the training dataset. Deep learning researchers have also devised more complex modular systems that explicitly combine many subsystems responsible for tasks like segmentation, depth detection, and other complex picture representations. Another option was to take inspiration from biology.
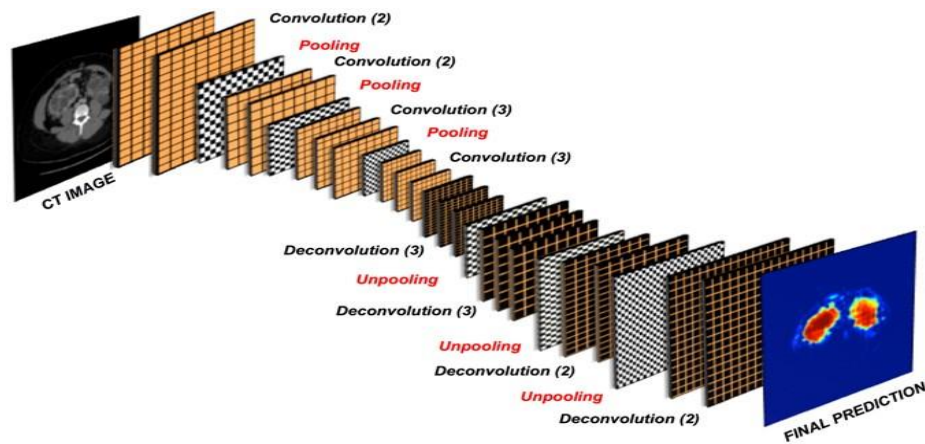

Figure 3.3. An architectural diagram of CNN[53].

The proposed CNN network uses twelve convolutional layers and three fully connected layers. The classification of a brain tumor in brain tumor sample photos differs significantly from ImageNet classification. The classification of ordinary objects such as animals, household items, and so on is required by ImageNet. Similarly, brain tumor sample images are medical data to detect and categorize glaucoma symptoms. As a result, it's safe to believe that the fully connected classification layers were trained from scratch, and the deeper convolutional layers were most likely replaced. Looking back at the training review can be beneficial; the fact that lesser training losses were still associated with better testing performance does not support the overfitting theory. As a result, these gadgets are costly. Active gadgets are accurate and simple, but they can be inconvenient because they require physical contact between the user and the instrument. While computationally demanding, passive gadgets do not require physical contact and are more user-friendly than active devices.

It can be seen that image networks, rather than feedforward networks, have a stronger inclination to suit the data. Second, the plot illustrates that networks with two retrained layers can achieve lower training losses than models with only one retrained layer.
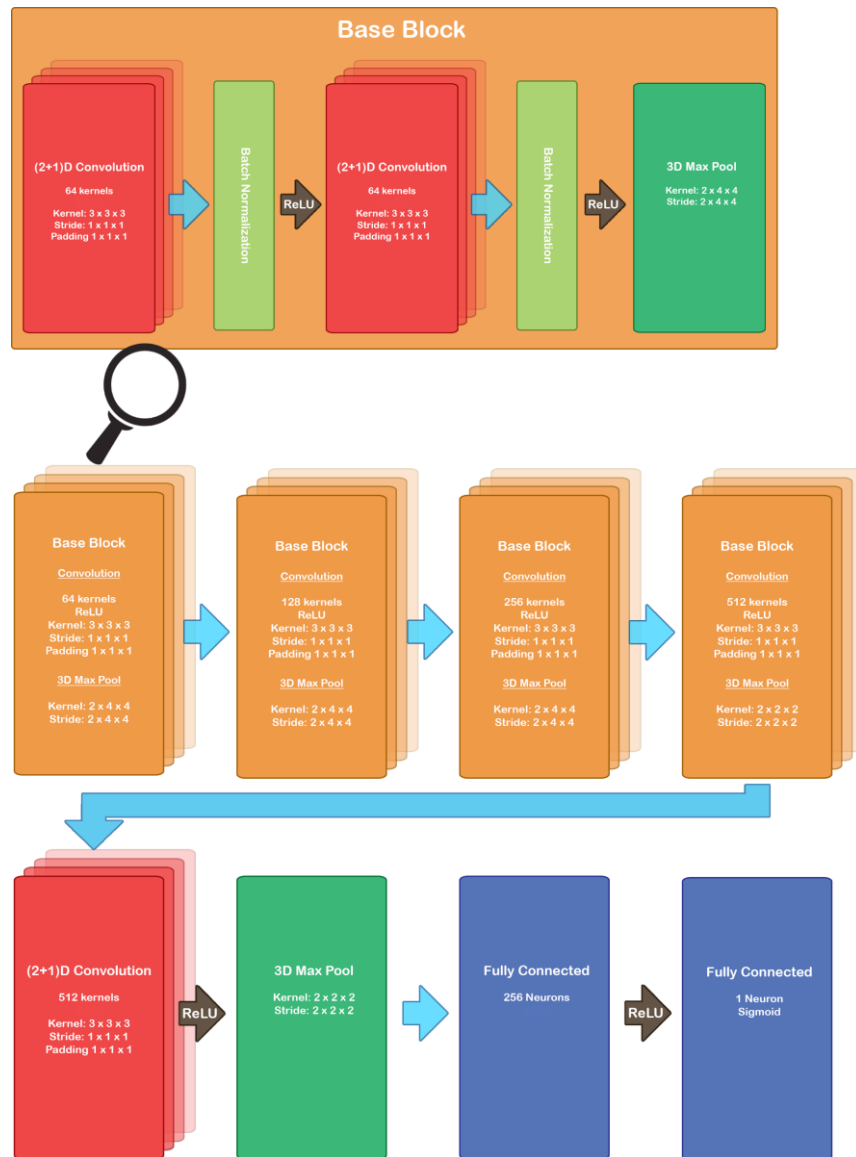

Figure 3.4. CNN with a description of layers in every singular block.

3.4.1. Dimensionality of Images

The concept of convolution and how it is applied to images. However, a few important details were left out. A two-dimensional (2D) image with color is not 2D for a convolutional neural network.

Color images have channels, usually one for red, one for green, and one for blue. Therefore, the actual dimensions of such an image are channels, height, width, and three sizes. The kernel applied will consequently be 3D. Even though the image is 3D, the convolution applied is called 2D convolution. This is because when depth is considered a channel, the depth of the kernel is always equal to the depth of the image. The seed only has room to move horizontally and vertically (two dimensions). Additionally, the output image will be 2D because the kernel outputs one value at the center of the seed—the difference between convolution with channels and convolution with spatial depth.

3.4.2. Convolutional Layer

Layers based on convolution exist in CNNs. Rather than having layers of neurons, like in fully linked networks, one layer has many kernels, each with its own set of trainable parameters. As shown in figure 5, a forward pass entails applying convolution to each kernel in a layer and then adding a bias to each kernel. In the output image, convolution with one kernel creates one channel. Because the kernel covers all tracks in the input image but only outputs one value, resulting in a single channel, this is the case. If the input data is a 2D image with channels, the output channels are stacked depth-wise, resulting in a 2D image with a channel for each kernel. In Figure 3.5 we are showing depth-wise convolution and regular convolution. Depth-wise convolution treats each depth-wise slice independently and therefore outputs a value for each depth-wise piece seen, each with its color in the output. Regular convolution treats the depth as channels and thereby calculates with all channels at once. This will output one value for the 3x3x3 kernel.
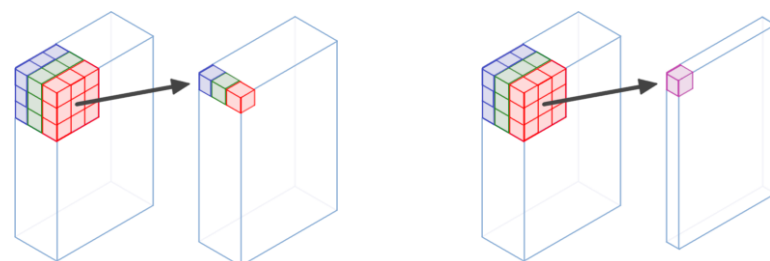
(a) Depth-wise convolution.   (b) Regular convolution with channels

Figure 3.5. Depth-wise convolution vs. regular convolution with channels [54].

The concepts explained here can be applied to any higher dimension. For example, medical images can be 3D color images. This means images with dimensions channels depth height width, in the same way as before the kernel is now 4D, with the channel dimension equal to the channel dimension of the input volume. The kernel will move in the three dimensions depth x height x width.
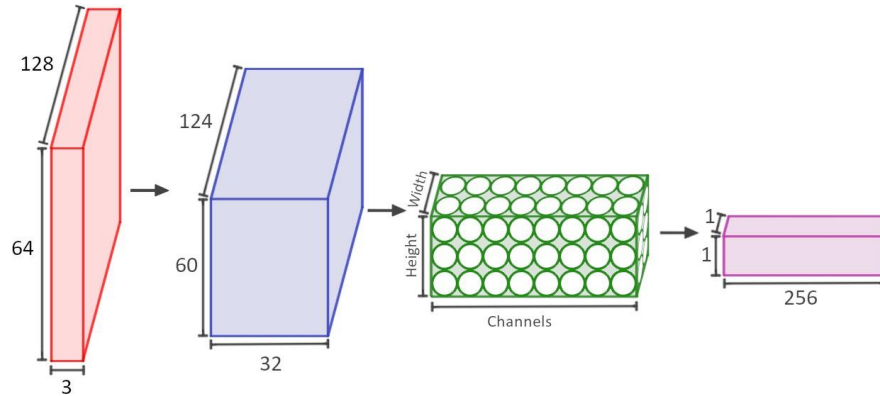

Figure 3.6. Layers of process

In Figure 3.6 Red volume is the 3 x 64 x 128 (channels height width) input image. Thirty-two kernels of size 3 x 5 x 5 with a stride of 1 are applied to the input image. The output from each kernel becomes a channel "slice" stacked depth-wise in the blue volume. The blue volume can be seen as the activations after the first layer. As no padding was applied, the height and width were reduced. The green volume shows how these shapes can be viewed as neurons stacked in a 3D formation. Each neuron in the green volume is only connected to a select group of neurons in the blue volume.

3.4.3. Down sampling and Image Sampling

A convolutional neural network does not necessarily only consist of convolutional layers. Even though kernels have reduced the number of parameters substantially, it is often helpful to lower the parameter count further. Thus downsampling is used. Downsampling can be done in many different ways. We can reduce the output image simply by making the stride bigger than 1. A natural downsample happens if padding is not utilized, and techniques such as dilation can reduce the output image. Dilation is a way to spread the kernel, as seen in figure 3.7.
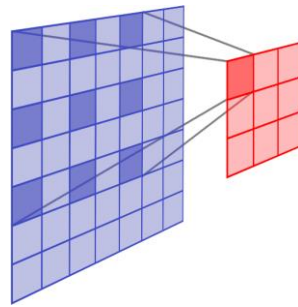
Figure 3.7. Illustration of dilation

In Figure 3.7 the blue plane is the input image, and the red plane is the output image. Dark blue is the input value used to compute the dark red output value. Dilation is the concept of spacing the dark blue values apart. Another technique that has become very common is pooling, proposed in [36] for CNNs. It should be mentioned that pooling had been a well-known concept long before 2016. We presented the variation called max pooling. It works similarly to a convolutional layer by utilizing the sliding window method and applying a function to a local selection of the input at a time. However, max-pooling operates on a per-channel basis.

Backpropagation through a max pool layer is done by setting the gradient for all not local maximums values to 0. Then only compute the gradient for the max values M going from the layer after the max pool to the layer before the max pool. In a way, adding the gradient as if the max pool layer was not there on selected connections. If kernels overlap, one must accumulate several error signals in one unit.

3.4.4. Batch Normalization

Normalizing the input of the convolutional layer improves the total training time significantly [47]. The normalization is usually done by setting the mean and variance of the input features to 0 and 1, respectively. Due to the adjusted distribution of the input, the network only needs to handle numbers in one range for all input neurons. Batch normalization takes this a step further and applies this concept to the network's hidden layers. Among the reasons why batch normalization work is that it reduces covariant shift. One way to imagine what this means for a neural network goes as

follows: You are making a network to say whether there is a brain tumor in an image or not. The boundary function the network has learned has only seen one part of the problem, brown brain tumors. It lacks the information to know how the function should look for brain tumor of more colors. As the input has not been normalized, the new images of colored brain tumors are too far from the original distribution, so the network is unable to generalize the new brain tumor images.
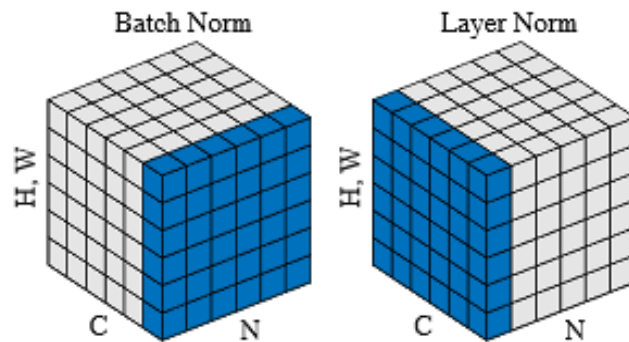

Figure 3.8. Difference between batch normalization and layer normalization

An important detail to notice about batch normalization is that it does normalization and scaling over a mini-batch, a selection of input-target pairs sent through the network as one to compute an average gradient. Calculating the mean and variance only considers the mini-batch, not the whole dataset. This has a slight regularizing effect on the network. The normalization will be slightly noisy due to the mean and variance being a little different be- tween each mini-batch. Bigger mini-batches have mean and variance closer to the dataset's mean and variance; thus, smaller mini-batches have a more significant regularizing effect.

3.4.5. Feature Extraction

Before the training and testing phases, feature extraction is crucial. This procedure entails extracting key features from the image collection. Contrast, Correlation, Energy, Homogeneity, and Entropy are all part of this property.

The GLCM is a technique that uses the spatial relationship of pixels to analyze the texture of a picture. Feature extraction is critical in this study because it allows

researchers to distinguish between brain tumors and other disorders quickly. The matrices' distance is commonly expressed in various ways, with values ranging from 0 to 45, 90, and 135 in most cases. We can raise the number of features called to more to improve accuracy. An adjustment layer in CNN is introduced after the feature extraction process is frozen to compensate for the disparities between classifying slices and brain tumor features. After the adaption layer comes to the classification layer, which is not frozen in CNN, this will finally determine whether the volume shows signs of a brain tumor or not. CNN model will also use the volume labels.

3.5. BRAIN IMAGE PRE-PROCESSING

The term "image processing" refers to the process of adjusting pixels. They're resizing an image's pixels to the appropriate shape. Data pre-processing is commonly used to reduce image contrast, undesired noise, and brightness. The image is transformed to grayscale, black and white, histogram equalization, and thresholding for the pre-processing component. Using a developed GUI on MATLAB software, more image pre-processing techniques were applied to the image. The deep learning model can be used to repurpose a neural network for a brain tumor classification task. A model, such as CNN, has shown excellent performance on image classification tasks, which on an abstract level, is the same domain. The idea is that earlier layers in a deep convolutional network detect more fundamental features. The first layers may see simple shapes such as ed ges, then the following layers raise the complexity slightly, finding geometric shapes, and for each layer, more complex features are represented. The most fundamental elements a network finds are similar to deep convolutional networks. Therefore, one should take the first layers from a well-trained model and reduce the parameters that require training.
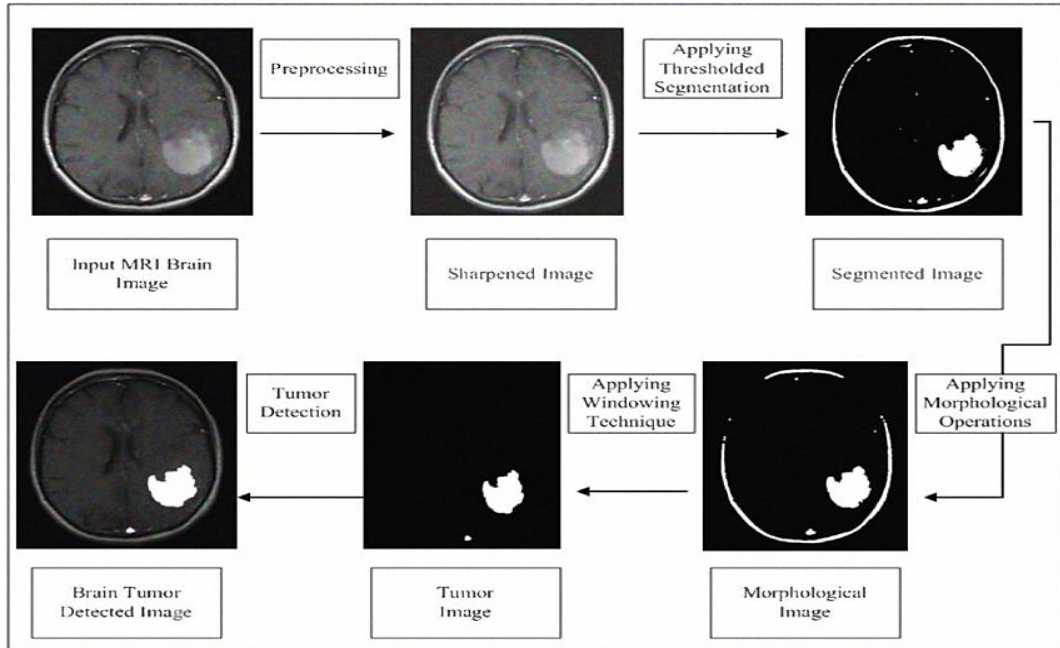
Figure 3.9. Brain image sample to acquire the interest of tumor area [55].

However, it should be noted that there is no guarantee that max-pooling will not remove data that could be useful for the CNN model. There are several pooling techniques other than max pooling. They generally work the same way, using a different reduction function, for example, average.

The goal is to increase spatial invariance by reducing the representation to the most important features. If the input has been transformed or exposed to a lot of noise, this can confuse the CNN. Max pooling attempts to fix this by reducing the representation to keep the most important spatial relations while removing unnecessary information.

3.6. TRAINING AND TESTING

The dataset was split into three parts 70% training, 20% testing, and 10% Validation. A convolutional neural network back propagation was created using the MATLAB tool. With a total of 60 epochs, each was set. The number of accuracies can also be increased if we retrain the neural network repeatedly. Figure 3.10 shows train and test of CNN concerning model loss and 60-epochs training.

Table 3.1. The description of parameters being used for training and testing an expert system.

Parameter/Decision	Choice
Training Mini-Batch Size	1
Validation Mini-Batch Size	1
Learning Rate	0.005
Architecture	CNN
Training	70%
Testing and Validation	20% and 10%
No. of Epochs	60
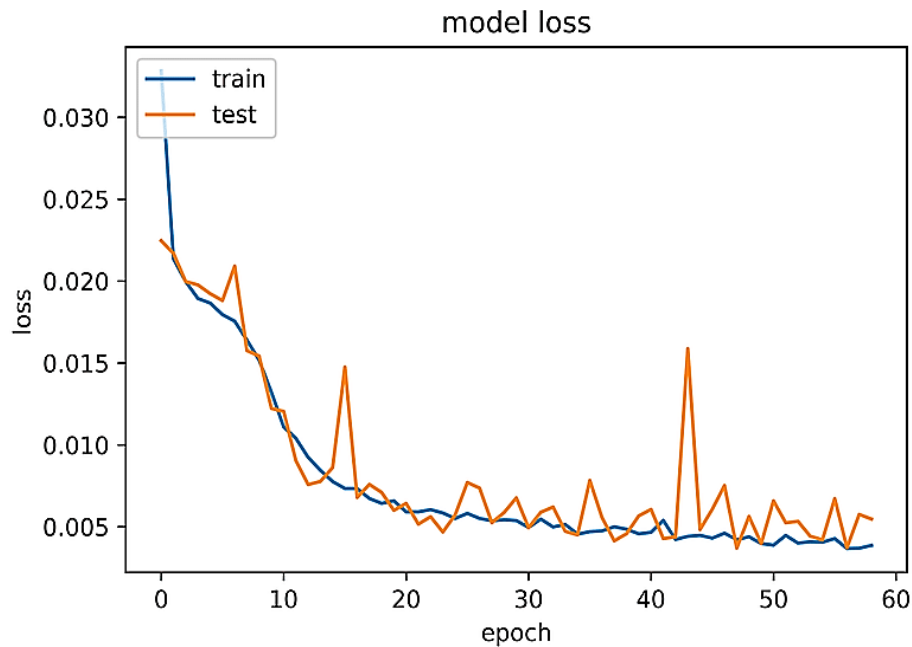
Figure 3.10. The training and testing parameters for CNN

The mini-batch size was limited to the storage capacity of the GPU, and as it turned out, it gave a pretty good performance. Therefore, little effort was put into multi-GPU training, which would allow bigger mini-batches. The training process stored the model parameters every time it found a better validation accuracy. This method was used instead of early stopping. When training multiple models sequentially on one GPU, storing models and using time limits was ideal because server guidelines require a total time limit on the GPU resource. The training period had a set time of 3 hours per model. The training time was decided after finding that a model would usually reach peak validation loss and accuracy during this period.

A much more significant time frame was set if a new design decision was tested and the network was periodically manually monitored. Training loss was logged every step to aid in evaluating how the network performed. Validation loss and accuracy were calculated every ten steps. Both loss and ac- curacy were calculated for the whole validation set and averaged. A prediction for accuracy was made by thresholding the network output at 0.5.

3.7. SUMMARY

The CNN architecture is made after increasing more layers to the convolutional neural networks. The famous CNN model VGG16 inspires the use of kernels of size 3 in this work. The use of batch normalization is inspired by ResNet and other models that have performed well in ImageNet for detecting and classifying medical diseases. The activation function ReLU and max pooling for downsampling were used for the same reasons. The number of convolutional layers was derived by trial and adjustment and fit in the restrictions in resources available. A repeating pattern in the network was abstracted to its layer called a base block. Reducing a block to only one convolution leads to a significant decrease in validation accuracy for brain tumor detection and classification. Furthermore, there was no capacity for a network much more extensive than CNN in the experimental setup. Each block contained two convolutional layers, which used CNN. We saw similarities in the field of detecting and classifying brain tumor disease. The CNN seemed ideal for training where high complexity is wanted, but fewer parameters are required because the dataset is large. The architecture can, however, quickly switch to using 3D convolution.

PART 4

RESULTS AND DISCUSSION

4.1. INTRODUCTION

This chapter presents the results obtained from the methodology outlined in Chapter 3. We discussed the analysis of the results and what was learned from each experiment. This chapter concludes with detecting and classifying brain tumors with a deep learning-based CNN model in terms of performance and accuracy. In a setting where we only have partial information necessary for people, CNN operates well based on knowledge and makes judgments. Fortunately, it is a requirement that we can easily meet, used Neural network toolbox and Deep learning toolbox. All observations in dataset are nicely distributed with 10-fold cross validation.

Table 4.1. CNN results like Specificity, Sensitivity, F1-Score, and Mean AUC

Outcome of the Test Performed	Condition (e.g tumor) As determined by the Standard of Truth		
	Positive	Negative	Mean AUC
Sensitivity	57	84	70.50
Specificity	79	33	56.00
F1-Socre	45	92	68.50

First and foremost, because the algorithms are based on reflections from moving time, there are no environmental lighting restrictions. Second, processing reviews with ultrasonic waves reduces computational complexity compared to deep learning techniques. One method for deep learning-based categorization uses ultrasonic waves to determine the range of the moving time and the received signal strength. Time of flight can be used to estimate range in various ways.

The series occurrence can be detected by determining the received signal strength. The kind of the performed series can then be classified using range estimation. Only brain tumors and health diseases are used to train the convolutional neural network to reconstruct inputs from a latent space representation. As a result, when given a healthy disease sample as input, the convolutional neural network has an easier time detecting the disease, resulting in increased accuracy. A convolutional neural network takes longer to process when there is enough brain tumor in a disease sample image. Still, it may be utilized to discover anomalous regions by passing through a comprehensive processing pipeline. Figures 4.11, 4.12 and 4.13 showed the brain's input image, segmented brain image, and no brain tumor were detected and classified within the region of interest (ROI) using the CNN approach
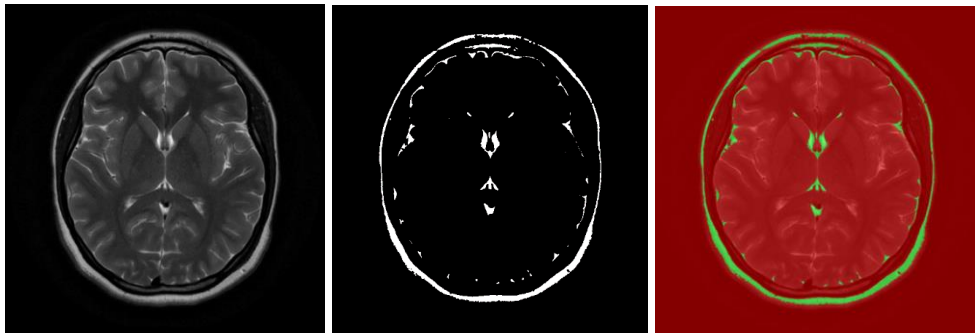

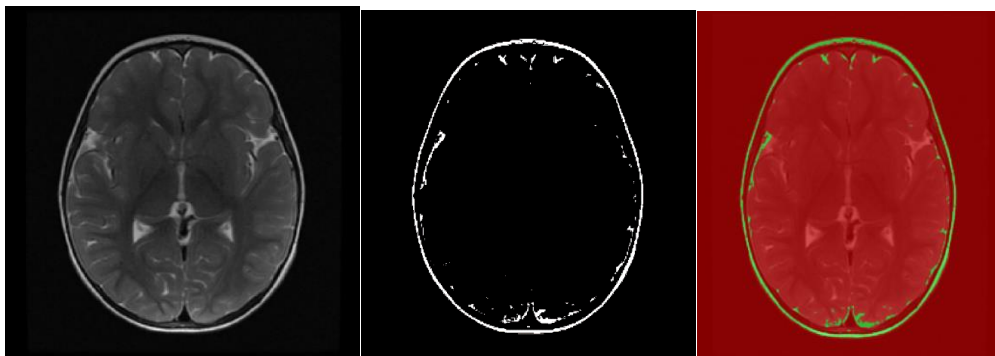Figure 4.11. Test illustration 1
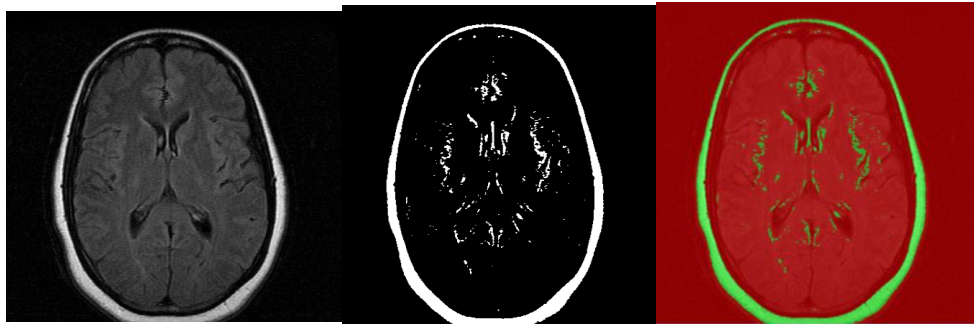

Figure 4.12. Test illustration 2

Figure 4.13. Test illustration 3

The positive tumor detection accuracy was selected for storing the" best" model during training. Precision and recall were chosen for details on how the network evaluates data. Finally, AUC is selected as the overall performance measure as it works similarly to accuracy but further considers the degree of certainty for the predictions. The convolutional neural network shows a precision of 0.98, which indicates that when the network diagnoses a patient with a brain tumor, CNN will get it right 98% of the time. This is of interest because it urges caution when using the network. If CNN is used blindly, it would have a 2% chance of giving the wrong diagnosis. This can be costly for the hospital because resources that do not help the patient can be spent. Furthermore, recall indicates that of all the patients with a brain tumor, CNN will detect 98% of them. With collaboration and the critical use of CNN, this gap can be further reduced. The visualization closes the gap between the health professional and the model by giving an idea of how CNN made its decision. Figures 4.14, 4.15 and 4.16 showed the input image of the brain, segmented image of the brain, and brain tumor being detected and classified within the region of interest (ROI) using the CNN approach
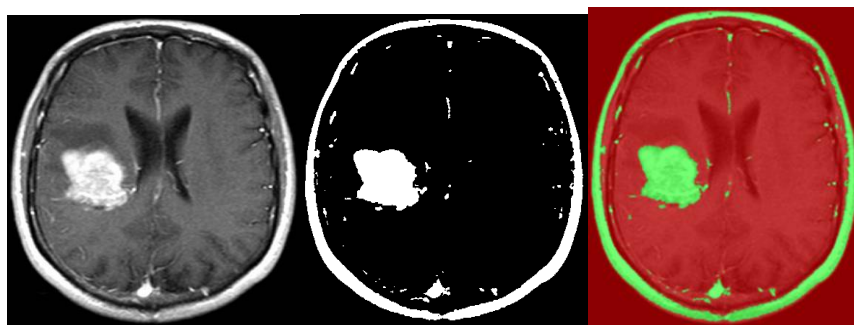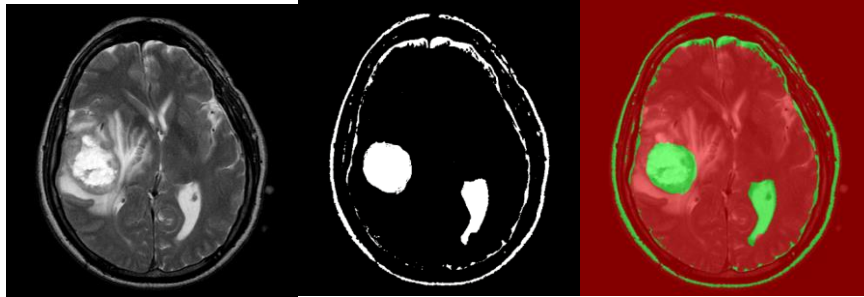

Figure 4.14. Test illustration 4

Figure 4.15. Test illustration 5
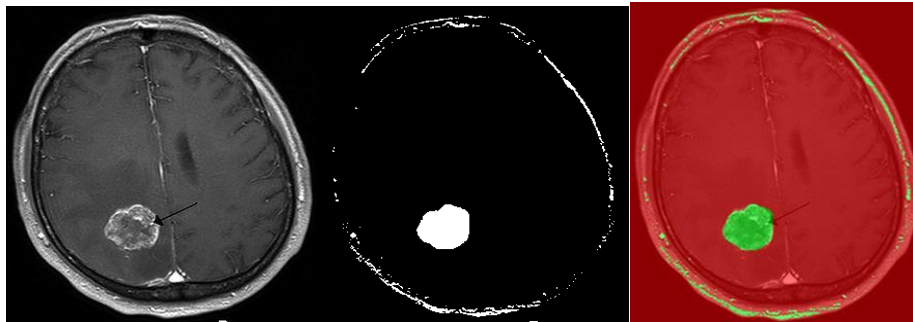
Figure 4.16. Test illustration 6

The results reveal that deep convolution performs better than simple convolution on all metrics when trained on the Kaggle dataset. Recall makes up the most significant difference of all the metrics measured, with a 0.01 difference in the mean recall. This is reflected in their AUC values, where the deep convolution neural network performs significantly better in detecting and classifying brain tumor disease. Furthermore, for the Kaggle dataset, the CNN model was trained with a randomly initialized train/test split in the ratio of approximately 70/20 and 10 separately for validation. This was done by collecting all cases into one array, shuffling them, and finally splitting the array so that both partitions had the same number of issues as they originally had. Finally, the shuffled indices were stored with the model to ensure the evaluation process would not use any training cases.

Table 4.1. CNN accuracy metrics results are shown in fractions

Metric	Convolutional neural network	Artificial Neural Network
Accuracy	0.97917 ± 0.025039	0.91667 ± 0.028464
Precision	0.98361 ± 0.019689	0.98554 ± 0.024118
Recall	0.98541 ± 0.026435	0.88958 ± 0.055941
AUC	**0.99765 ± 0.0036011**	**0.98993 ± 0.0063338**

Table 4.2. The Brain tumor images list with risks

Sample Image	Brain tumor Risk
IMG1.jpg	0.28218
IMG2.jpg	0.34816
IMG3.jpg	0.027847
IMG4.jpg	0.28081
IMG5.jpg	0.28086
IMG6.jpg	0.77814
IMG7.jpg	0.23869
IMG8.jpg	0.35365
IMG9.jpg	0.28825
IMG10.jpg	0.24779
IMG11.jpg	0.018874
IMG12.jpg	0.22376
IMG13.jpg	0.23201
IMG14.jpg	0.3038
IMG15.jpg	0.24816
IMG16.jpg	0.24682
IMG17.jpg	0.37032
IMG18.jpg	0.39568
IMG19.jpg	0.24506
IMG20.jpg	0.6983

The matrices of brain tumor disease detection and classification in the framework had to be created based on descriptions on CNN. Max pooling already finds the highest contributing values. Thus one only needs to go back through the max pool layer from a discriminative location to find the following discriminative place. Batch normalization normalizes the values, which means the highest contributing values remain the same. In this case, the discriminating locations got passed on to the next layer.

Table 4.3. Compare accuracy in same dataset

Cites	Model	Accurcy %
[56]	DCNN	98.97
[57]	RCNN	91.66
[58]	CNN	97.13
[59]	CNN	96.0
[60]	CNN	96.0
Proposed	**CNN**	**99.7%**

4.2. DISCUSSION

Convolutional neural networks (CNN) are effective when working with imagery data consisting of many examples, as shown in Table 6, A general comparison between several existing systems with our proposed architecture.

Table 4.4. A general comparison table

Cited	Brain tumor Disease Detection		
	Architecture	Accuracy	Dataset
[61]	DBN	95.78 %	BRATS
[62]	LSTM	99.23 %	MRS dataset
[63]	SVM	78 %	Rhizome Image
[64]	LSTM-based learning	97%	BRATS
	CNN	99.76 %	Kaggle

In other published papers, we have evaluated existing systems that detect and classify brain tumours with reasonable accuracy. Comparing this to the AUC value, one can argue that if CNN is ever used in practice, it might be more productive in returning the output probability of a brain tumor. This would provide additional information on uncertainty. This gives a good lesson in being skeptical of the results. Even though CNN performs well, signs of weakness were revealed through visualization. On the positive side, the tools used to make this discovery show the usefulness of visualization and deep learning methods.

A system displaying the output probability and visualization can ease the work of health professionals and reduce uncertainty, making it a more viable tool to use in practice.

Some of the significant points for discussion are provided following:

- Like many related works, CNN shows that deep learning is a viable approach to detecting and classifying brain tumor disease.
- Testing the deep convolutional neural network on brain vessel coherence tomography (BVCT) scans with promising results.
- A CNN architecture, without any pre-training, trained on one GPU, can perform at a state-of-the-art level.
- The use of CNN fixations to display symptoms from a medical classification with CNN.
- Implementation and use of CNN grab more accurate results for making an expert system.

The introduction and use of a new dataset from an open-source repository,' Kaggle,' was a good experience for visualizing results

4.3. CONCLUSION

In this novel research work, we have developed an intelligence expert system to detect the most dangerous disease using a convolutional neural network. To conclude this research, we observed CNN techniques and networks for training at 70% of data, testing at 20%, and validation at the rest of the 10% of data. This research was vital as it worked on the CNN patterns of different comparisons with existing deep learning and machine learning techniques. The system's main strength was that the CNN technique could be set by considering the imaging network for comparison recognition and applying it to learn using only the un-provided instance as input. CNN is very important and has high accuracy and low complexity. Still, it can be uncomfortable since it needs physical contact between the user and the device using CNN layers. The

CNN technique is computationally less demanding, doesn't require physical contact, and is friendly compared to active devices.

Deep learning-based approaches rely on tracking the natural user movements without requiring users to wear or hold any sensor for series classification. This research also presents a method for comparing patterns to improve their robustness in classifying provided comparison instances for chronic brain tumor disease detection. This works shows that the overall accuracy of deep learning models can be mitigated with the convolutional neural network technique and achieve an accuracy of up to 92.78% with an execution time of 5.33s only. For the confusion matrix of brain tumor detection and classification, 97.9% was recorded, and the precision of 98.3% was accounted for with a recall of 98.5%. Ultimately, an AUC of 99.76% was recorded and calculated for this dedicated research work.

4.4. FUTURE RECOMMENDATIONS

In the future, three aspects will be of the highest interest that needs improvement in future:

- Progress of CNN with adding more layers to make it DCNN.
- Improvement of visualization and improvement of the data.
- Progress by creating an expert system more heterogeneous with more predictions of diseases under a single system.

One way that might improve CNN's performance would be depth. With more computer resources, a deeper network can be tested. A convolutional neural network might perform better with a deeper network. On top of this, one can add skip connections to uphold performance once the network gets deeper. With more computer resources, bigger mini-batches could potentially improve training as well. Introducing some pre-processing such as noise reduction, might aid in the cases where DCNN makes the correct prediction but is based on strange focus points.

A final suggestion is to proceed with a semi-supervised method where only a tiny part of the dataset needs labeling. This method allows for more training without the need for doctors manually label new cases in the dataset.

In the future, a technique capable of doing so would bring valuable insight into the reasoning of a model. One part of CNN fixations that can potentially be improved is the localization map in its architecture. One could attempt to further adjust the sigma parameter in the 3D Gaussian blur. This parameter affects how far the "blobs" of interest stretch over the map for a brain tumor or other disease detection and classification. One could also attempt to perform 2D Gaussian blur for each slice or another technique to display the density of points.

A more extensive dataset with more variation can better prepare CNN for real-life use. One of the best ways to improve a deep learning method is to give it more data. The Kaggle dataset could eventually become a new benchmark in the field. The dataset can grow significantly larger once permissions are granted. Benchmarking allows for better comparison between approaches which is advantageous for the field. We have also discussed testing against human professionals. Comparison to human performance is among the best indicators of how well an automated system could perform in practice. A dataset with human performance statistics and specific guidelines could be an excellent benchmark for the field.

REFERENCES

1. GURUNATHAN, Akila; KRISHNAN, Batri. "Detection and diagnosis of brain tumors using deep learning convolutional neural networks" *International Journal of Imaging Systems and Technology* (2021)

2. HS, Santhosh Kumar; KARIBASAPPA, K. "An approach for brain tumour detection based on dual-tree complex Gabor wavelet transform and neural network using Hadoop big data analysis" *Multimedia Tools and Applications* (2022).

3. KIRAN, P.; PARAMES HACHARI, B. D. "Resource Optimized Selective Image Encryption of Medical Images Using Multiple Chaotic Systems" *Microprocessors and Microsystems* (2022)

4. SHAN, Chengxiang; LI, Qiang; WANG, Ching-Hsin. "Brain Tumor Segmentation using Automatic 3D Multi-channel Feature Selection Convolutional Neural Network" *Journal of Imaging Science and Technology* (2022)

5. ILHAN, Ahmet; SEKEROGLU, Boran; ABIYEV, Rahib "Brain tumor segmentation in MRI images using nonparametric localization and enhancement methods with U-net" *International Journal of Computer Assisted Radiology and Surgery* (2022)

6. SALVI, Massimo, et al. "The impact of pre-and post-image processing techniques on deep learning frameworks: A comprehensive review for digital pathology image analysis" *Computers in Biology and Medicine* (2021)

7. CHEN, Hanting, et al. "Pre-trained image processing transformer. In: Proceedings of the IEEE/CVF" *Conference on Computer Vision and Pattern Recognition* (2021)

8. SCHAPIRO, Denis, et al. MCMICRO " A scalable, modular image-processing pipeline for multiplexed tissue imaging" *Nature methods* (2022)

9. XIONG, Yihui; ZUO, Renguang "Robust feature extraction for geochemical anomaly recognition using a stacked convolutional denoising autoencoder" *Mathematical Geosciences* (2022)

10. PILLAI, Abhiram, et al." Breast Cancer Detection in Mammograms Using Deep Learning. In: Applied Information Processing Systems" (2022)

11. SMITH, Melvyn L.; SMITH, Lyndon N.; HANSEN, Mark F "The quiet revolution in machine vision-a state-of-the-art survey paper, including historical review, perspectives, and future directions" *Computers in Industry* (2021)

12. QI, Ping, et al. "Integrating functional data analysis with case-based reasoning for hypertension prognosis and diagnosis based on real-world electronic health records" ***BMC Medical Informatics and Decision Making*** (2022)

13. SAIBENE, Aurora; ASSALE, Michela; GILTRI, Marta. "Expert systems: Definitions, advantages and issues in medical field applications. Expert Systems with Applications" (2021)

14. ALHARAN, Abbas FH; ALI, Nabeel Salih; ALGELAL, Zahraa M. "AN ADAPTIVE NEURO-FUZZY INFERENCE SYSTEM AND PRINCIPAL COMPONENT ANALYSIS: A HYBRIDIZED METHOD FOR VIRAL HEPATITIS DIAGNOSIS SYSTEM" ***Colloquium-journal. Голопристанський міськрайонний центр зайнятості***, (2022).

15. MCMONNIES, Charles W. "Why the symptoms and objective signs of dry eye disease may not correlate" **Journal of Optometry** (2021)

16. DHARMAWAN, Dhimas Arief. "Assessing fairness in performance evaluation of publicly available retinal blood vessel segmentation algorithms" ***Journal of Medical Engineering & Technology*** (2021).

17. ABDULSAHIB, Aws A., et al. "Comprehensive review of retinal blood vessel segmentation and classification techniques: intelligent solutions for green computing in medical images, current challenges, open issues, and knowledge gaps in fundus medical images" ***Network Modeling Analysis in Health Informatics and Bioinformatic*** (2021).

18. FIGUEROA, Anna G., et al. "Levodopa positively affects neovascular age-related macular degeneration" ***The American journal of medicine*** (2021).

19. VIVEK, Pratyush, et al. "CNN Models and Machine Learning Classifiers for Analysis of Goiter Disease. In: 2022 IEEE International Students" ***Conference on Electrical, Electronics and Computer Science (SCEECS). IEEE*** (2022).

20. LAHMOOD HAMEED, Fakhri; DAKKAK, Omar "Brain Tumor Detection and Classification Using Convolutional Neural Network (CNN)" ***International Congress on Human-Computer Interaction, Optimization and Robotic Applications (HORA). IEEE*** (2022)

21. REZAIE, Tayebeh, et al. "Adult-onset primary open-angle glaucoma caused by mutations in optineurin" (2002).

22. HEINSCH, Milena, et al. "Supporting friends and family of adults with a primary brain tumour: A systematic review" ***Health & Social Care in the Community*** (2022)

23. HUANG, Zheng, et al. "AMF-Net: An adaptive multisequence fusing neural network for multi-modality brain tumor diagnosis" ***Biomedical Signal Processing and Control*** (2022)

24. Ramdas Vankdothu, Mohd Abdul Hameed, Husnah Fatima, "A Brain Tumor Identification and Classification Using Deep Learning based on CNN-LSTM Method" *Computers and Electrical Engineering* (2022)

25. S K Rajeev, M. Pallikonda Rajasekaran, G. Vishnuvarthanan, T. Arunprasath, "A biologically-inspired hybrid deep learning approach for brain tumor classification from magnetic resonance imaging using improved gabor wavelet transform and Elmann-BiLSTM network" *Biomedical Signal Processing and Control*, (2022)

26. R. Sindhiya Devi, B. Perumal, M. Pallikonda Rajasekaran, "A hybrid deep learning based brain tumor classification and segmentation by stationary wavelet packet transform and adaptive kernel fuzzy c means clustering" *Advances in Engineering Software*, (2022)

27. LEI, Xiaoliang, et al. "Brain tumor segmentation in MR images using a sparse constrained level set algorithm" *Expert Systems with Applications*, (2022).

28. SHINY, K. V., et al. "Study and Analysis of Various Automatic Brain Tumour Segmentation and Classification: A Challenging Overview" *Turkish Journal of Computer and Mathematics Education (TURCOMAT)* (2022)

29. UGALE, Vivek Dhruv; PAWAR, Swati S.; PAWAR, Sheetal. "Brain Tumour Detection using Image Processing". *In: 2022 IEEE 11th International Conference on Communication Systems and Network Technologies (CSNT). IEEE* (2022)

30. PURE, M. Tech Scholar Nayan; TIWARI, Ashish. "MRI Image Segmentation and Classification Using KFCM and Convolution Neural Networks" (2021)

31. MZOUGHI, Hiba, et al. "Towards a computer aided diagnosis (CAD) for brain MRI glioblastomas tumor exploration based on a deep convolutional neuronal networks (D-CNN) architectures" *Multimedia Tools and Applications* (2021)

32. Sudharani, K., Sarma, T. C., & Rasad, K. S "Intelligent Brain Tumor lesion classification and identification from MRI images using k-NN technique" *In 2015 International Conference on Control, Instrumentation, Communication and Computational Technologies (ICCICCT) IEEE* (2015)

33. Ahmmed, R., Swakshar, A. S., Hossain, M. F., & Rafiq, M. A"Classification of tumors and it stages in brain MRI using support vector machine and artificial neural network". *In 2017 International Conference on Electrical, Computer and Communication Engineering (ECCE)* (2015)

34. Machhale, K., Nandpuru, H. B., Kapur, V., & Kosta, L " MRI brain cancer classification using hybrid classifier (SVM-KNN)" *In 2015 International Conference on Industrial Instrumentation and Control (ICIC)* (2015)

35. Melanie Bauer, Celine Berger, Kathrin Gerlach, Eva Scheurer, Claudia Lenz, Post "mortem evaluation of brain edema using quantitative MRI", *Forensic Science International* (2022)

36. Shinsuke Koike, Saori C. Tanaka, Tomohisa Okada, Toshihiko Aso, et al. "Brain/MINDS beyond human brain MRI project: A protocol for multi-level harmonization across brain disorders throughout the lifespan, NeuroImage: Clinical" (2022)

37. Noman Haleem, Matteo Bustreo, Alessio Del Bue, "A computer vision based online quality control system for textile yarns" *Computers in Industry*, (2022).

38. Suman Paneru, Idris Jeelani, "Computer vision applications in construction: Current state, opportunities & challenges" (2021)

39. Prashant Saurabh Minz, Charanjiv Singh Saini, "Comparison of computer vision system and colour spectrophotometer for colour measurement of mozzarella cheese, " (2021).

40. N. Rozendorn, G. Greenberg, O. Madgar, I. Gluck, M. Vered, E. Alon, A. "Dobriyan , Preoperative MRI for oral tongue squamous cell carcinoma: timing and correlation to histopathology" *International Journal of Oral and Maxillofacial Surgery* (2022)

41. SCHÖLKOPF, Bernhard. "Causality for machine learning. In: Probabilistic and Causal Inference: The Works of Judea Pearl" (2022)

42. MURPHY, Kevin P. "Probabilistic machine learning: an introduction. MIT press" (2022)

43. PHOON, Kok-Kwang; ZHANG, Wengang. "Future of machine learning in geotechnics. Georisk: Assessment and Management of Risk for Engineered Systems and Geohazards" (2022)

44. BHAT, Nayeem Ahmad; FAROOQ, Sheikh Umar. "An Improved Method for Training Data Selection for Cross-Project Defect Prediction. Arabian Journal for Science and Engineering" (2022)

45. KOSTOPOULOS, Georgios; KOTSIANTIS, Sotiris "Exploiting semi-supervised learning in the education field: A critical survey" *Advances in Machine Learning/Deep Learning-Based Technologies* (2022)

46. BHAGYA RAJ, G. V. S.; DASH, Kshirod K. "Comprehensive study on applications of artificial neural network in food process modeling" Critical Reviews in Food Science and Nutrition (2022)

47. Available Online: *https://www.kaggle.com/navoneel/brain-mri-images-for-brain-tumor-detection*

48. Available Online : *https : // docs . ecognition . com / v9.5.0 / eCognition_documentation / Reference%20Book/23%20Convolutional%20Neural%20Network%20Algorithms/Convolutional%20Neural%20Network%20Algorithms.htm*

49. Acharya, U.R.; Sree, S.V.; Ribeiro, R.; Krishnamurthi, G.; Marinho, R.T.; Sanches, J.; Suri, J.S. "Data mining framework for brain tumor disease classification using SVM: A hybrid feature extraction paradigm" (2016)

50. E. Dervisevic, S. Pavljasevic, A. Dervisevic, S.S. Kasumovic, "Challenges In Early Brain tumor Detection using LTSM and RNN," (2016)

51. R. Bock, J. Meier, L. G. Nyl, G. Michelson, "Brain tumor risk index: automated brain tumor detection from color chronic images using Deep Belief Network DBN," *Medical Image Analysis* (2017)

52. *https://eng.snu.ac.kr/online/eng_med/06_%eb%b0%95%ec%b2%a0%ea%b8%b0%ec%9c%a4%ec%84%b1%eb%a1%9c_%ea%b5%90%ec%88%98%eb%8b%98.pdf*

53. *https://machinethink.net/blog/googles-mobile-net-architecture-on-iphone/*

54. Akram, M. U., & Usman. "Computer aided system for brain tumor detection and segmentation" *In International conference on Computer networks and information technology* (2022)

55. VEERAMUTHU, A., et al. "MRI brain tumor image classification using a combined feature and image-based classifier" *Frontiers in Psychology*, 2022

56. Salçin, K "Detection and classification of brain tumours from MRI images using faster R-CNN" (2022)

57. BRINDHA, P. Gokila, et al. "Brain tumor detection from MRI images using deep learning techniques" *In: IOP Conference Series: Materials Science and Engineering* (2021)

58. Younis, A., Qiang, L., Nyatega, C. O., Adamu, M. J., & Kawuwa, H. B. "Brain Tumor Analysis Using Deep Learning and VGG-16 Ensembling Learning Approaches" (2022)

59. Dehkordi, A. A., Hashemi, M., Neshat, M., Mirjalili, S., & Sadiq, A. S. "Brain Tumor Detection and Classification Using a New Evolutionary Convolutional Neural Network" (2022)

60. T. A. Jemimma and Y. J. V. Raj, "Brain Tumor Segmentation and Classification Using Deep Belief Network," Second International Conference on Intelligent Computing and Control Systems (ICICCS)" (2018)

61. Dandıl, E., & Karaca, S. "Detection of pseudo brain tumors via stacked LSTM neural networks using MR spectroscopy signals" *Biocybernetics and Biomedical Engineering* (2021)

62. Mawaddah, S., Mufid, M. R., Basofi, A., Fiyanto, A., Aditama, D., & Nurlaila, N. "Rhizome Image Classification Using Support Vector Machine". *In International Conference on Applied Science and Technology on Social Science* (2021)

63. Amin, Javaria & Sharif, Muhammad & Raza, Mudassar & Saba, Tanzila & Sial, Rafiq & Shad, Shafqat "Brain tumor detection: a long short-term memory (LSTM)-based learning model" *Neural Computing and Applications*. (2020)

APPENDIX A.

THE IMPORTANT CODES

```matlab
brain(varargin)
function varargout = brain(varargin)
gui_Singleton = 1;
gui_State = struct('gui_Name',       mfilename, ...
   'gui_Singleton',  gui_Singleton, ...
   'gui_OpeningFcn', @brain_OpeningFcn, ...
   'gui_OutputFcn',  @brain_OutputFcn, ...
   'gui_LayoutFcn',  [] , ...
   'gui_Callback',   []);
if nargin && ischar(varargin{1})
   gui_State.gui_Callback = str2func(varargin{1});
end
if nargout
   [varargout{1:nargout}] = gui_mainfcn(gui_State, varargin{:});
else
   gui_mainfcn(gui_State, varargin{:});
end
% --- Executes just before brain is made visible.
function brain_OpeningFcn(hObject, eventdata, handles, varargin)
handles.folder_name=[cd '\images.new'];%dataset.mat
handles.imageDataset = load([cd '\corel_1000_dataset.mat']);
handles.numOfReturnedImages = 10+1;
% Choose default command line output for CBIR
handles.output = hObject;
% Update handles structure
guidata(hObject, handles);
% --- Outputs from this function are returned to the command line.
function varargout = brain_OutputFcn(hObject, eventdata, handles)
varargout{1} = handles.output;
% --- Executes on button press in pushbutton1.
function pushbutton1_Callback(hObject, eventdata, handles)
[query_fname, query_pathname] = uigetfile('*.jpg; *.png; *.bmp');
if (query_fname ~= 0)
```

```matlab
query_fullpath = strcat(query_pathname, query_fname);
imgInfo = imfinfo(query_fullpath);
[pathstr, name, ext] = fileparts(query_fullpath); % fiparts returns char type
if ( strcmpi(ext, '.jpg') == 1 || strcmpi(ext, '.png') == 1 || strcmpi(ext, '.bmp') == 1 )
    queryImage = imread( fullfile( pathstr, strcat(name, ext) ) );
    % display query image
    axes(handles.axes2)
    imshow(queryImage, []);
    queryImage = imresize(queryImage, [384 256]); %make the image size standard

    disp(imgInfo);
    disp(name);
    % update global variables to be used in next stage

    handles.queryImage = name;
    handles.img_ext = ext;
    guidata(hObject, handles);
  else
    errordlg('You have not selected the correct file type');
  end
else
  return;
end
% --- Executes on button press in pushbutton2.
function pushbutton2_Callback(hObject, eventdata, handles)
%Define parameters to be used in search
numOfReturnedImgs = handles.numOfReturnedImages;
I = handles.queryImage;
str = '.jpg';
I=append(I,str);
training(I);
```

Training

```matlab
function training(image)
dbimg = 'image.new';
% Query Image
% imgName = '1.jpg';
imgName = image;
numSim = 5; %Find n number of closest similar images

I = [dbimg '/' imgName];
Qimg = imread(I);

% Query Image: Extract Features
feature_query = featureVectorImg(Qimg);
disp(['Feature Extraction of Query Image done']);
load('corel_1000.mat');
list_img = dir(dbimg);
for i=1:size(list_img,1)
    n = list_img(i).name;
    imgname = [dbimg '/' n];
    if (n(1) ~= '.')
        ed(i,:) = euclidian_dist(feature_query, fvect(i,:));
    end
end
m = max(ed);
mod_ed = zeros(size(ed,1), 1);
for i=1:size(ed,1)
    if (ed(i)==0)
        mod_ed(i) = 2*m;
    else
        mod_ed(i) = ed(i);
    end
end
```

```matlab
figure,
imshow(imread(I));
title('Query Image');

for i=1:numSim
    %Based on distance calculation find closest object with CNN
    idx = find(mod_ed == min(mod_ed));

    figure,
    imshow(imread([dbimg '/' list_img(idx).name]))
    title(['Found similar image :' num2str(i)]);

    mod_ed(idx) = m;
end

% clear filename idx imagepath imgname imgpath m
end
function dist = euclidian_dist(x1, x2)
sub = x1-x2;
dist = sqrt(sub * sub');
end
```

Testing

```matlab
function varargout = testing(varargin)
% Begin initialization code - DO NOT EDIT
gui_Singleton = 1;
gui_State = struct('gui_Name',      mfilename, ...
    'gui_Singleton',  gui_Singleton, ...
    'gui_OpeningFcn', @CBIR_OpeningFcn, ...
    'gui_OutputFcn',  @CBIR_OutputFcn, ...
    'gui_LayoutFcn',  [] , ...
```

```
    'gui_Callback',   []);
if nargin && ischar(varargin{1})
    gui_State.gui_Callback = str2func(varargin{1});
end

if nargout
    [varargout{1:nargout}] = gui_mainfcn(gui_State, varargin{:});
else
    gui_mainfcn(gui_State, varargin{:});
end
% End initialization code - DO NOT EDIT
% --- Executes just before CBIR is made visible.

function CBIR_OpeningFcn(hObject, eventdata, handles, varargin)
handles.folder_name=[cd '\images.new'];%dataset.mat
handles.imageDataset = load([cd '\fvect.mat']);
handles.numOfReturnedImages = 10+1;
% Choose default command line output for CBIR
handles.output = hObject;

% Update handles structure
guidata(hObject, handles);

% --- Outputs from this function are returned to the command line.
function varargout = CBIR_OutputFcn(hObject, eventdata, handles)
varargout{1} = handles.output;
% --- Executes on button press in pushbutton1.
function pushbutton1_Callback(hObject, eventdata, handles)

[query_fname, query_pathname] = uigetfile('*.jpg; *.png; *.bmp');
if (query_fname ~= 0)
    query_fullpath = strcat(query_pathname, query_fname);
    imgInfo = imfinfo(query_fullpath);
```

```matlab
[pathstr, name, ext] = fileparts(query_fullpath); % fiparts returns char type
if ( strcmpi(ext, '.jpg') == 1 || strcmpi(ext, '.png') == 1 || strcmpi(ext, '.bmp') == 1 )
    queryImage = imread( fullfile( pathstr, strcat(name, ext) ) );
    % display query image
    axes(handles.axes2)
    imshow(queryImage, []);
    queryImage = imresize(queryImage, [384 256]); %make the image size standard
    % extract query image features
    queryImageFeature=Extract_features(queryImage,imgInfo,name);
    disp(imgInfo);
    disp(name);
    % update global variables to be used in next stage
    handles.queryImageFeature = queryImageFeature;
    handles.img_ext = ext;
    guidata(hObject, handles);
else
    errordlg('You have not selected the correct file type');
end
else
    return;
end

featureVectorImg

function varargout = testing(varargin)
% Begin initialization code - DO NOT EDIT
gui_Singleton = 1;
gui_State = struct('gui_Name',       mfilename, ...
    'gui_Singleton',  gui_Singleton, ...
    'gui_OpeningFcn', @CBIR_OpeningFcn, ...
    'gui_OutputFcn',  @CBIR_OutputFcn, ...
    'gui_LayoutFcn',  [] , ...
    'gui_Callback',   []);
```

```matlab
if nargin && ischar(varargin{1})
    gui_State.gui_Callback = str2func(varargin{1});
end

if nargout
    [varargout{1:nargout}] = gui_mainfcn(gui_State, varargin{:});
else
    gui_mainfcn(gui_State, varargin{:});
end
% End initialization code - DO NOT EDIT
% --- Executes just before CBIR is made visible.

function CBIR_OpeningFcn(hObject, eventdata, handles, varargin)
handles.folder_name=[cd '\images.new'];%dataset.mat
handles.imageDataset = load([cd '\fvect.mat']);
handles.numOfReturnedImages = 10+1;
% Choose default command line output for CBIR
handles.output = hObject;

% Update handles structure
guidata(hObject, handles);

% --- Outputs from this function are returned to the command line.
function varargout = CBIR_OutputFcn(hObject, eventdata, handles)
varargout{1} = handles.output;


% --- Executes on button press in pushbutton1.
function pushbutton1_Callback(hObject, eventdata, handles)

[query_fname, query_pathname] = uigetfile('*.jpg; *.png; *.bmp');
if (query_fname ~= 0)
    query_fullpath = strcat(query_pathname, query_fname);
```

```matlab
    imgInfo = imfinfo(query_fullpath);
    [pathstr, name, ext] = fileparts(query_fullpath); % fiparts returns char type
    if ( strcmpi(ext, '.jpg') == 1 || strcmpi(ext, '.png') == 1 || strcmpi(ext, '.bmp') == 1 )
        queryImage = imread( fullfile( pathstr, strcat(name, ext) ) );
        % display query image
        axes(handles.axes2)
        imshow(queryImage, []);
        queryImage = imresize(queryImage, [384 256]); %make the image size standard
        % extract query image features
        queryImageFeature=Extract_features(queryImage,imgInfo,name);
        disp(imgInfo);
        disp(name);
        % update global variables to be used in next stage
        handles.queryImageFeature = queryImageFeature;
        handles.img_ext = ext;
        guidata(hObject, handles);
    else
        errordlg('You have not selected the correct file type');
    end
else
    return;
end


Feature extrctor


dbimg = 'image.new'; %Database/Folder of images~1000; 100 samples each


% Find Feature Vector of each image
list_of_imgs = dir(dbimg);
for i=1:size(list_of_imgs,1)
    n = list_of_imgs(i).name;
    imagename = [dbimg '/' n];
    if (n(1) ~= '.')
```

```
        findImgfv = imread(imagename);
        fvect(i, :) = featureVectorImg(findImgfv);
        disp(['Feature vector extracted for image: ' imagename]);
    end
end

save('fvect.mat','fvect');
```

CNN

```
% folder for the images
imgpath = '/brain_tumor_dataset/Yes/Y32';

% query image. Change your image name here
filename = 'test.jpg';

% threshold set for minimum eucledian distance that is considered similar
th = 3.6e3;

imagepath = [imgpath '/' filename];
imgquery = imread(imagepath);

% get feature vectors
feature_query = featureVector(imgquery);
disp(['feature fector for query image has been extracted']);

% similarity matching using Eucledian distance
imglist = dir(imgpath);
for i=1:size(imglist,1)
    n = imglist(i).name;
    imgname = [imgpath '/' n];
    if (n(1) ~= '.')
```

```matlab
        % only find vector for other file than the query
      if (~strcmp(imgname, imagepath))
         imgfind = imread(imgname);
         fvect(i, :) = featureVector(imgfind);
         eudist(i, :) = euclid(feature_query, fvect(i,:));
         disp(['feature fector and eucledian distance for ' imgname ' has been
extracted']);
      end
   end
end

% choose highest similarity
% zero should not be choosen, so make it any number biggest
m = max(eudist);

modeudist = zeros(size(eudist,1), 1);
for i=1:size(eudist,1)
   if (eudist(i)==0)
      modeudist(i) = 2*m;
   else
      modeudist(i) = eudist(i);
   end
end

% find closest object according to eucledian distance
idxclosest = find(modeudist == min(modeudist));

% show query image
figure,
imshow(imread(imagepath));
title('query image');

% find any image closest with certain threshold (th variable)
```

```
idxchosen = find(modeudist < th);

for i=1:length(idxchosen)
    figure,
    imshow(imread([imgpath '/' imglist(idxchosen(i)).name]));
    title(['closest image on rank ' num2str(i)]);
end



segmentation

dbimg = 'image.new';
% Query Image
imgName = '1.jpg';

numSim = 5; %Find n number of closest similar images

I = [dbimg '/' imgName];
Qimg = imread(I);

% Query Image: Extract Features
feature_query = featureVectorImg(Qimg);
disp(['Feature Extraction of Query Image done']);
load('fvect.mat');

list_img = dir(dbimg);
for i=1:size(list_img,1)
    n = list_img(i).name;
    imgname = [dbimg '/' n];
    if (n(1) ~= '.')
        ed(i,:) = euclidian_dist(feature_query, fvect(i,:));
    end
```

```matlab
end


m = max(ed);
mod_ed = zeros(size(ed,1), 1);
for i=1:size(ed,1)
   if (ed(i)==0)
      mod_ed(i) = 2*m;
   else
      mod_ed(i) = ed(i);
   end
end


figure,
imshow(imread(I));
title('Query Image');


for i=1:numSim
   %Based on distance calculation find closest object
   idx = find(mod_ed == min(mod_ed));


   figure,
   imshow(imread([dbimg '/' list_img(idx).name]))
   title(['Found similar image :' num2str(i)]);


   mod_ed(idx) = m;
end


% clear filename idx imagepath imgname imgpath m


function dist = euclidian_dist(x1, x2)
sub = x1-x2;
dist = sqrt(sub * sub');
end
```

RESUME

Fakhri lahmood Hameed was graduated from software engineering department in musal, Al-Hadba'a University College. Started Master of computer engineering in Karabük since 2019-2020 and work in detergent company in salahaldeen