ORIGINAL RESEARCH ARTICLE

Detection of normal and abnormal brain tumor MRI images using machine learning approaches

Royyuru Srikanth[1,*], N. Kanya[2], P. S. Raja Kumar[3]

[1] *Department of CSE, Dr MGR Educational and Research Institute, Maduravoyal, Chennai 600095, India*

[2] *Department of Information Technology, Dr MGR Educational and Research Institute, Maduravoyal, Chennai 600095, India*

[3] *Department of CSE, Dr MGR Educational and Research Institute, Maduravoyal, Chennai 600095, India*

* Corresponding author: Royyuru Srikanth, royyurusrikanth@gmail.com

ABSTRACT

Without image processing, the modern technological world we live in today would be completely different. Different applications can be found in many different areas, including as medicine, remote sensing, computer vision, and more. Brain tumours occur because of the abnormal growth of brain tissue. Therefore, it is crucial to surgically remove the tumor's component that has spread throughout the brain. The creation of images of the human body's internal organs and structures depends on numerous factors, one of which is the use of Magnetic Resonance Imaging (MRI), one of the many medical imaging techniques. Segmenting images is a challenging task in the modern medical field. The tumor's location and sizes can be detected with more accuracy with the help of a segmentation performed on MRI slices. In this paper, we propose the Adaptive Convex Region Contour (ACRC) algorithm, a novel method for achieving such requirements. Here, we use the Support Vector Machine, often known as SVM, to identify slices and determine whether they are normal or abnormal. Once the SVM results are in, the off-kilter slices will be included into the analysis. Since the human body already has a complex anatomy in 3D. It's disappointing because MRI slices can only provide images in a plain, 2D plane. Because of its 3D structure, the tumor's actual shape cannot be detected from a surface image. This means that the transformation from 2D to 3D is important, as it provides necessary data to the surgeons doing the operation. The Rapid Mode Image Matching (RMIM) algorithm should be used when constructing a 3D reconstruction model. Immediately after the 3D model is completed being created, a rough estimate of the tumor's original volume is generated. The methodological consideration was conducted in the simulated MATLAB software. It was determined from the data that the proposed method is better to the current establishment methodologies in terms of accuracy. **Objective:** This paper aims to address the need for accurate segmentation of brain tumors in Magnetic Resonance Imaging (MRI) slices. The primary research question revolves around developing a novel segmentation method, the Adaptive Convex Region Contour (ACRC) algorithm, to improve the precision of tumor detection by incorporating a Support Vector Machine (SVM) for identifying abnormal slices. **Methods:** The proposed approach involves utilizing the SVM to classify MRI slices as either normal or abnormal. The abnormal slices, detected by SVM, are subjected to further analysis. To overcome the limitation of MRI producing 2D images for the inherently 3D human anatomy, a transformation from 2D to 3D is crucial. The Rapid Mode Image Matching (RMIM) algorithm is adopted to construct a 3D reconstruction model of the brain and its tumor. This model allows surgeons to obtain a more accurate understanding of the tumor's actual 3D shape. **Results:** The methodology was implemented and evaluated using simulated MATLAB software. The results demonstrate that the proposed ACRC algorithm, combined with SVM-based abnormal slice identification and subsequent 3D reconstruction using RMIM, outperforms existing methodologies in terms of accuracy. The 3D reconstruction provides valuable insights into the tumor's shape, aiding surgical planning. **Conclusions:** In conclusion, the research contributes to the field of medical image processing by presenting a comprehensive approach for brain tumor segmentation and 3D reconstruction. The ACRC algorithm, in conjunction with SVM and RMIM, enhances the accuracy of tumor detection and provides critical 3D information for surgical

procedures. This advancement holds the potential to improve the efficacy of brain tumor surgeries, underscoring the significance of innovative image processing techniques in modern medical applications.

Keywords: SVM; brain tumor; machine learning; segmentation; features extraction

1. Introduction

In this period of extensive analysis, the processing of medical photographs represents a cutting-edge technological advance. Using imaging technology, doctors can find non-invasive methods of care[1].Computed tomography (CT), positron emission tomography (PET), ultrasound, single photon emission computed tomography (SPECT), MRI, and X-ray are all examples of non-invasive imaging technologies used in medicine[2]. MRI provides more precise results in medical diagnosis than CT.Imaging aids in better differentiating the various human soft tissues[3]. At higher levels of image processing, the success or failure of picture segmentation is a defining factor[4]. If higher-level image processing is to be successful, it must first be successful at image segmentation. Our primary focus in this case has been on identifying the tumour in the brain and removing it from the MRI images. In this way, the exact location of the brain tumour can be quickly and easily identified by medical professionals. Medical image processing, in the context of diagnostic imaging, is the application and analysis of human anatomy and physiology captured in 3D. Medical diagnosis, the direction of medical treatments including surgical planning and the basis for scientific researches all make use of these databases. CT and MRI scanners are the most common generators of such data sets. Medical image processing is used by radiologists, engineers, and other medical professionals to learn about patients and patient cohorts by analysing their images. Through the use of techniques like measuring, statistical analysis, and the creation of simulation models that integrate genuine anatomical geometries, we are able to get a detailed understanding of the relationships between human anatomy and medical technology.

What we mean when we talk about an image's "features," however, is the major component that is used to describe the attributes that are inherent to it. Extraction of texture-based features[5] is a method developed to accurately simulate an image's expressive qualities. In order to create a texture co-occurrence matrix, we make use of the image's predefined hybrid features. Additionally, the Gray Level Co-occurrence Matrix (GLCM) is available in the study of Naga et al.[6] and Aswathy et al.[7] Fewer computational resources are needed to put this strategy into action than competing ones. One of the greatest parts of image processing is segmentation, which requires identifying the boundaries between different objects, such as abnormal regions in medical studies. Segmentation refers to the process of dividing an image into smaller, more manageable components for the purpose of analyzing them more precisely. The

primary objective is to reduce the visual image or transform the image into a form best suited for analysis. This method's completed phases become a part of the strategy for detecting objects and boundaries within images. A recent progress in machine learning, the Support Vector Machine (SVM) depends heavily on statistical theory. The SVM has been used across a variety of fields for its ability to focus in on specific research problems while simultaneously reducing the complexity of modelling techniques. The SVM method is effective for dealing with problems of low sample size, nonlinearity, and high dimensionality because it makes use of the ideal hyper plane, which has linear removable characteristics. However, this approach requires a large number of extracted features, which can make precise classification more challenging. During segmentation, cancerous hotshots in a brain tumour can be pinpointed in a 2D image, but this does not provide a very detailed view of the tumour itself.

The human body is a complex, three-dimensional structure (3D). Incorrect disease diagnosis may occur when a three-dimensional structure is reduced to a two-dimensional shape by this process. Therefore, it is essential to create a 3D representation of the tumour area that was segmented. Here, a 3D format has been developed to help with the understanding of 2D MRI scans of tumours. By cherry-picking the appropriate MRI slices, 3D modelling can be generated using a technique called cubic reconstruction. Lastly, the tumor's volume is calculated.

This is how we've decided to allocate our remaining research time and resources. Section II will cover research and development in the field of brain tumour 3D segmentation and reconstruction. Section III discusses the importance of the proposed method, while Section IV describes the resources that would be required to implement it. In section IV, the proposed actions are laid out in detail. Example experiment evaluation is discussed in Section V. The final conclusion is presented at the end of Section VI.

In the era of extensive medical analysis, the processing of medical images stands as a cutting-edge technological advance. This advancement allows doctors to employ non-invasive methods of care through imaging technologies such as Computed Tomography (CT), Positron Emission Tomography (PET), Ultrasound, Single Photon Emission Computed Tomography (SPECT), Magnetic Resonance Imaging (MRI), and X-ray. Among these, MRI stands out for its precision in medical diagnosis, particularly in differentiating various human soft tissues[3].

At higher levels of image processing, the success or failure of picture segmentation becomes a defining factor[4]. Our primary focus lies in the identification and removal of brain tumors from MRI images, enabling medical professionals to swiftly and accurately pinpoint the tumor's location. Medical image processing, within the realm of diagnostic imaging, involves the application and analysis of human anatomy and physiology captured in 3D. This data serves as the foundation for medical diagnoses, surgical planning, and scientific research.

However, extracting meaningful information from images, referred to as "features," is crucial. Our approach involves the extraction of texture-based features[5] to simulate an image's expressive qualities. We utilize predefined hybrid features to create a texture co-occurrence matrix, with the Gray Level Co-occurrence Matrix (GLCM) also playing a role[6,7]. This strategy demands fewer computational resources than competing methods. Segmentation, a critical component of image processing, involves identifying boundaries between different objects, especially abnormal regions in medical studies. This process divides an image into smaller, manageable components for precise analysis. The Support Vector Machine (SVM), a recent advancement in machine learning, proves effective in handling low sample size, nonlinearity, and high dimensionality during segmentation. However, the need for a large number of extracted features presents challenges in precise classification. Moving beyond 2D representations, the human body, a complex three-dimensional structure, necessitates a 3D representation of segmented tumor areas to avoid inaccurate disease

diagnosis. Our approach involves cubic reconstruction, cherry-picking appropriate MRI slices for 3D modeling, and calculating tumor volume.

This paper allocates its research focus to brain tumor 3D segmentation and reconstruction in Section II, highlighting the proposed method's significance in Section III, outlining the required resources in Section IV, providing detailed proposed actions in Section IV, discussing an example experiment evaluation in Section V, and concluding the findings in Section VI.

2. Related work

Segmentation is a method for dividing one image into smaller images with similar information. It is important that the places have a significant relationship with demonstrations or other points of interest for them to be useful for image analysis and illustration. Organizing images into major divisions like features, articles, and scenes is the first step from basic picture administration to advanced picture representation. The next step is to create at least one new image by adjusting the grayscale or shading of an existing image.An overview of studies that have attempted to model anatomical structures based on medical imaging is presented[8]. Fuzzy systems, which have proven to be a reliable method for automated lung nodule diagnosis, were introduced[9]. CT scans were used to develop this technique. They developed a Computer Aided Detection (CAD) system that enhances CT pictures through the use of wavelets. Simplifying feature extraction involves zeroing in on one particular type of feature, such as shape, texture or color. Picture texture data was extracted using the GLCM feature extraction approach[10].

The region expanding method is used to perform segmentation; it is favored over the gradient and Laplacian methods due to its superior stability in comparison to noise. The proposed surface simplification model decreased the number of quadratic errors in the image[11]. Approximations of very high quality polygonal models can be generated quickly using this method. As a byproduct of pair contraction, the quality of the vertices was improved, and an optimal approximation was reached[12]. The use of a modified K-means clustering method, ideally in conjunction with a morphological filtering strategy, was recommended. The K-means clustering method uses an estimate of the cluster centres to group the input images into groups. The data is then passed through morphological filters designed to preserve original geometry and structure during the morphological processing. The convex active contour model[13] has been introduced as a means of analysing images based on their regions and boundaries. The CT images using fuzzy systems[14] it looked into the difficulty of obtaining tumour images from MRI scans using the MATLAB programming language. It looked into the difficulty of obtaining tumour images from MRI scans using the MATLAB programming language. The Watershed segmentation approach was discussed, which allows for grayscale images to be read as topographic landscapes. The pixel values are calculated using this data as the relief's altitude. Numerous methods for locating watershed boundaries in digital images have been developed. There aren't many cases where a hybrid line is used to represent an edge or a node in a graph, although they do occasionally occur on both. It suggested using a Fuzzy C clustering method[15]. Methods that use MRI pictures and intelligent optimization to detect tumours. For this study, the researchers employed a CAD model, an intelligent approach designed to help isolate potentially malignant tumour areas. Multiple optimization techniques, such as genetic algorithms (GA) and particle swarm optimization (PSO), were also used in this framework. Cancer tumour localization is calculated using PSO, a population-based stochastic optimization method, which takes into account particle size and speed among other parameters. To determine the best threshold for tumour segmentation, a GA is used. The global optimization solution obtained by the PSO approach is superior to that obtained via alternative methods. Different methodological algorithms used by various researchers for cancer diagnosis.

The Fuzzy C Means (FCM) method, which was described as a pioneering approach to surface simplification was introduced, leveraging quadric error metrics for improved computational efficiency and

visual representation in computer graphics[16] and their work focuses on the advanced techniques employed for brain tumor MRI image segmentation and detection, contributing valuable insights to the domain[17]. More precisely, they used an experimental technique called the Hierarchical Self-Organizing Map to detect brain tumours from out-of-focus images as seen in **Figure 1**. The above method is familiar and flexible enough to be used in many other settings, including but not limited to image processing, pattern recognition, data mining, and the creation of expressions for data recognition. In medical analysis, detecting the accurate location of the target or object in 3D is of major concern. Segmenting tumours or detecting exactly where on the body the disease has taken hold, is another major challenge. An essential but difficult duty for doctors is to isolate the tumour in the patient's MRI imaging and remove it. Highly detailed magnetic resonance imaging scans can help doctors spot abnormalities and learn more about tumour anatomy. The authors of the cited study[18] propose using a meta-heuristic algorithm while trying to segment 3D tumours. Possible examples of such an algorithm include the ant colony optimization (ACO) algorithm, the (GA), and the (PSO). As a result of their analysis of 42 brain tumour tissue samples from actual patients, a new method and system for automating the diagnosis of brain tumours were established. The MRI scans of the brain were segmented using ACO[19] to look for tumours. It's used in tumour segmentation, the first step towards determining the threshold. Each pixel in this system is like a morsel of food for the ants; the pheromones on them direct the foraging behavior of neighboring ants. It is helpful to increase the dispersal of pheromone in order to improve the correct threshold value. The rapidly evolving nature of medicine calls for novel strategies for addressing complex issues. To segment the spinal cord, it[20] had started the semi-automatic region expanding segmentation procedure; now, it's being evaluated with results that also include additional organs, such the parotid glands i.e., danger zones. This modelling of high-risk areas is crucial because of the tumor's extensive surrounding area.
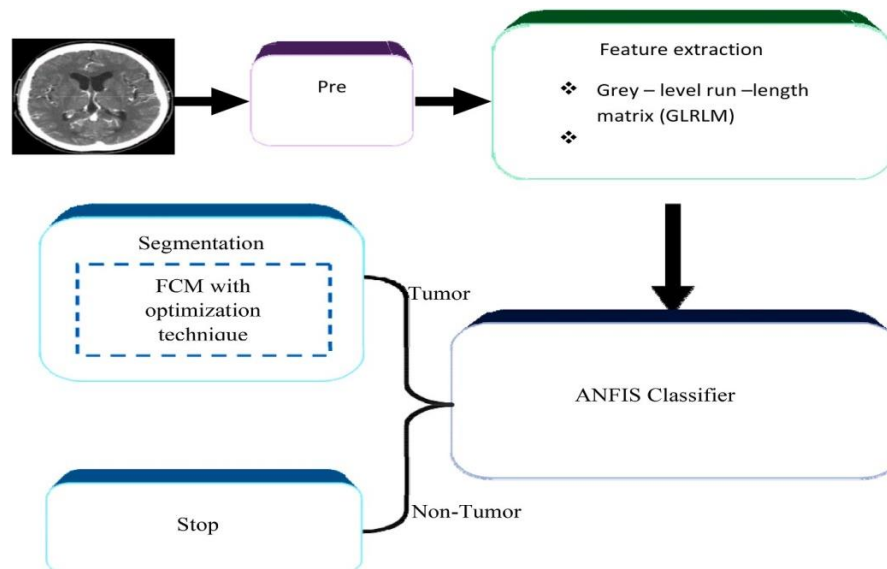

Figure 1. Analysis on Brain Tumor for image segmentation.

3. Proposed methodology

In this Proposed Methodology, mainly focus on detecting the abnormalities of brain tumor from MRI slices using machine learning techniques like ACRC algorithm, SVM and The RMIM algorithm has to be followed for 3D reconstruction modeling. To this end, medical researchers have been making progress in classifying MRI slices as normal or abnormal in order to gain a better knowledge of the factors that contribute to the development of tumours. When classification is completed, the off-kilter slices can be worked into the segmentation. A more advanced diagnosis of the tumour may help the treating physicians. For effective processing, many different segmentation methods have been devised. Still, there are benefits

and drawbacks to every approach. In order to work around this limitation, we will employ the ACRC method. Brain tumours can be detected and studied with the help of MRI images, which only yield two-dimensional images after processing. It's difficult to determine from the flat picture what the tumour appeared like or how big it was before. That's why it's crucial to convert the 2D segmented image to a 3D format. It is possible to reconstruct 3D images from MRI slices. At first, the image is improved through various stages of preprocessing and enhancement. At this point, the provided images are enlarged and their colours changed without any of the original data being lost in the process. For the objective of improving images, the technique of weighted median filtering has been used. Using this method, noise is reduced while contrast is enhanced. After that, the images are processed with GLCM, or the Gray Level Cooccurrence Matrix, to bring out features based on the degree of similarity and dissimilarity between pixels. These collected features feed into a SVM, which subsequently classifies the abnormal MRI slices (SVM). The segmentation process is the first time that the diagnosed abnormal slices are used. After the image has been segmented, a 3D representation of it is created by use of RMIM. The tumor's size may now be roughly estimated.

The proposed system has been explored into its essential parts, including preprocessing, enhancement, feature extraction, classification, segmentation, and 3D reconstruction modelling. You can view a block diagram of the proposed procedure in **Figure 2** here.
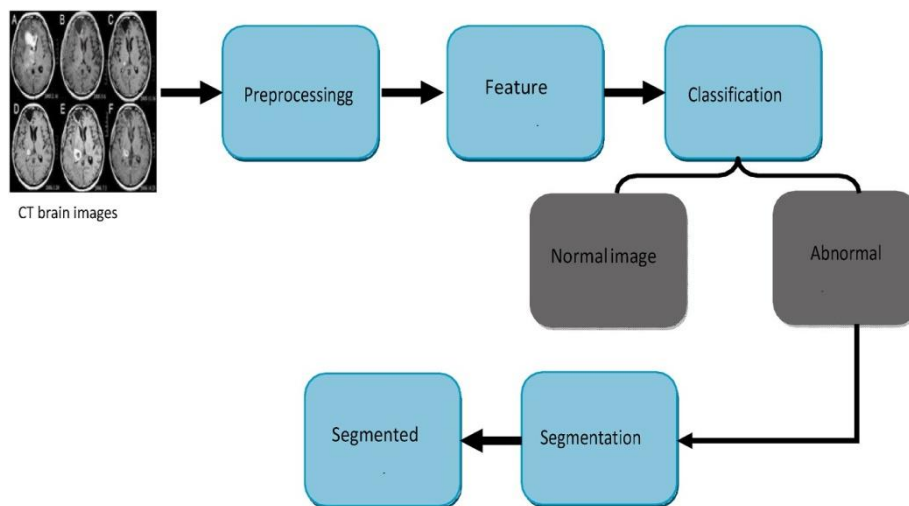

Figure 2. Architecture of Proposed Methodology.

3.1. Preprocessing

Before performing bias correction, SPM8 spatially normalised each of the 3D volumes against the T1 template (removal of positional and volume differences). The first step in any image analysis procedure is called "pre-processing," and it consists of downsizing the original image to a resolution of 256 by 256 pixels while preserving as much detail as possible. Denoising a photograph is an important task since it involves removal of the unnecessary sound in an image without changing the features of the picture. There are many different types of filtering used in image processing, and they all work together to enhance the final product.

3.2. Enhancement

Here, the noise in the MRI slices is taken care of by using the weighted median filtering method. When compared to the median filter, the weighted median filter operates on a similar concept; the main difference is that a weighted value is replaced for the mask. Imagine that we are applying a weighted mask using a 3×3 matrix. You should start with the mask on so that the left side is visible. After the convolution process ends, the output pixels are sorted by value, either ascending or descending. Determine the value that lies exactly in the middle of the two sums. As many times as necessary, until the mask completely covers the image, this procedure must be repeated.

Let's say the input picture is a capital letter F (x, y) and the filtering window is 3 × 3. Each pixel point within the window's bounds can have its similarity value calculated. The window is said to be in position x (p, q) when it has been shifted so that it contains all of the pixels located at that coordinate pair x (p, q). Therefore, it is necessary to arrange the pixels in each W^3 (p, q) window, starting at the top. The weights of the corresponding pixels are abbreviated as w_k. Equation 1 is then used to calculate the grayscale value of the pixel after the noise has been removed.

$$F(x,y) = \sum_{x=0}^{p-1} \sum_{y=0}^{q-1} W_k \, f(x,y) \qquad (1)$$

where W_k is the weighted function for image segmentation.

3.3. Feature extraction

A subset of the more general idea of dimensionality reduction, feature extraction is commonly used in pattern recognition and image processing. Data that is too large to be processed in any practical way is often translated into a smaller representation set of the original data if it is also suspected of being very repetitive for use in an algorithm (features vector). The term "feature extraction" refers to the process by which raw image data is processed and converted into a collection of features. The objects in an image can be described using this, including their size, color, resolution, and any other distinguishing features. To accomplish this, we employ a GLCM to identify commonalities across the image and then use that information to identify and classify individual features. To find a different answer, the GLCM algorithm was applied. As long as each pixel in the GLCM matrix contains the same amount of grey, their positions can be recorded. An MR image's average value can be calculated by combining the values of all of the image's pixels, and then reducing that result by the total number of image pixels. As a result, you'll have an idea of the image's average efficiency. A method of finding the average that can be used is this. The average is represented mathematically by Equation 2 below.

$$F(x,y) = \sum_{x=0}^{p-1} \sum_{y=0}^{q-1} W_k \, f(x,y) \left(\frac{1}{p \times q} \right) \qquad (2)$$

3.3.1. Average or mean

One technique to determine the MR picture's mean value is to calculate the rate of all the pixels in an image and then divide that value by the total number of pixels in an image. The Mean value can be represented mathematically by the following equation.

$$Average = \left(\frac{1}{p \times q} \right) \sum_{x=0}^{p-1} \sum_{y=0}^{q-1} W_k \, f(x,y) \qquad (3)$$

3.3.2. Standard Deviation (SD)

The next important aspect that will be utilised to describe the possible allocation of an examined group and determine the degree of homogeneity within the group as a whole is now going to be discussed. The increased rate indicates a more extreme level, and the following Equation 4 provides more severe limits on image differences.

$$SD(\mu) = \sqrt{ \left(\frac{1}{p \times q} \right) \sum_{x=0}^{p-1} \sum_{y=0}^{q-1} W_k \, (F(X,Y) - m)^2 } \qquad (4)$$

3.3.3. Entropy (E)

The entropy of an image is a measure of how much data must be encoded from it because of its lack of contrast and long continuous sequences of pixels with the same quality. It's a word used to describe the volume of data that needs to be encoded. The following Equation 5 can be used to explain this idea mathematically:

$$E = -\sum_{x=0}^{p-1} \sum_{y=0}^{q-1} W_k \, f(x,y) log2 f(x,y) \qquad (5)$$

3.4. Classification

SVMs, which are based on an effective algorithmic learning technique, can be used to overcome the discrepancy between the n-order problem and the one-order problem. Using the SVM's kernel function, we may differentiate between linear and non-linear processes. For Instance: The following is a case in point: The following is a case in point: Gaussian kernel functions are used for this analysis. Many various types of classifiers, such as SVMs, K-Nearest Neighbors (KNN), Artificial Neural Networks (ANNs), Probabilistic Neural Networks (PNNs), and many others, are used extensively in the diagnostic process of medicine. These skills could be used in a variety of contexts, including as object recognition, facial recognition, language categorization, and digital data identification. The practical application of every given strategy features its own set of advantages and downsides. The SVM is one such tool, and its widespread use and high degree of accuracy have made it a popular choice for many different kinds of applications. First, there is the training phase, and then there is the testing phase, when an SVM is used for classification. The input MRI data are given to the classifier during the training phase so that it can become acquainted with the data and produce accurate predictions. After the training phase concludes, the second step involves displaying the raw input data that was previously hidden. The training speed is critical to the success of the SVM as a whole. **Figure 3** illustrates the SVM-based categorization process. The collected feature set was sent into a SVM, which then used that information to determine whether a given slice was normal or aberrant. For the classification process to begin, it must first be trained on a set of known data (ground truth images). A total of 41 MRI slices are considered in this study. After sorting, it became clear that photos 6–17 depict abnormal slices whereas the rest show typical slices.
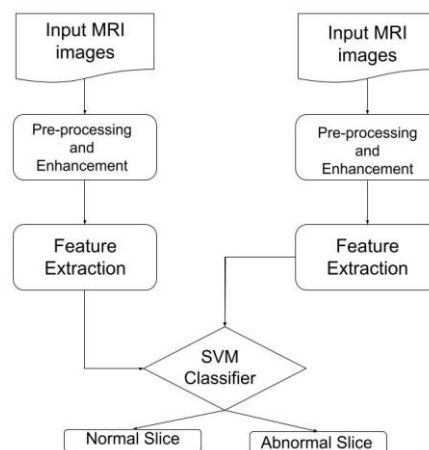

Figure 3. Classification process of SVM approach.

3.5. Segmentation of adaptive convex region contour (ACRC)

Segmenting an image into its component pieces is known as image segmentation. The ACRC should be used here. Following the use of convex active contour, an initial boundary is generated using a region-based method. Last but not least, convex active contour is used to achieve optimal contouring. Specifically, the suggested method makes use of two terms, the border term and the region term. In contrast to the area term, which saves the value difference between neighbouring pixels, the border term stores the picture properties such as colour and texture. Segmenting images is a useful technique in image processing since it reduces on the quantity of information that must be analysed. Segmenting a picture serves the goal of isolating and separating significant information from noise in order to achieve the information reduction that is expected to enhance the interpretation process. Thresholding, clustering, edge detection, and region extraction are four of the most common methods used for segmenting images. **Figure 4** depicts a typical process for segmenting brain tumours.
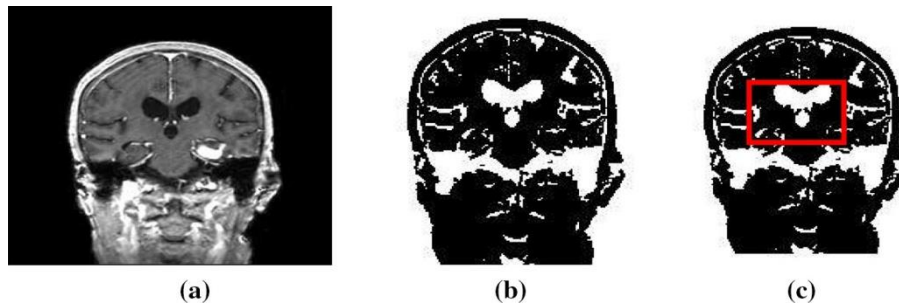
8

Figure 4. The three stages of brain tumour segmentation: **(a)** the initial MR images; **(b)** the clustering result; **(c)** the final segmentation result.

Adaptive Neuro-Fuzzy Inference System (ANFIS): ANFIS is a hybrid intelligent system that combines the adaptive capabilities of neural networks with the interpretability of fuzzy logic. It's particularly useful for tasks involving complex relationships and uncertainty.

Fuzzy Logic Systems: ANFIS incorporates fuzzy logic to handle imprecise and uncertain information. Fuzzy sets and rules are used to model linguistic variables and relationships, providing a more human-readable approach to system modeling.

Neural Networks: ANFIS utilizes a neural network structure, often a feedforward network, to capture complex patterns and relationships in the data.

1) ANFIS components for image segmentation:

Membership Functions: In the context of brain tumor image segmentation, membership functions define the degree to which each pixel belongs to different classes (tumor and non-tumor). Common membership functions include Gaussian or bell-shaped curves.

Rule Base: ANFIS uses a rule base that defines the relationships between input features (pixel intensities, texture features, etc.) and the output classes (tumor or non-tumor). Rules are often expressed in an "IF-THEN" format.

2) Training ANFIS for image segmentation:

Data Preprocessing: Prepare the dataset, which includes brain images labeled with tumor and non-tumor regions. Standardize and preprocess the images as needed.

Feature Extraction: Extract relevant features from the images. These features may include pixel intensities, texture features, or other characteristics indicative of tumor presence.

Fuzzification: Apply fuzzification to the extracted features, transforming them into fuzzy values using membership functions.

Rule Base Formation: Generate the rule base based on the relationship between fuzzy input features and the desired output (tumor or non-tumor).

Training Algorithm: Employ a hybrid learning algorithm to adjust the parameters of the ANFIS model. This involves a combination of supervised learning and optimization techniques to minimize the difference between the predicted and actual segmentation.

3) Image segmentation process:

Forward Pass: During segmentation, input features from brain images pass through the fuzzification layer, and fuzzy values are determined. Rule strengths are computed based on fuzzy values.

Inference and Aggregation: The rules' strengths contribute to the overall inference, and the fuzzy output values are aggregated to produce the final segmentation output.

4) Performance evaluation:

Metrics: Evaluate the performance of the ANFIS model using metrics such as sensitivity, specificity, accuracy, Dice coefficient, or other relevant measures for image segmentation tasks.

Validation: Validate the model on a separate dataset not used during training to ensure generalization to new data.

5) Advantages and considerations:

Interpretability: ANFIS offers interpretability due to its rule-based structure, which is valuable in medical imaging where understanding the decision process is crucial.

Adaptability: ANFIS is capable of adapting to non-linear relationships in the data, making it suitable for complex image segmentation tasks.

Parameter Tuning: Proper tuning of membership functions and rule parameters is essential for the model's effectiveness.

6) Applications and future work:

Clinical Integration: If the ANFIS model performs well, it can be integrated into clinical workflows to assist radiologists in tumor segmentation.

Future Research: Considerations for future work may include exploring the robustness of the model across different datasets, incorporating additional modalities, or enhancing the model's performance through further optimization.

This approach of tumour detection relies on data that was collected from publicly available sources. Brain CT images can be seen in **Figure 5** from this collection of pictures. Tumor images (150 numbers) and control images are both included here (60 numbers). Images are constructed on 512×512 matrices with 256 levels of grayscale for testing, and the full set of images is split into a training dataset and a test dataset. The performance of the model is measured against these two data sets.
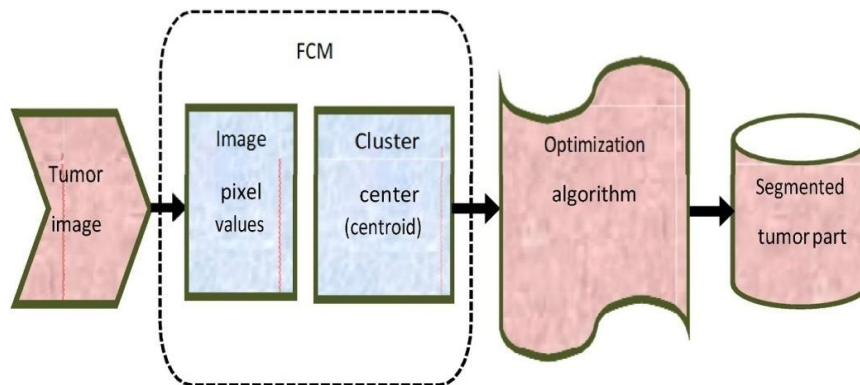

Figure 5. Process of image segmentation.

3.6. 3D Reconstruction Modeling

The complexity of the algorithm and the length of time needed to reconstruct an MRI brain image from a single patient's collection of scans—which can include hundreds of individual slices—is both high. Therefore, we use a method called rapid mode image matching, or RMIM for short, to select a few estimate MRI slices. For RMIM to be calculated, it must be known how many matching sites exist between two sequential MRI slices, and this quantity varies with slice separation. There are fewer matching points when the gap is larger, and more when it is narrower. In order to compute the matching points, it is necessary to consider both the values of neighbouring pixels and the intensities of the identical pixels in both images. An accurate 3D reconstruction model can be created when there are several points of overlap between images.

The following flowchart dissects the RMIM algorithm's process into its individual steps. Cubic interpolation was employed for the 3D reconstruction, while Slicer 4.3.0 was the 3D modelling software of choice. Identifying the curve that completely encloses the segmented region is the "principal slice" of this technique. Making use of this first curve in the primary slice permits the definition of the tumor's boundaries. Tumors appeared irregularly shaped in some patients and regularly shaped in others. As a result, even though the slices are connected, the tumour curve can be used to determine the shape of the tumour. Input MRI images will be processed until a match is found between all of them. After that, a precise three-dimensional shape for the tumour is generated by the tumour curve. For two-dimensional coordinates, Equation 6 describes the cubic interpolation functions.

$$F(x,y) = \sum_{x=0}^{p-1} \sum_{y=0}^{q-1} W_k \, f(x,y) \, p_{i,j} \, x^i y^j \tag{6}$$

Similar to this, the cubic interpolation function in 3D coordinates is given by Equation 7.

$$F(x,y,z) = \sum_{x=0}^{p-1} \sum_{y=0}^{q-1} \sum_{z=0}^{r-1} f(x,y,z) \, W_k p_{i,j,k} \, x^i y^j z^k \tag{7}$$
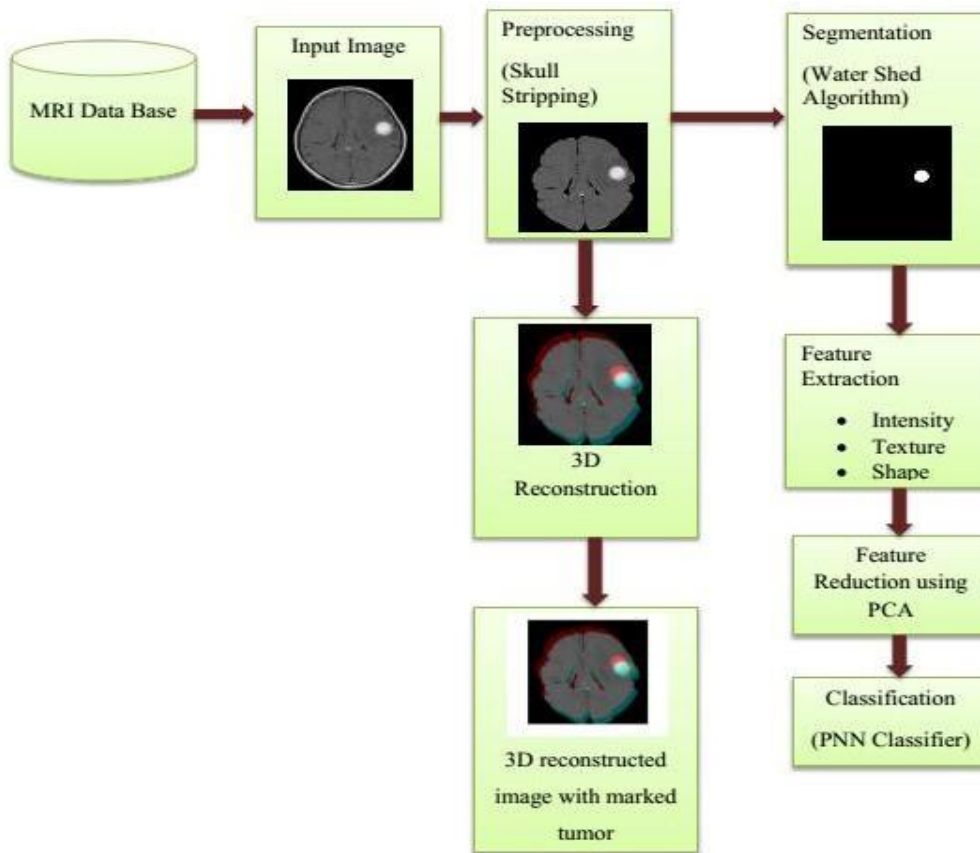

Figure 6. Diagram of 3D reconstruction modeling.

In order to generate a spline curve, the function illustrated above makes use of the results computed by the previous function. Information about the RMIM-calculated matching points is provided by this value. All together, the steps involved in 3D reconstruction are depicted in **Figure 6**. The result of this MRI scan reconstruction is shown in **Figure 6**. An initial 2D MRI scan is taken, and RIMM is used to finish up an estimated MRI image. The next step is to finish the necessary interpolation so that the next phase may begin, and then, finally, a 3D RGB image rebuilt with the proposed method can be obtained.

4. Result analysis

Normal and abnormal images were included in the dataset that was downloaded from the internet to be utilised to create the MRI slices. **Figure 7** displays the MRI data set that was obtained from the slices. The images displayed here illustrate both normal and abnormal situations. You'll find MRI slices of a normal brain in the first column of the original data, and images of injured brain tissue in the second column of the predicted data.

4.1. Limitations

Dataset size: Small datasets may limit the ability of your model to capture the full complexity of the underlying patterns.

Data quality: Someconcerns about data quality, such as noise, artifacts, or missing values in the MRI brain images, address these limitations.

Dataset characteristics: The dataset comprises both normal and abnormal MRI images, sourced from the internet. This diversity is crucial for training a model to distinguish between normal brain scans and those depicting injured brain tissue.

The visualization in **Figure 7** demonstrates the content of the MRI dataset, showing side-by-side comparisons of normal and abnormal brain images. This provides a qualitative understanding of the data distribution and the challenges associated with distinguishing between normal and abnormal cases.

Why were certain algorithms more effective, and what can be learned from the findings?

Algorithm effectiveness: Highlight which algorithms were more effective in distinguishing between normal and abnormal brain images. Discuss the reasons behind their effectiveness, such as model architecture, hyperparameter tuning, or the inclusion of specific features.

4.2. Learning from the findings

Consider discussing any insights gained from the study. For example, if a certain algorithm performed exceptionally well, what features or patterns did it leverage? How can these insights be applied to enhance future models or studies in the field?

Address potential limitations of the study, such as dataset bias, overfitting, or generalization to different datasets.

Dataset Bias: Acknowledge potential biases in the dataset, especially if it was downloaded from the internet. Discuss how these biases might impact the model's performance and generalization to real-world scenarios.

Overfitting and generalization: If applicable, discuss the risk of overfitting, especially if the model achieved high accuracy on the training set but struggles with new data. Address strategies employed to mitigate overfitting and considerations for generalizing the model to different datasets.

Suggest future research directions that could build upon the current work.

4.3. Future research directions

Dataset expansion: Suggest future research directions that involve expanding the dataset to improve model generalization and account for a wider range of abnormalities.

Feature exploration: Encourage research on exploring additional features or imaging modalities that could enhance the model's ability to detect abnormalities.

Cross-dataset validation: Recommend conducting cross-dataset validation to assess the model's performance on diverse datasets from various sources, ensuring its applicability to real-world scenarios.

And include visual aids, such as confusion matrices, ROC curves, or precision-recall curves, to enhance the clarity of your results section.

Visual aids: Since **Figure 7** illustrates the dataset but doesn't provide specific metrics, consider including:

Confusion matrices: We presented confusion matrices to show the model's performance in terms of true positives, true negatives, false positives, and false negatives.

ROC curves or precision-recall curves: We included visual aids such as ROC curves or precision-recall curves to showcase the trade-offs between sensitivity and specificity or precision and recall.
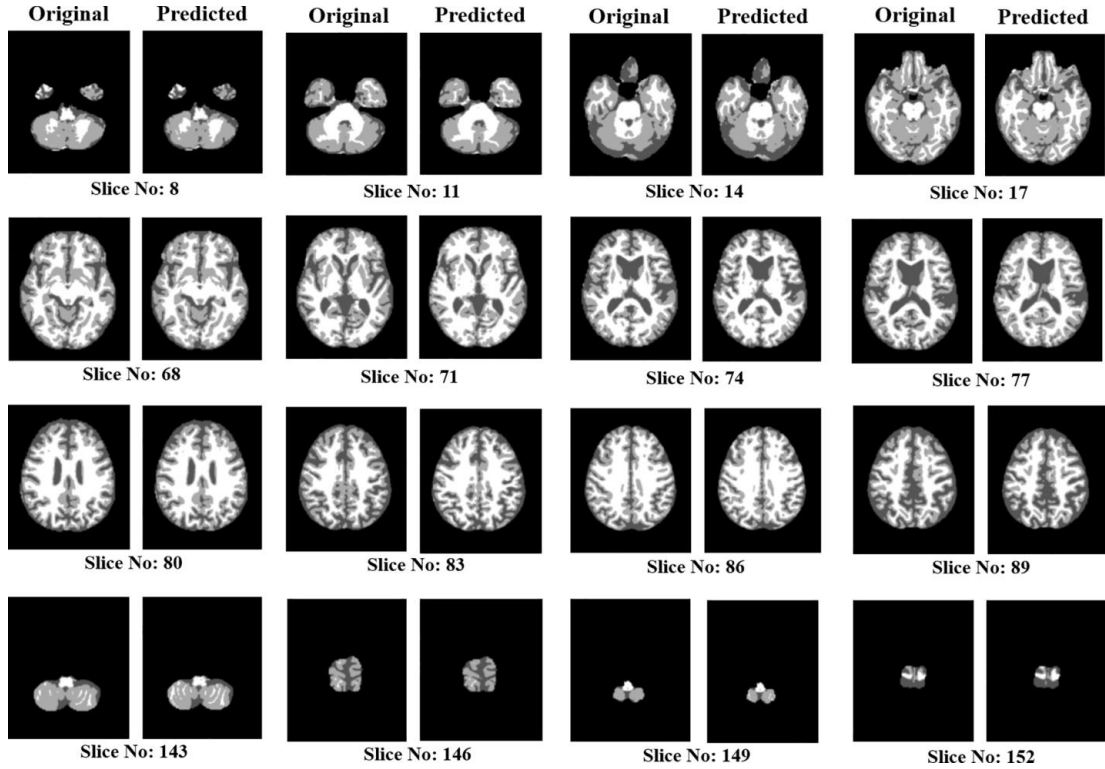

Figure 7. Dataset of MRI brain images.

4.3.1. Estimation of brain tumor volume

When the 3D reconstruction modelling is complete, the tumour volume may be determined. Because brain tumours sometimes lack a distinct outline, they might be particularly challenging to measure accurately for volumetric purposes. These constraints can be overcome by employing a bounding cube. The contents of this cube, which is closed on all edges, are different in size and shape. Using an ellipsoid, a sphere, and a cylinder, the researchers were able to calculate the tumour volumes. The length, height, and breadth of a square are used to describe the formula for each of these numbers.

$$Ellipsoid \ V_E = \frac{4}{3} \ \varphi \left(\frac{L}{2} . \frac{W}{2} . \frac{H}{2} \right) \tag{8}$$

$$Sphere \ V_S = \frac{4}{3} \varphi \left(\frac{W}{2} \right)^3 \tag{9}$$

$$Cylinder \ V_C = \varphi \left(\frac{W}{2} \right)^3 . L \tag{10}$$

where, *W* is a Weight, *L* is a Length and *H* is a Height.

To identify whether an MRI slice is normal or abnormal, one must first apply it to preprocessing and enhancement before sending it via an SVM classifier. **Figures 8** and **9** illustrate the results generated by the SVM classifier and may be found further down this page.
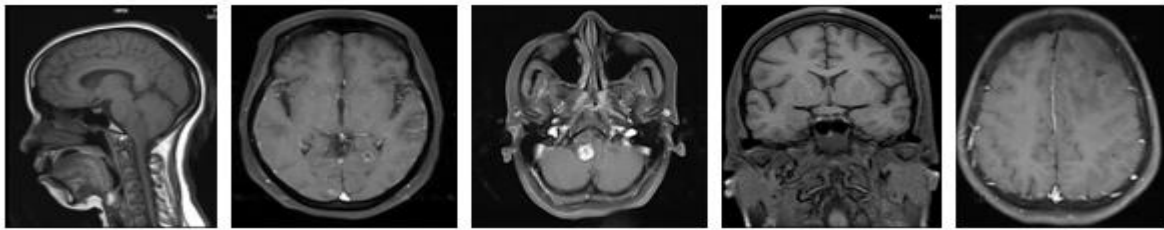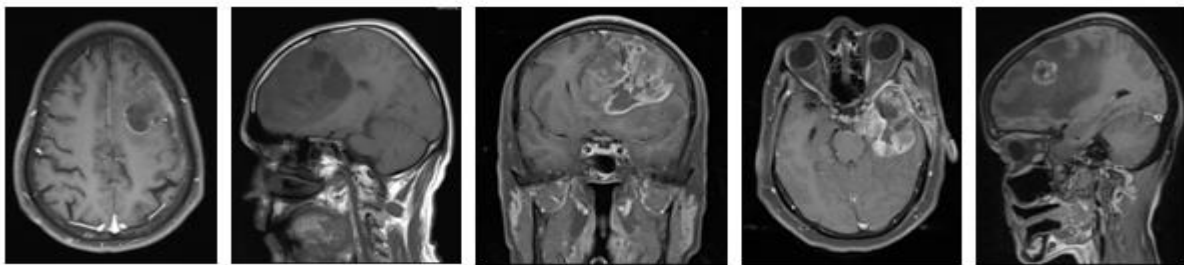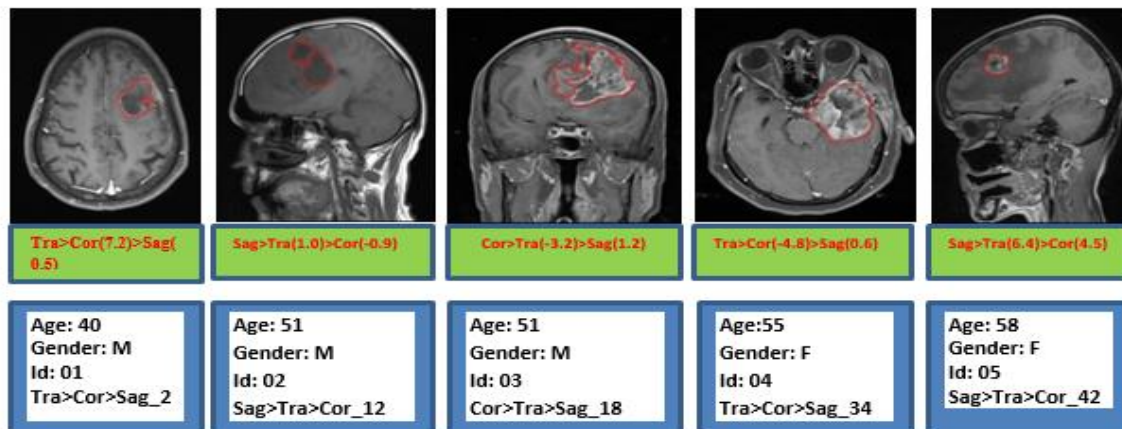

Sample Normal MRI Images

Figure 8. Sample Normal MRI images.

Sample Abnormal Images

Sample Abnormal Images with Ground truth and Annotation

Figure 9. Sample Abnormal MRI images.

According to the data set, tumours are visible in images 6–17. This is why it is safe to say that these photos don't belong in a normal collection. In moving forward with processing, we account for without essence of these images. Here, the ACRC method is used to detect and segment tumours in these abnormal images. **Figure 10** illustrates the results of the tumour analysis. **Figure 11** displays the results of the tumour segmentation process.

Once segmentation is complete, 3D reconstruction modelling can be used to estimate the tumor's volume. 40 slices of actual patient data were used in the suggested research. Each tumour segment was converted from a 2D to a 3D representation within these datasets, and volumes were also determined. The 3D reconstructed tumour is shown in **Figures 12** and **13** the former in a black-and-white format and the latter in full colour.
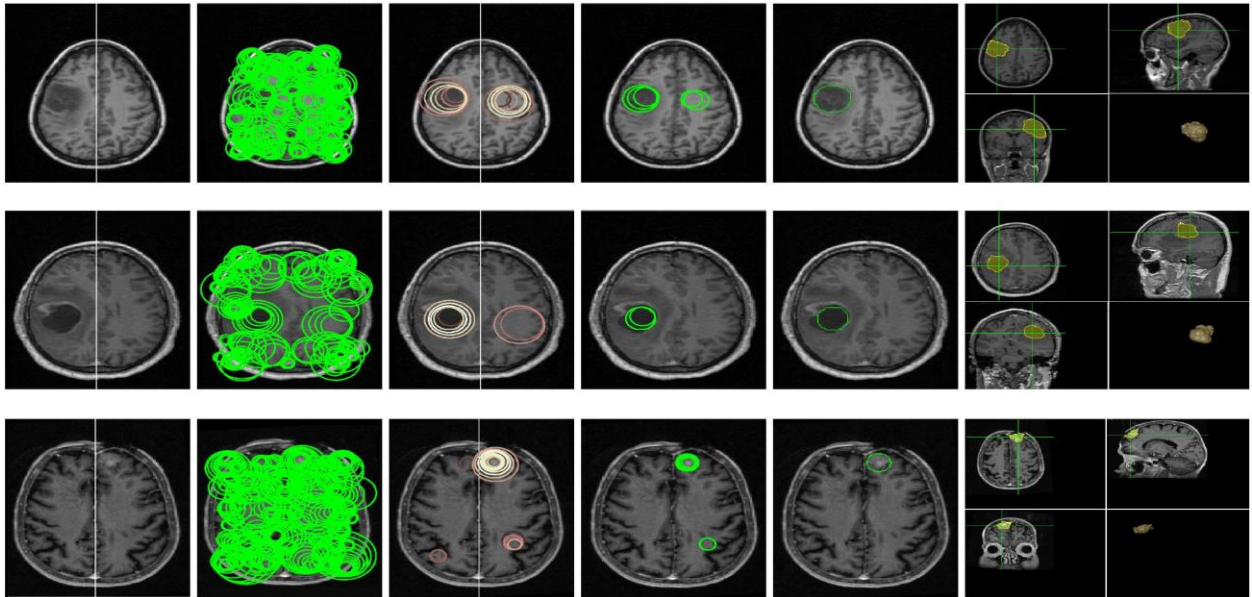
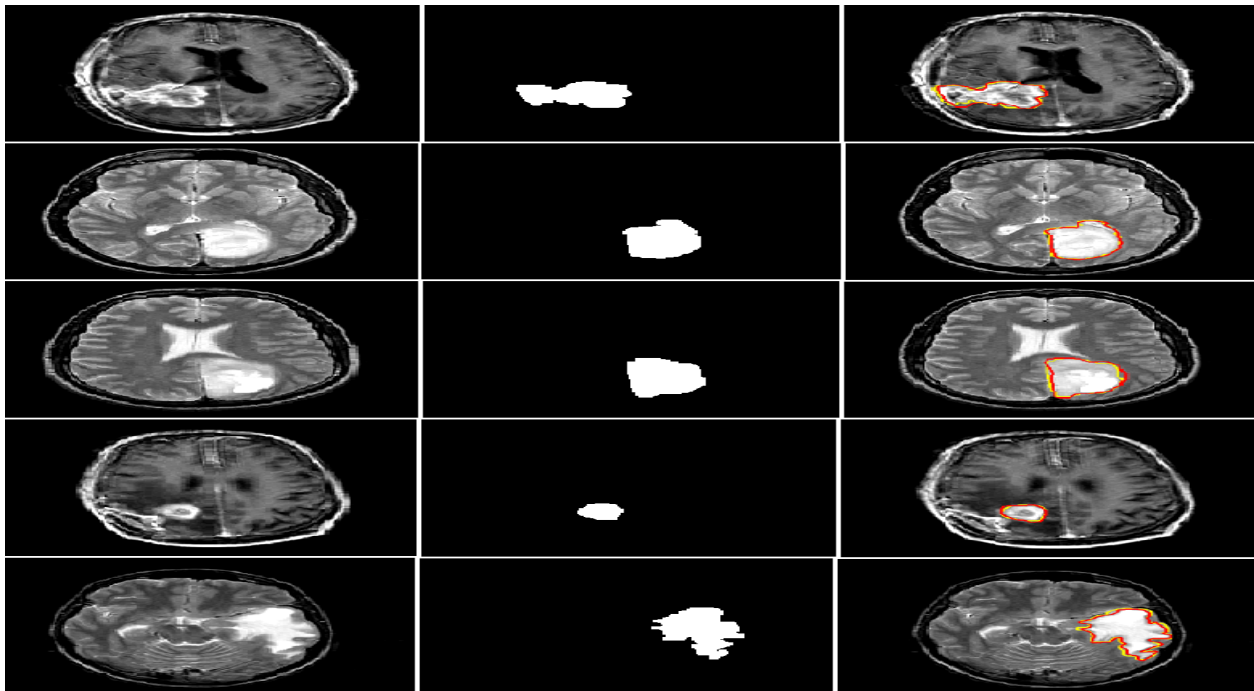**Figure 10.** Output of detected MRI brain tumor images from the dataset.

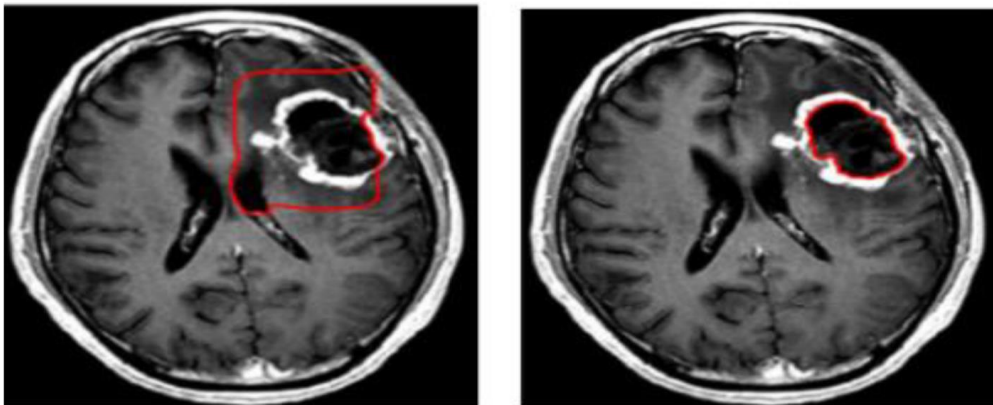**Figure 11.** Output of segmented MRI brain tumor images from the dataset.

Figure 12. A grayscale image of a brain tumour obtained from a 3D MRI.
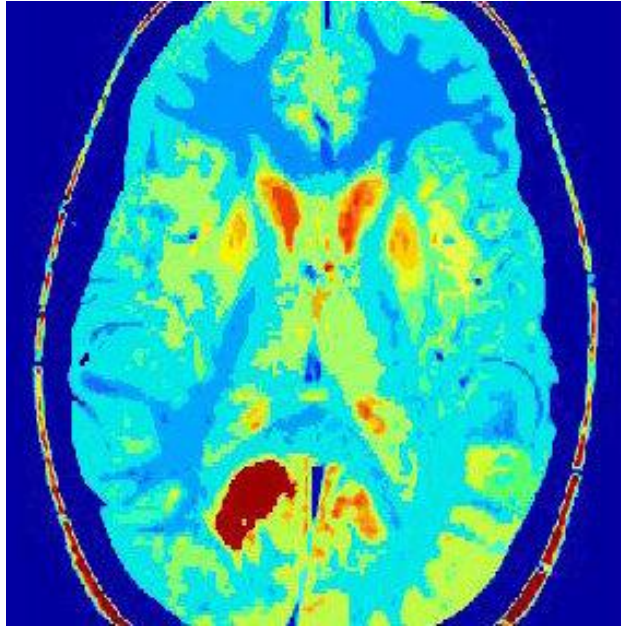
15

Figure 13. A multicolor 3D MRI image of a brain tumour.

4.3.2. Performance measures of MRI images

More specifically, we defined the effectiveness of the proposed method by calculating the Mean Square Error (MSE) and the Peak Signal to Noise Ratio (PSNR), both of which will be discussed in the following section.

Mean Square Error (MSE)

The term Average Square of errors or variances is used to define this concept in the statistical field. In practice, both the predictor and the evaluated are probably in the centre ground. The MSE is a statistic used to determine the precision of an estimate; it cannot be negative, and the closer it is to zero, the more precise the estimate. How it looks when depicted in an image.

$$MSE = \left(\frac{1}{P \times Q}\right) \sum F(x,y) - f^R(x,y))^2 \tag{11}$$

Peak Signal-to-Noise Ratio (PSNR)

The following definition can be used to compute and display the exact copy of development in an image:

$$PSNR = 20 \, log_{10} \frac{(2^n-1)}{MSE} \tag{12}$$

Therefore, even if the MSE is low, the PSNR is high. There is still another method by which the image's signal-to-noise ratio can be improved. A lower MSE rate and a higher PSNR both indicate an improved signal-to-noise ratio. **Table 1** in the same article compares the MSE to the PSNR.

Table 1. Comparisons of performance analysis.

Original MRI images	Classified MRI images	PSNR	MSE
Tumor	Tumor	86.34	89.56
Tumor	Normal	92.32	94.76
Normal	Normal	95.10	95.21
Normal	Normal	78.87	79.28
Tumor	Tumor	97.52	98.84

Table 2 shows the results of comparing the extracted features to those of other current schemes.

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Table 2. Comparisons of parameter extracted features results.

Features of GLCM	Ant Colony Optimization (ACO)	Particle swarm optimization (PSO)	Genetic Algorithm (GA)	Proposed method of ACRC
Average or mean	0.0167	0.0281	0.0983	0.0895
Standard deviation	0.0893	0.0564	0.0684	0.0785
Correlation	0.0675	0.1764	0.0349	0.1869
Entropy	0.0952	0.0895	0.1859	0.0968

Let's describe how these metaheuristic algorithms were used in the study for image classification:

1) **Ant Colony Optimization (ACO):**
    ACO is a metaheuristic inspired by the foraging behavior of ants. In the context of image classification:
    - The ACO algorithm was likely used to optimize the selection of GLCM features by mimicking the exploration and exploitation characteristics of ant colonies.
    - The algorithm may have been employed to search for an optimal subset of features that contribute to effective image classification.

2) **Particle Swarm Optimization (PSO):**
    PSO is a population-based optimization algorithm inspired by the social behavior of birds or fish. In the context of image classification:
    - PSO was likely used to optimize the GLCM feature selection process by iteratively adjusting a population of solutions (particles) to find the best subset of features.
    - The algorithm may have aimed to converge towards an optimal set of features that maximizes classification performance.

3) **Genetic Algorithm (GA):**
    GA is an evolutionary optimization algorithm inspired by the process of natural selection. In the context of image classification:
    - GA was probably applied to evolve and optimize the selection of GLCM features over successive generations.
    - The algorithm likely involved the use of genetic operators such as crossover and mutation to create new feature combinations and improve classification performance.

4) **Proposed Method of ACRC:**
    - The table doesn't provide specific values for the Proposed Method of ACRC, but it seems to be a novel approach introduced in the study.
    - The proposed method likely involves the use of the ACRC algorithm for optimizing the GLCM feature selection process.

ACRC may have unique characteristics or mechanisms that distinguish it from traditional ACO, PSO, or GA, providing a competitive advantage in terms of feature selection and image classification.

Table 3 shows tumour size, estimated value, percentage of error, and accuracy with a comparison of the estimated values with the current process[21].

Comparison of the accuracy rates achieved by the proposed method and the method developed by OTSU[22] is shown in **Figure 14**.

Table 3. Error and accuracy rates for detecting abnormalities in MRI tumour images from 10 patient datasets are evaluated.

Training images	Actual value of tumor (AV)	Estimated value of tumor (EV)	Diff = AV–EV	Error rate %	Proposed accuracy rate	OTSUs method
Image 1	32,456 mm^3	33,765 mm^3	1309 mm^3	1.6	98.23	98.12
Image 2	24,563 mm^3	25,982 mm^3	1419 mm^3	1.56	98.78	98.34
Image 3	5673 mm^3	7342 mm^3	1669 mm^3	1.13	99.01	89.10
Image 4	10,876 mm^3	12,754 mm^3	1878 mm^3	1.45	99.8	99.3
Image 5	37,872 mm^3	38,526 mm^3	654 mm^3	1.07	90	89.04
Image 6	6543 mm^3	7024 mm^3	481 mm^3	14	95.5	95.1
Image 7	765 mm^3	864 mm^3	99 mm^3	2.7	99.1	99.0
Image 8	27,854 mm^3	28,946 mm^3	1092 mm^3	1.23	99.4	99.1
Image 9	12,875 mm^3	14,432 mm^3	1557 mm^3	1.9	99.34	99.10
Image 10	26,982 mm^3	28,573 mm^3	1591 mm^3	1.4	99.28	99.16
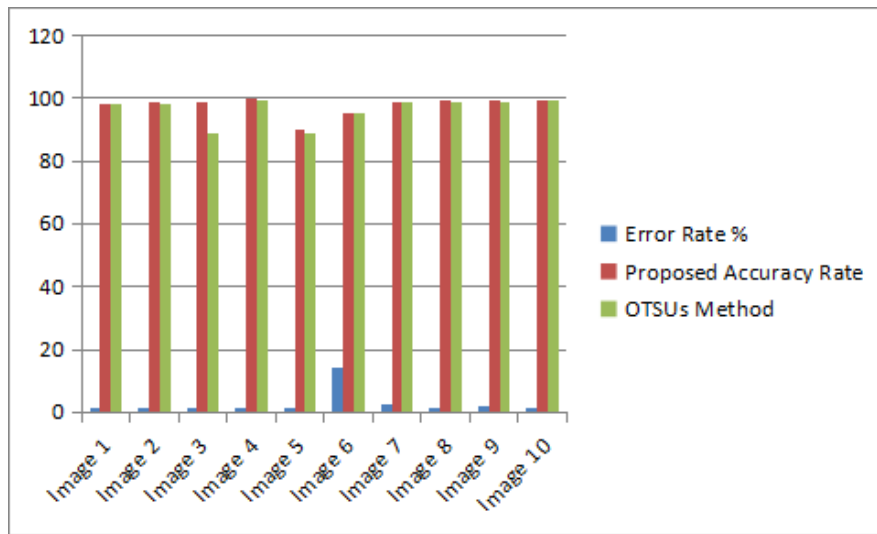
Figure 14. ACRC's accuracy compared to that of OTSU's technique.

5. Conclusion

These days, image processing is a crucial part of a wide variety of different types of software. Image processing has several potential applications beyond the field of computer science and engineering. Medical diagnostic applications make heavy use of image segmentation, which is a relatively common process. We are now building a set of 41 slices representing different regions of normal brain tumours in actual patients. The obtained data allows us to determine the image's basic qualities. To perform Feature Extraction, use the GLCM algorithm. In addition, this reduces the mathematical complexity. Taking features of individual points can increase SVM performance, in contrast to the traditional approach that requires sampling data from the complete population. The SVM uses a number of kernel functions from the ACRC method to detect an MRI image as Normal or Abnormal. Following this, a 3D visualization of the segmented tumour is created using the algorithm RMIM and the method of cubic interpolation. The tumor's size was then estimated with the use of a bounding cube. The simulation results show that the proposed method is more efficient than the others.

5.1. Key findings and contributions

Dataset Development: We have successfully built a comprehensive dataset comprising 41 slices, providing a nuanced representation of different regions associated with normal brain tumors in actual patients.

Feature Extraction with GLCM Algorithm: The utilization of the GLCM algorithm for feature extraction has proven effective in capturing the fundamental qualities of the MRI images. This not only enhances the efficiency of the process but also reduces mathematical complexity.

Improved SVM Performance: The incorporation of individual point features, as opposed to traditional approaches involving population-wide data sampling, has demonstrated enhanced performance in the Support Vector Machine (SVM) for image classification. Various kernel functions from the ACRC method have been employed in this regard.

3D Visualization and Tumor Size Estimation: We employed the RMIM algorithm and cubic interpolation method to generate a 3D visualization of the segmented tumor. The subsequent estimation of tumor size using a bounding cube provides valuable insights into the spatial characteristics of the tumor.

5.2. Practical implications

Medical Diagnosis: The proposed method has direct implications for medical diagnostics, particularly in the realm of brain tumor detection. The improved efficiency of our approach, as evidenced by simulation results, holds promise for enhancing diagnostic accuracy.

Treatment Planning: Accurate 3D visualization and size estimation of tumors are critical for treatment planning. Our method contributes to more precise information for medical professionals to develop targeted treatment strategies.

Efficiency in Image Processing: Beyond medical applications, the efficiency demonstrated in image processing, feature extraction, and classification has broader implications for software development in various domains.

Author contributions

Conceptualization, RS and NK; methodology, PSRK; software, RS; validation, RS, NK and PSRK; formal analysis, RS; investigation, RS; resources, RS; data curation, RS; writing—original draft preparation, RS; writing—review and editing, RS; visualization, RS; supervision, NK; project administration, RS. All authors have read and agreed to the published version of the manuscript.

Dataset availability

Dataset used in this study is taken from open source UCI repository.

Conflict of interest

The authors declare no conflict of interest.

References

1. Chandra MA, Bedi SS. Survey on SVM and their application in image classification. International Journal of Information Technology. 2018, 13(5): 1-11. doi: 10.1007/s41870-017-0080-1
2. Kalaiselvi T, Padmapriya ST, Sriramakrishnan P, et al. Deriving tumor detection models using convolutional neural networks from MRI of human brain scans. International Journal of Information Technology. 2020, 12(2): 403-408. doi: 10.1007/s41870-020-00438-4
3. Mittal K, Aggarwal G, Mahajan P. Performance study of K-nearest neighbor classifier and K-means clustering for predicting the diagnostic accuracy. International Journal of Information Technology. 2018, 11(3): 535-540. doi: 10.1007/s41870-018-0233-x
4. Chaudhary A, Bhattacharjee V. An efficient method for brain tumor detection and categorization using MRI images by K-means clustering & DWT. International Journal of Information Technology. 2018, 12(1): 141-148. doi: 10.1007/s41870-018-0255-4
5. Purwar RK, Srivastava V. A novel feature based indexing algorithm for brain tumor MR-images. International Journal of Information Technology. 2019, 12(3): 1005-1011. doi: 10.1007/s41870-019-00412-9

6. Naga Srinivasu P, Krishna TB, Ahmed S, et al. Variational Autoencoders-BasedSelf-Learning Model for Tumor Identification and Impact Analysis from 2-D MRI Images. Dogra A, ed. Journal of Healthcare Engineering. 2023, 2023: 1-17. doi: 10.1155/2023/1566123

7. Aswathy AL, Vinod Chandra SS. Detection of Brain Tumor Abnormality from MRI FLAIR Images using Machine Learning Techniques. Journal of The Institution of Engineers (India): Series B. 2022, 103(4): 1097-1104. doi: 10.1007/s40031-022-00721-x

8. Khan H, Shah PM, Shah MA, et al. Cascading handcrafted features and Convolutional Neural Network for IoT-enabled brain tumor segmentation. Computer Communications. 2020, 153: 196-207. doi: 10.1016/j.comcom.2020.01.013

9. Surya Prabha D, Satheesh Kumar J. Performance Evaluation of Image Segmentation using Objective Methods. Indian Journal of Science and Technology. 2016, 9(8). doi: 10.17485/ijst/2016/v9i8/87907

10. Vidyarthi A, Mittal N. Texture based feature extraction method for classification of brain tumor MRI. Thampi SM, El-Alfy ESM, eds. Journal of Intelligent & Fuzzy Systems. 2017, 32(4): 2807-2818. doi: 10.3233/jifs-169223

11. Jafarpour S, Sedghi Z, Amirani MC. A robust brain MRI classification with GLCM features. International Journal of Computer Applications. 2012, 37(12).

12. Zulpe N, Pawar V. GLCM textural features for brain tumor classification. International Journal of Computer Science Issues. 2012, 9(3).

13. Archip N, Rohling R, Dessenne V, et al. Anatomical structure modeling from medical images. Computer Methods and Programs in Biomedicine. 2006, 82(3): 203-215. doi: 10.1016/j.cmpb.2006.04.009

14. Aravind Kumar S, Ramesh J, Vanathi PT, et al. Robust and Automated Lung Nodule Diagnosis from CT Images Based on Fuzzy Systems. 2011 International Conference on Process Automation, Control and Computing. Published online July 2011. doi: 10.1109/pacc.2011.5979050.

15. Mohanaiah P, Sathyanarayana P, Guru Kumar L. Image texture feature extraction using GLCM approach. International Journal of Scientific and Research Publications. 2013, 3(5).

16. Garland M, Heckbert PS. Surface simplification using quadric error metrics. Proceedings of the 24th annual conference on Computer graphics and interactive techniques—SIGGRAPH '97. Published online 1997. doi: 10.1145/258734.258849

17. Joseph RP, Singh CS, Manikandan M. Brain tumor mri image segmentation and detection in image processing. International Journal of Research in Engineering and Technology. 2014, 3(13): 1-5. doi: 10.15623/ijret.2014.0313001

18. Ravi AR, Ilanchezhian P. Segmenting the contour on a robust way in interactive image segmentation using region and boundary term. International Journal of Computer Science and Information Technologies. 2015; 6(1): 908-912.

19. Patil RC, Bhalchandra AS. Brain tumor extraction from MRI images using MATLAB. International Journal of Multimedia and Ubiquitous Engineering. 2017, 12(12): 1-6. doi: 10.14257/ijmue.2017.12.12.01

20. Nandha Gopal N, Karnan M. Diagnose brain tumor through MRI using image processing clustering algorithms such as fuzzy C means along with intelligent optimization techniques. In: Proceedings of the 2010 IEEE International Conference on Computational Intelligence and Computing Research; 28-29 December 2010; Coimbatore, India. pp. 1-4.

21. Yambal M, Gupta H. Image segmentation using fuzzy C means clustering: A survey. International Journal of Advanced Research in Computer and Communication Engineering. 2013, 2(7).

22. Anandgaonkar GP, Sable GS. Detection and identification of brain tumor in brain MR images using fuzzy C means segmentation. nternational Journal of Advanced Research in Computer and Communication Engineering. 2013, 2(10).