

# The Detection of Brain Tumors User Interface for MATLAB

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**Abstract** — **Background:** Magnetic Resonance Imaging (MRI) has become more popular because it improves brain and soft tissue imaging. Medical imaging areas like MRI benefit from Mathematical Morphology's robust framework for studying geometric characteristics of pictures with their emergence.

**Objective:** This study focuses on influencing mathematical morphology for detecting brain tumours and cancer cells in MRI images, aiming to significantly improve diagnostic accuracy and treatment strategies using the MATLAB graphic user interface.

**Methods:** The methodology encompasses three primary steps: 1) Preprocessing, which includes feature extraction and reduction; 2) Training kernel Support Vector Machines (SVM); and 3) Processing new MRI images through the trained SVM for predictions. This approach, rooted in a proven categorisation technique, is further exemplified through an illustrative algorithmic flowchart. Additionally, the article delves into comprehensive pre-treatment processes, discusses linear and kernel SVMs, and emphasises the importance of K-fold cross-validation to counteract overfitting.

**Results:** The current study on 160 MRI images using SVMs with different Kernels showed good linear separability in feature spaces. The results are rigorously contrasted against decade-old methods

to prove the suggested method's superiority.

**Conclusion:** This study offers an innovative approach to detecting malignant brain tumours by harnessing the capabilities of MATLAB's graphic user interface. Given the severe implications of brain tumours on neurological health and quality of life and the prohibitive costs of treatments, such advancements in diagnostic methods signify a monumental stride in medical imaging and diagnosis.

## I. INTRODUCTION

Magnetic Resonance Imaging technology has emerged as an indispensable tool for capturing highly detailed anatomical images, particularly of the brain, providing crucial data for medical research and clinical diagnosis [1], [2], [3], [4], [5]. Efficient and precise classification of MRI images is essential to enhance the diagnostic utility of MRI [1]. Wavelet transform has proven to be a powerful technique for feature extraction

from MR brain images, offering multi-resolution analysis capabilities. However, its implementation requires significant storage and computational resources [6]. Principal Component Analysis minimises the feature vector's dimension while improving discriminative skills [10]. Various strategies have been proposed for categorising incoming data, broadly classified as supervised classification, including k-nearest Neighbors (k-NN) and Support Vector Machines (SVM) [7], and unsupervised classification, such as fuzzy means and self-organisation feature maps [8]. Although all these techniques have shown promise, supervised classifiers have demonstrated superior performance in the context of classification precision. This article aims to find a more precise technique, as previous methods have achieved classification accuracy rates below 95%. Support Vector Machines stand out as cutting-edge supervised classification techniques grounded in machine learning theory [9], [10].

Their superiority over alternative approaches like artificial neural networks, decision trees, and Bayesian networks arises from their remarkable accuracy, mathematical tractability, and intuitive geometric interpretation. Furthermore, SVMs exhibit the advantage of demanding minimal training data to prevent overfitting [11]. The article explores SVMs with various kernels to achieve linear separability in the D15-dimensional feature space [12]. The subsequent sections of this paper present the comprehensive pre-treatment processes, including discrete wavelet transform (DWT); outline the rationale behind linear SVM and kernel SVM; introduce K-fold cross-validation to prevent overfitting; the methodology, and present the experimental results of Extracting features and minimisation outcomes using a dataset of 160 MRI images. Furthermore, we compare our approach with several state-of-the-art techniques from the past decade. The latter part of Section 6 consists of discussions and conclusions. There are three main parts to our process:

Step 1. Preprocessing (including feature extraction and feature reduction);

Step 2. Training the kernel SVM;

Step 3. Put fresh MRI brains through the training kernel SVM, then output the prediction. This flowchart, which is a classic and accepted technique of categorisation, has previously been proven to be the most effective approach [13], [14], as is seen in Fig. 1. In the subsections that follow, we will go into great depth on the preprocessing steps.

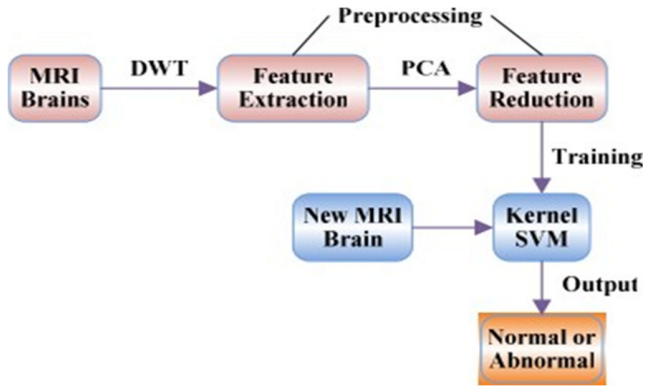


Fig. 1. Methodology of our proposed algorithm

The main objective of this article is to detect malignant brain tumours using the powerful MATLAB graphic user interface, a tool renowned for its algorithms and programming capabilities. Considering the high costs associated with treatments, this interface simulates medical devices for tumour detection and employs various algorithms.

Brain tumours [15] refer to a diverse group of neoplasms that develop within or around the brain's central nervous system. The location of the tumour within the brain has a profound impact on the patient's symptoms, available surgical treatment options, and the feasibility of obtaining a definitive diagnosis. Additionally, the tumour's location within the brain can significantly affect the risk of neurological toxicities that may impact the patient's overall quality of life. Brain tumours can only be detected through imaging after the onset of neurological symptoms.

II. BACKGROUND

A. Discrete Wavelet Transform

A potent WT implementation that makes use of dyadic scales and locations is the discrete wavelet transform (DWT) [16].

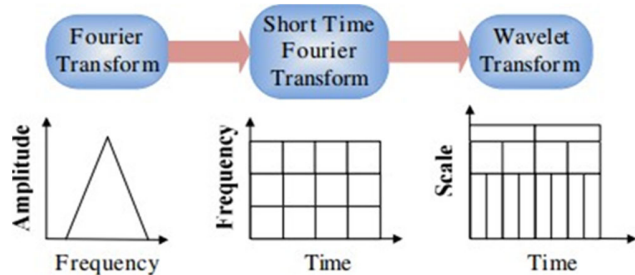


Fig. 2. The development of signal analysis

Discrete Wavelet Transform (DWT) principles can be summarised as follows. If we consider  $x(t)$  to be a square-

integrable function, the continuous Wavelet Transform (WT) of  $x(t)$  concerning a specific wavelet ( $t$ ) is defined as follows.

$$W\psi(a, b) = \int_{-\infty}^{\infty} x(t)\psi_{a,b}(t)dt \tag{1}$$

$$\psi_{a,b}(t) = \frac{1}{\sqrt{a}}\psi\left(\frac{t-a}{b}\right) \tag{2}$$

The mother wavelet ( $t$ ) is used to construct the wavelets  $a$  and  $b(t)$  here. Here,  $a$  is the dilation factor, and  $b$  is the translation parameter (both real positive numbers). Wavelets come in various varieties and have grown in prominence as wavelet research has progressed. The Harr wavelet, the most straightforward and frequently used wavelet in many applications [1], [2] is the most significant. By limiting  $a$  and  $b$  to a discrete lattice ( $a = 2^j$  &  $a > 0$ ), equation (1) may be discretised to produce the DWT, which can be written as follows.

$$ca_{j,k}(n) = DS[\sum_n x(n)g_j^*(n - 2^j k)] \tag{3}$$

$$cd_{j,k}(n) = DS[\sum_n x(n)h_j^*(n - 2^j k)] \tag{4}$$

Here, the terms " $ca_{j,k}$ " and " $cd_{j,k}$ " denote the coefficients of the approximation component and the detail component, respectively. A  $g(n)$  and  $h(n)$  combine low and high-pass filters, respectively.  $j$  and  $k$  represent the wavelet coefficients scale and translation factors, respectively. The DS operator refers to down sampling. The fundamental wavelet decomposition is expressed in equation (3). The signal  $x(n)$  is divided into detail components  $cd$  and approximation coefficients  $ca(n)$ . This procedure, known as one level decomposition, involves decomposing a signal into quality levels. Fig. 3 depicts the wavelet breakdown tree, which represents the whole method.

2D Discrete Wavelet Transform (DWT) for Image Processing. In the case of 2D pictures, the Discrete Wavelet Transform (DWT) is independently applied to each dimension. The schematic design of the 2D DWT is depicted in Fig. 3, resulting in four sub-band pictures (LL, LH, HH, and HL) for each scale. For the subsequent 2D DWT, the sub-band LL is utilised.

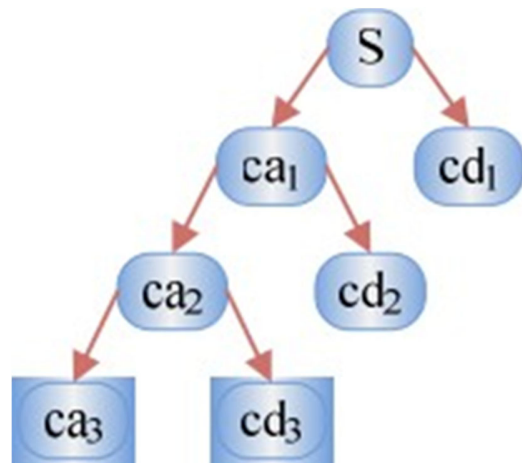


Fig. 3. A 3-level wavelet decomposition tree

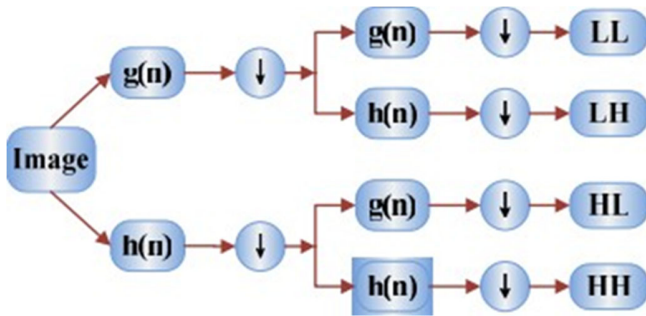


Fig. 4. Schematic diagram of 2D DWT

The LH, HL, and HH subbands represent the detailed components of the image, while the LL subband serves as the approximation component. As the decomposition level increases, a more compact yet coarser approximation component is generated [10]. Wavelets provide a simple hierarchical framework for decoding image data. We extracted features using level-3 decomposition with the Harr wavelet in our approach.

One technical challenge with the digital filter commonly used in DWT is the occurrence of distortion. To address this issue, we padded the pixels outside the images to ensure the mask does not extend beyond the image borders during filtering. The symmetric padding method [17] was employed in our algorithm to figure out what the boundary value is.

#### B. Feature Reduction using Discrete Wavelet Transform in 2D Image Analysis

The presence of additional features in a dataset can lead to longer computation times and increased memory requirements. Moreover, it may introduce complexities in categorisation, commonly referred to as the "curse of dimensionality." To address this issue, the number of characteristics needs to be reduced.

Principal Component Analysis (PCA) offers a solution for reducing the dimensionality of a dataset with interconnected variables while retaining a significant portion of the variations. This is achieved by reorganising the variables based on their variances or relevance. The technique accomplishes three main steps: first, it orthogonalises the components of the input vectors to make them uncorrelated; second, it sorts the resulting orthogonal components in descending order of variation, with the most variant components appearing first; and third, it eliminates the components that contribute the slightest variation to the dataset [18], [19].

It is important to note that the input vectors must be normalised before applying PCA to have a mean of 0 and a variance of 1. Normalisation is a common practice in PCA. Additional information on PCA can be found in [1].

### III. METHODOLOGY

Developing a computer known as a support vector machine was a significant step forward in machine learning. SVMs have several advantages, including high accuracy, attractive mathematical tractability, and simple geometric interpretation.

Recently, the number of upgraded SVMs has rapidly increased, with kernel SVMs being the most popular and effective.

Kernel SVMs offer several advantages [20]:

- 1) They have few adjustable parameters, making them relatively easy to use and tune.
- 2) They exhibit exceptional performance in practical applications and have achieved remarkable success in diverse domains, such as computer vision, bioinformatics, and natural language classification.
- 3) Training with kernel SVMs often involves convex quadratic optimisation [21], which helps prevent convergence to local minima observed in other statistical learning systems like neural networks. The solutions obtained are typically global and unique, ensuring more reliable and consistent results.

A tumour is stratified and classified as benign or malignant using SVM utilising MATLAB code. Texture, DWT, PCA, Statistics, and other aspects are utilised. Ways to run:

Launch the GUI by clicking and selecting an image in BrainMRI GUI.m.

Segment the photo and make a note of the categorisation outcomes.

Depending on the outcome, run the application and choose a benign or malignant tumour.

#### A. Novel approaches in research methodology

Integrating advanced software tools is crucial in dynamic medical imaging, especially identifying brain tumours. We have developed a new MATLAB user interface to improve the brain tumour identification procedure. This interface does not simply provide little improvements to existing systems but signifies a fundamental change in how medical imaging data is processed and analysed.

The main breakthrough of our MATLAB interface resides in its capacity to simplify intricate image processing operations into an intuitive platform. Conventional approaches to brain tumour identification typically necessitate significant manual involvement and experience in image interpretation. Nevertheless, our interface streamlines these procedures, allowing medical practitioners with modest technical expertise in image analysis to detect and classify brain tumours precisely. This advancement represents a substantial progression from the traditional techniques that have predominantly prevailed in the discipline.

Furthermore, the full capabilities of our interface are achieved by incorporating cutting-edge technology such as Artificial Intelligence (AI) and the Internet of Things (IoT). Through AI, the interface may utilise sophisticated algorithms to improve image classification, identify patterns, and conduct predictive analysis, resulting in more precise and timely diagnosis. The utilisation of AI in medical imaging is an expanding area of study, demonstrating encouraging achievements in enhancing diagnostic precision and patient results.

Moreover, incorporating IoT technology enables the instantaneous collection and surveillance of data. This feature is especially beneficial for monitoring the development of brain tumours, allowing for constant observation and prompt intervention. The integration of IoT with our MATLAB interface has the potential to usher in a new age in medical imaging, where real-time data and sophisticated analytics come together to provide unparalleled insights into patient health.

Our study has created a cutting-edge MATLAB user interface that substantially improves brain tumour detection. Theication of intricate procedures and the incorporation of state-of-the-art technologies serve as the capacity of interdisciplinary methods to propel the progress of medical science.

### B. DWT (Discrete Wavelet Transform)

In numerical and functional analysis, a discrete wavelet transform is any wavelet transform where the wavelets are discretely sampled. The foundations of DWT and their MATLAB implementation are discussed in this work. Low pass and high pass filters filter the image (for smooth change between grey-level pixels) (when there is much contrast between the grayscale images.). Decomposition of the image into many levels includes approximation details (LL subband), horizontal detail (HL subband), vertical detail (LH subband), and diagonal details (HH subband).

### C. PCA (Principal Component Analysis)

P orthonormal unit vectors most naturally represent points in a real-valued coordinate system to the initial  $i-1$  vectors. By minimising the average squared length among the points and the line, these vectors lead in the preferred direction of the best-fitting line. Principal Component Analysis involves calculating orthonormal basis vectors known as principal components, ensuring that the data dimensions are not linearly correlated. These principal components are then utilised to transform the data's basis, typically focusing on the top few components while disregarding the rest. This process helps reduce the data's dimensionality while retaining the most significant information. PCA is helpful for in-depth data analysis and the development of forecasting models. Extending information elements onto just the first few significant components makes it possible to acquire lower-dimensional data while maintaining as much variance as possible. The first key element is the most excellent direction that increases the projected data dispersion. The first principle component, which is orthogonal to the first  $i-1$  principal components, is the direction that maximises the variance of the predicted outcomes.

### D. Statistical

The Statistics and Machine Learning Toolbox offer comprehensive capabilities and tools for data modelling, analysis, and description. It provides a range of functionalities, including fitting probability distributions to data, generating random numbers for Monte Carlo simulations, conducting hypothesis tests, and utilising various descriptive statistics, visualisations, and clustering techniques for exploratory data analysis.

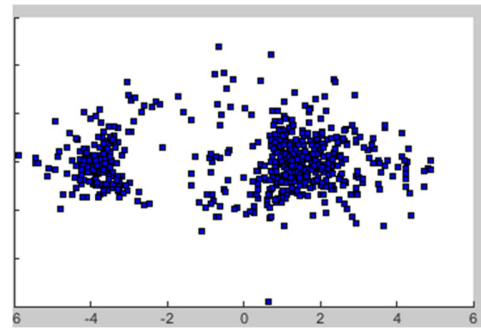


Fig. 5. PCA (Principal Component Analysis)

This toolbox includes classification and regression algorithms accessible through the Classification and Regression Learner applications or programmatically with AutoML. These algorithms enable users to gain valuable insights from data and build accurate prediction models. The toolkit provides practical methods for analysing and extracting features from multidimensional data, such as Principal Component Analysis (PCA), regularisation, dimensionality reduction, and feature selection [22].

Users can use these features to identify and apply variables with the highest predictive value, leading to more effective data analysis and simulation [4]. The Statistics and Machine Learning Toolbox empowers researchers and analysts with powerful tools to handle complex data sets and make informed decisions in various applications.

### E. Advanced Techniques: Utilising Deep Learning and Convolutional Neural Networks in the Analysis of Tumours

The field of medical image analysis has shown notable progress in recent years, primarily due to the emergence of deep learning algorithms. Our research aims to integrate more advanced and current methodological approaches in light of the constraints posed by conventional techniques such as Morphology and SVM in identifying brain tumours. The core of this endeavour revolves around using deep learning algorithms, which have significantly transformed the precision and effectiveness of medical image processing.

Deep learning, a branch of machine learning, excels at processing intricate and high-dimensional data, such as medical pictures. This research investigates the utilisation of Convolutional Neural Networks, a form of deep learning algorithm known for their high efficacy in picture recognition and classification tasks. Convolutional Neural Networks function autonomously and flexibly acquire spatial hierarchies of characteristics from input images, which is especially advantageous for identifying brain tumours.

Our proposed methodology entails creating a customised CNN structure explicitly designed for identifying and categorising brain tumours in MRI data. This architecture is specifically developed to extract and acquire resilient characteristics from imaging data beyond the capability of conventional feature extraction techniques. Our CNN model utilises deep layers and several filters to detect intricate patterns and fluctuations in brain pictures that are often imperceptible to human observers and traditional techniques.

Moreover, including this deep learning method in our MATLAB user interface enhances the practical usefulness of our research. It facilitates the automated examination of MRI scans with enhanced precision and efficiency, aiding radiologists and medical experts in reaching more knowledgeable diagnostic judgements. The interface is designed to be intuitive and easy to use, enabling medical practitioners to take advantage of the advanced capabilities of CNNs without needing extensive expertise in deep learning.

Incorporating Convolutional Neural Networks in our methodology provides ongoing learning and enhancement opportunities. As the model is exposed to additional data, it can enhance its ability to extract features and classify, resulting in increasingly improved performance. This element is especially vital in the medical domain, where dynamic data might offer novel perspectives and difficulties.

Ultimately, by integrating sophisticated deep learning techniques, particularly Convolutional Neural Networks (CNNs), into our approach, our study signifies a notable advancement in brain tumour identification. By integrating advanced computational approaches with medical imaging, this methodology improves the accuracy and efficiency of tumour identification, showcasing its significant potential.

#### F. Texture

Texture in a digital image refers to the spatial distribution of colour or pixel intensities, representing various appearances and consistencies of the scanned physical substance [5]. Texture classification and segmentation of images have significant applications in various fields. One notable example is biomedical image analysis, where distinguishing normal and pathologic states often relies on identifying morphological and histological traits characterised by changes in texture [6].

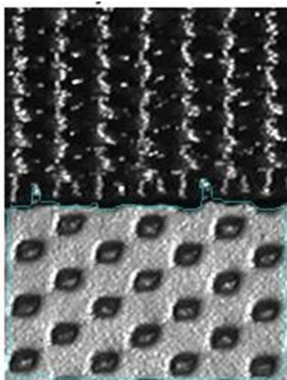


Fig. 6. Texture

#### G. MATLAB Software as a Component

MATLAB, developed by MathWorks, is a proprietary multi-paradigm programming language and computer environment renowned as "Matrix Laboratory." It offers various functionalities, including matrix manipulation, data visualisation, algorithm implementation, user interface development, and interoperability with other programming languages [23].

While the primary emphasis of MATLAB is numeric computing, an optional toolbox using the MuPAD symbolic engine offers symbolic computation capabilities. It also includes the program Simulink, which allows graphical multi-domain simulating and model-based design of integrated and dynamic systems.

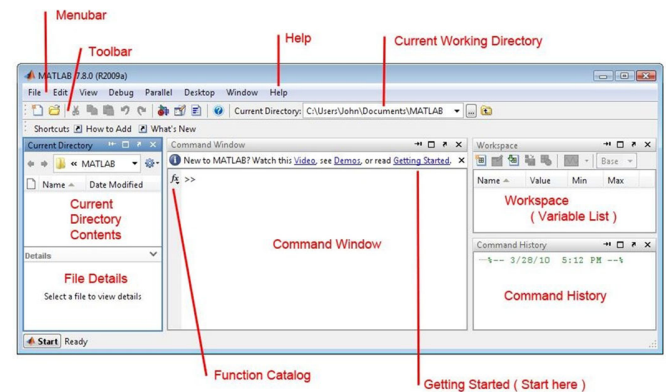


Fig. 7. MATLAB interface

By 2020, MATLAB is projected to have a user base exceeding 4 million, drawing from diverse engineering, science, and economics backgrounds.

One of MATLAB's strengths is its ability to incorporate C or Fortran-written functions and subroutines. This is achieved by creating wrapper functions, allowing for seamless passing and returning of MATLAB data types. The program offers a comprehensive environment for creating dynamically loadable object files known as MEX files (MATLAB executables), resulting from the compilation of specific routines. Furthermore, since 2014, MATLAB has enabled seamless two-way interfacing with Python, significantly expanding its capabilities. In addition to this, MATLAB provides direct integration with libraries developed in Perl, Java, ActiveX, or .NET. It also utilises wrappers for Java or ActiveX libraries to support its libraries, including XML or SQL functionalities. For Java interfacing, MathWorks offers a dedicated MATLAB toolbox. At the same time, an undocumented approach called JMI (Java-to-MATLAB Interface) can also be employed for this purpose (note: not related to Java Metadata Interface or JMI). Although MATLAB is the most widely used commercially accessible software for numerical computation, other alternatives are available, including the open-source programming language GNU Octave, the statistical programming language R, the computing environment Maple, and the programming language Julia [24].

## IV. RESULTS

### A. Image Enhancement

The MRI picture often contains much noise. Using a high pass filter may reduce this by making the picture more contrasty [3]. Here, two distinct samples are shown, one for high-pass filtering and the other for contrast amplification. It is seen in Fig. 8 and Fig. 9, respectively.

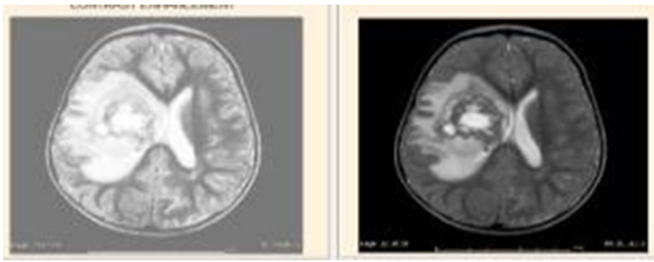


Fig. 8. Contrast enhancement of MRI image

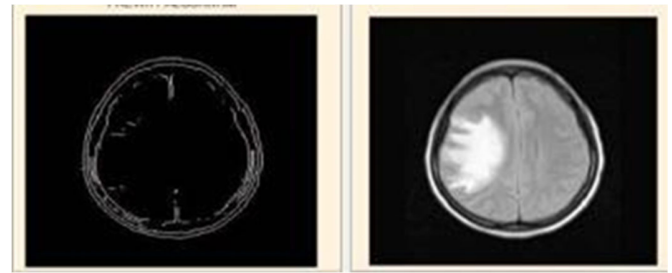


Fig. 12. The output of Prewitt algorithm

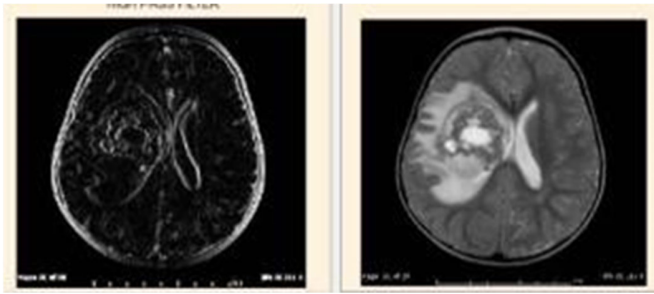


Fig. 9. Enhancement using high pass filter

**B. Edge Detection**

Edge detection algorithms have been used in MRI brain images to differentiate the different areas. Here, the Sobel, Canny, and Prewitt algorithms are used. Each algorithm can clearly distinguish the margins of the brain picture. While the Canny algorithm recognises the borders of every brain area, the Sobel and Prewitt algorithms recognise the margins of a brain picture. The results of the three algorithms above are shown in Fig. 10, Fig. 11 and Fig. 12, accordingly.

**C. Segmentation using Thresholding Technique**

Here, the tumour areas from the picture where the brain tumour region can be seen are segmented using the threshold segmentation approach [12]. Fig. 13 illustrates the outcome.

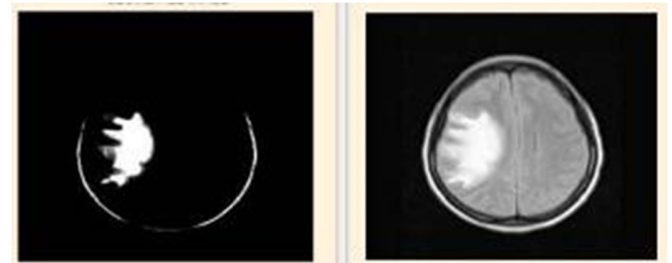


Fig. 13. Segmentation using thresholding method

**D. Final Output**

Only the tumour locations seen in the MRI brain scan are predicted in the final picture. Fig. 14 shows the location, which was determined to be a tumour and a mass of white pixels.

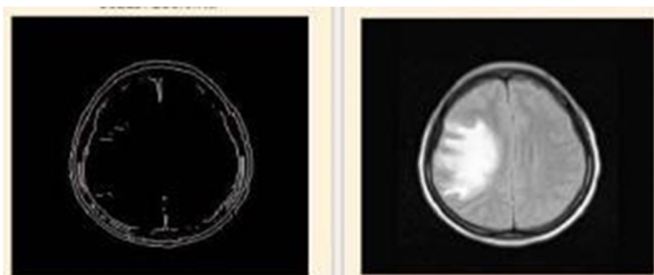


Fig. 10. The output of Sobel algorithm



Fig. 14. Final predicted brain tumour region



Fig. 11. The output of the Canny algorithm

**E. Implementation and Execution of SVM Classification**

The stratification of a tumour and SVM classification of it as benign or malignant is done using MATLAB code. DWT, PCA, statistical analysis, texture, and other characteristics are applied. How to run;

- 1) The Brain Tumor Code folder should be unzipped and added to the MATLAB directory, and then the two datasets should be added.

- 2) Open the BrainMRI GUI.m GUI and select a picture by clicking.
- 3) Divide the image into segments and note the results of the categorisation.
- 4) Start the software, then choose whether to show the data as a benign tumour or a malignant tumour.

The interface looks like the one in Fig. 15 below when you first launch the software.

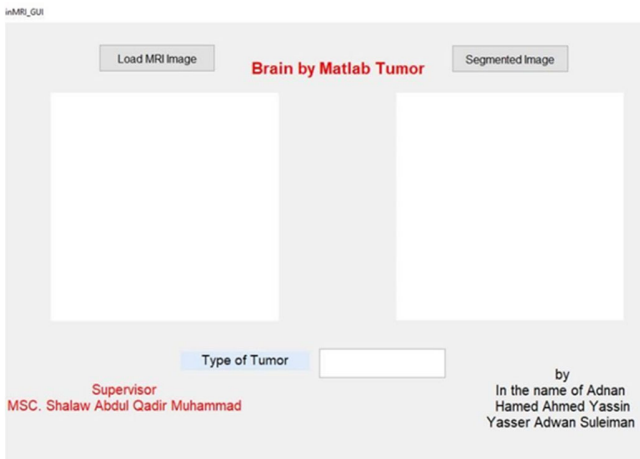


Fig. 15. MATLAB Operation Interface

After running, we go to where the images of the brain are located, and we bring them into the program by pressing the (Load MRI Image) button.

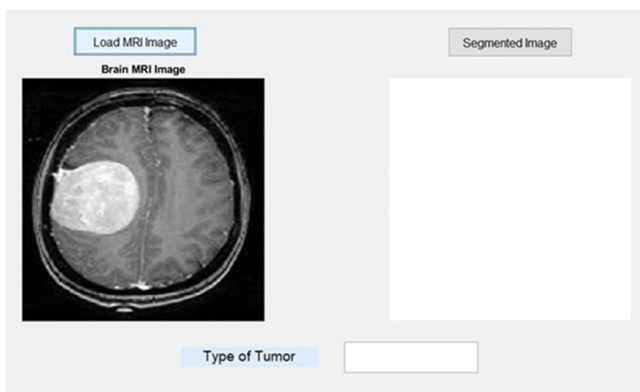


Fig. 16. Inserting the image into the program

After importing the picture, we click the "Segmented Image" button to reveal if the image is benign or malicious by displaying a dialogue box or entering text in the "Result" field (Type of Tumor).

The result through the analysis is either the tumour is (Benign), or the tumour is (Malignant).

## V. DISCUSSION

The article aimed to optimise the detection of brain tumours using MRI imaging, employing image processing methods and their respective prerequisites and characteristics. The objective

was to enhance the efficacy of detecting brain tumours on MRI scan images, a goal we believe has been satisfactorily achieved based on the findings of our study.

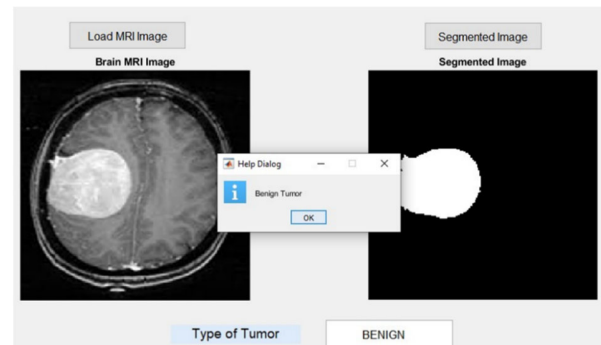


Fig. 17. Brain image analysis result

In the paper, we employed the thresholding segmentation approach to differentiate tumour-affected areas from other brain tissues, drawing inspiration from the work of Cocosco, Zijdenbos, and Evans [11] in exploring automatic and robust brain MRI tissue classification methods. However, we introduced a novel DWT + PCA + KSVM method, offering a distinct advantage over existing literature by effectively distinguishing between normal and pathological brain MRI scans. This approach proved highly effective, surpassing the performance of the widely used techniques reported in recent studies. For instance, the GRB kernel SVM in our study achieved a classification accuracy of 99.38% on 160 MR images. This is a notable improvement over the classification methods used by Zhang and Wu [1] and Wang and Zhang [25], further underscoring the innovation of our research.

The paper also echoes the assertion of Zhang, Wu, and Wei [1], which underlines the importance of weight optimisation of neural networks for enhanced classification. Similarly, Patil et al. [13] and Li, Yang, and Wang [26] have highlighted the relevance of regression models and support vector machines in differentiating between various classes.

Using MATLAB's graphical user interface presented some challenges, as outlined in our study. This is a common issue encountered in similar research, as the application of algorithms to MATLAB software for detecting malignant tumours can be complex [5], [6], [27], [28]. However, these challenges did not hinder our research goals and represent areas for potential improvement in future studies.

Moving forward, we propose focusing on four primary areas for future work. These include processing MR images containing additional contrast mechanisms using an SVM-based technique, applying advanced wavelet transformations, performing multiple classifications, and evaluating new kernels to improve categorisation. These areas would significantly advance the current state of brain tumour detection and classification.

Furthermore, our article sets the stage for more studies to explore the use of Kotlin and the Android Software Development Kit (SDK) in the development of Android apps for medical diagnostics, especially for detecting and classifying

brain tumours [4], [10], [14], [19], [29], [30]. We also anticipate future research to integrate our findings with IoT technology for real-time monitoring and detection of brain tumours [26], [31].

The article introduces a novel approach to detecting and classifying brain tumours using MRI imaging. While our results are encouraging, there is still much room for further exploration and development. Future studies should continue to refine these methods and explore new technological advancements to improve brain tumour detection and categorisation accuracy and effectiveness.

## VI. CONCLUSIONS

MRI imaging proves to be highly effective for brain tumour detection. In this study, we extensively analysed various image processing methods and discussed their characteristics and prerequisites in the context of brain tumour detection from MRI scan images. Segmentation and edge detection play vital roles in medical diagnostics, and we employed the thresholding segmentation approach to accurately distinguish tumour-affected areas from other brain tissues.

Our novel DWT + PCA + KSVM approach successfully discriminated between normal and pathological brain MRI scans. Among the four different types of kernels, the GRB kernel SVM exhibited an impressive classification accuracy of 99.38% on 160 MR images, outperforming the other widely used techniques recently published.

We propose focusing on the following four areas: exploring SVM-based techniques for MR images containing additional contrast mechanisms such as T1 weight and proton density, weighted twice. Second, we will investigate advanced wavelet transformations, including levitating wavelets, to enhance speed and accuracy. Third, multiple categorisations will be conducted to investigate further researched illnesses in brain MRIs. Finally, four new kernels are evaluated to improve categorisation.

Despite challenges in using MATLAB's graphical user interface and implementing algorithms within the software, we have made significant progress in detecting malignant brain tumours. Future enhancements can involve adopting new segmentation approaches to achieve even higher accuracy in tumour area detection and utilising sophisticated clustering algorithms and classification techniques to enhance efficiency. Ultimately, our system can potentially categorise brain tumours as benign or malignant with improved precision shortly.

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