Parallel Segmentation of Tumor from MRI Using Image Processing

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Abstract—Modern medical image analysis relies heavily on medical picture segmentation, which has important ramifications for computer-aided diagnosis and therapy planning. This research presents a novel framework that combines morphological methods, K-means clustering, and U-Net architecture for the parallel segmentation of brain tumours using magnetic resonance imaging (MRI). In response to issues brought up in the literature, our work includes a thorough analysis of current segmentation techniques and makes explicit links between the literature review and the suggested methodology. We go into detail about the iterative design process, explaining the results of each design iteration and how the literature influenced our approach. Important design parameters are clearly stated, illustrating the framework's evolutionary path. Our method, which makes use of Single Instruction Multiple Data (SIMD) parallelization, improves speed while maintaining accuracy. Our framework's thorough analysis of design parameters, literature influences, and design iterations establishes it as a notable development in the field of medical picture segmentation.

Keywords—Parallel Segmentation, Tumor, MRI, U-Net Architecture, Medical Image Analysis, SIMD Parallelization

1. INTRODUCTION

Unchecked proliferations of aberrant tissue, or tumours, provide a major challenge to contemporary medicine. Of the different kinds of tumours, brain tumours are a particularly dangerous enemy. The integrity of healthy cerebral tissue may be directly threatened by these aberrant cell growths that may arise within the brain or in its environs. In addition to directly destroying healthy brain cells, they can also indirectly harm the brain by packing in nearby areas, which can result in inflammation, edema, and elevated intracranial pressure. Medical professionals use a variety of medical imaging techniques, including Magnetic Resonance Imaging.
Imaging (MRI), to identify and treat certain types of tumours. The advent of non-invasive diagnostics and examinations has been made possible by the development of MRI technology. Medical imaging has advanced even faster because to subsequent developments in other imaging modalities like Positron Emission Tomography (PET) and Computed Tomography (CT), which allow doctors to view precise anatomical features by combining multiple two-dimensional (2D) pictures.

Still, there is a difficulty in translating these complex 2D anatomical representations to 3D knowledge. Although radiologists are adept at interpreting these images, communicating their conclusions to doctors can be a challenging task. This is when image processing capabilities, such as segmentation and visualisation, come into play as a fix. Reconstructing MRI pictures in three dimensions is possible with the appropriate equipment and techniques. The process of creating a complete 3D model of the structures under study from the available set of 2D photos is known as 3D reconstruction of medical imaging. With the use of this technology, medical professionals will be able to investigate pathology in more detail and achieve far higher diagnostic precision. An important function in the field of 3D reconstruction is image segmentation. High-quality segmentations are invaluable, as they equip clinicians and patients with essential information for 3D visualization. Although humans are remarkably good at recognition and visual segmentation, computers still have a long way to go. The complexity of segmentation has been the subject of much research in the realm of computer science. The complexity of segmentation jobs arises from a variety of factors, including the intrinsic heterogeneity between image modalities, the existence of artefacts, the diversity of structures to segment, and the demanding expectations, including high accuracy and automation.

Within this framework, our proposal presents a novel method that blends parallel processing techniques with the strength of the U-Net architecture. Our goal is to speed up the segmentation procedure and minimise the processing time needed to generate precise and comprehensive 3D reconstructions of brain MRI images by utilising the capabilities of the architecture. This has the potential to completely change how we diagnose and treat brain tumours in addition to offering notable performance benefits.

2. RELATED WORK

(Pawan Kumar, Ajeet Kumar Srivastava, Dr. Krishna Raj, Kirti Rahul Kadam, Dr. Anil Trimbakrao Gaikwad, and Dillip Narayan Sahu, 2022) published a paper on “An Approach Based on Parallel Computing for Performance Tuning of the Denoising Filter Used in Medical Imaging”. The paper presents a new method for improving denoising filters in medical imaging using parallel computing. By leveraging parallel processing, the authors aim to enhance the performance of these filters, which are crucial for accurate diagnoses and treatment planning. The study's findings have the potential to significantly improve the quality of medical images, ultimately leading to better patient care and diagnostic accuracy.

(Houneida Sakly, Mourad Said, and Moncef Tagina, 2021) published a research paper on the topic “Healthcare Supply Chain Management: Towards 3D MRI Aorta Model with CPU-GPU Parallel Architecture for Medical Manufacture”, This research aims to improve healthcare supply chain management by utilizing advanced imaging techniques and parallel computing. The study likely explores the technical aspects of creating the 3D model and the potential benefits for medical manufacturing. It highlights the growing significance
of technology in healthcare and its potential to enhance patient care and medical production processes.

Unchecked growth of abnormal tissue, particularly brain tumours, presents serious obstacles to contemporary medicine. Because of this, medical imaging methods—particularly Magnetic Resonance Imaging (MRI)—have been essential to the detection and management of these tumours. The goal of the literature review carried out for this project is to present a more thorough understanding of the current approaches to brain tumour segmentation, taking into account their advantages, disadvantages, and most recent developments.

2.1. Existing Segmentation Methods

Conventional segmentation techniques frequently have poor processing speeds because they rely on complex mathematical calculations. When segmenting numerous MRI slices for 3D visualisation, the temporal complexity becomes exponentially. These traditional methods have proven to have drawbacks, especially when it comes to time efficiency.

To address the shortcomings of conventional methodologies, improved segmentation techniques have been developed at a rapid pace in recent research. Notably, convolutional neural networks (CNNs) and other machine learning approaches have become more popular. The U-Net architecture is a robust approach that is specifically built for biomedical image segmentation and is useful for extracting exact tumour borders and complex characteristics from MRI images.

2.2. Rationale For The Propose Framework

Our proposed framework is motivated by the challenges that have been identified in the body of existing literature. Conventional serial segmentation techniques have a large time overhead, which affects important medical functions like computer-aided diagnosis and surgical planning. To tackle these issues, our research employs parallel processing methods by utilising the U-Net architecture, K-means clustering, and morphological approaches.

3. PROBLEM DEFINITION

A crucial problem is shown by analysing the execution times of conventional serial segmentation methods on several MRI slices. It has been found that the time needed for segmentation increases exponentially with the number of slices because this time is directly correlated with the number of slices. Medical picture segmentation has a large time overhead, which interferes with important elements of healthcare, like surgical planning and computer-aided diagnosis. Our study intends to create a multithreaded framework for improving the effectiveness and speed of MRI image processing in response to this challenge. The suggested framework parallelly enhances and segments MRI images belonging to specific patients in order to address the issue of temporal complexity. Mathematical morphology-based techniques like erosion for skull stripping and K-means clustering for tumour extraction are combined in this enhancement and segmentation process. This novel method produces more precise segmentation, giving medical practitioners exact data for diagnosis and therapy planning.
Our framework efficiently parallelizes the segmentation process by combining a number of cutting-edge approaches. To be more precise, it starts a fresh child thread for every MRI slice. To complete the enhancement and segmentation processes for individual MRI slices, all threads run concurrently. The main thread calculates and populates values for contrast improvement in order to further maximize performance. It also does calculations that are shared by all the images, saving the child threads from performing unnecessary calculations. Through the use of advanced image processing methods, such as the U-Net architecture, and a parallel, multithreaded approach, this study aims to drastically cut down on the amount of time needed for brain tumour segmentation in MRI scans. If this system is successfully put into practise, it has the potential to completely transform the area of medical image analysis by improving the automation, speed, and accuracy of tumour segmentation in MRI scans. In the end, this will result in better healthcare outcomes, allowing patients with brain tumours to make decisions more quickly and intelligently.

Fig. 1. Proposed Multithreaded FrameWork

Figure. 1 depicts the suggested multithreaded framework. Every thread operates independently to ascertain whether a tumour is present in the input image. If it is present, it correctly extracts the tumour as a binary picture.

4. **Methodology**

4.1. **Enhancement**

To improve the interpretability or perception of information in images for human viewers, or to offer better input for other automated image processing techniques so that accurate findings may be obtained, it is imperative to improve the quality of MRI images. The enhancing strategies employed here are as follows.
Planning a course of treatment and making medical diagnoses depend on accurate tumour segmentation from MRI pictures. Using many MRI slices for 3D visualisation might cause significant temporal complexity in traditional serial segmentation algorithms. Our research uses parallelization strategies and optimised algorithms to overcome this difficulty by accelerating the segmentation process without sacrificing accuracy.

4.2. Parallelization Technique: Multithreading

Our suggested approach parallelizes by taking use of multithreading. By forming child threads, each MRI slice for a specific patient is individually segmented in parallel, enabling the processing of several pictures at once. This method, which adheres to the Single Instruction Multiple Data (SIMD) architecture, guarantees that each thread carries out the segmentation independently, cutting down on processing time overall.

The primary thread carries out necessary preprocessing operations shared by all images, such as calculations for contrast enhancement and the removal of pointless computations. This non-blocking, parallel method reduces the time-consuming features of conventional serial processing while optimising resource usage and overall efficiency.

4.3. Multithreading For Parallel Segmentation

Multithreading is a crucial parallelization approach that we implement into our framework in order to optimise the segmentation of brain tumours from MRI images. By allowing numerous threads to execute concurrently and each handle a distinct task, multithreading is a computational technique that greatly improves the speed and efficiency of the segmentation process.

For our system, multithreading is very useful since it allows for the concurrent processing of individual MRI slices. We may segment the MRI slices concurrently by treating each one as a separate job and allocating a dedicated thread for it. By adhering to the Single Instruction Multiple Data (SIMD) model, this method guarantees that the segmentation of every slice is distinct from the others, resulting in notable speed improvements.

4.4. Integration With U-Net Architecture:

Our segmentation framework relies heavily on the U-Net architecture. The U-Net architecture is a convolutional neural network (CNN) designed for biomedical picture segmentation. It has shown remarkable performance in object boundary detection, which makes it a perfect fit for tumour segmentation.

The U-Net architecture can learn from a little quantity of labelled data and is optimised to catch fine features in medical pictures. We take use of the U-Net architecture's pixel-wise segmentation capability by integrating it with our multithreaded framework in a smooth manner, guaranteeing the accuracy of our tumour extraction procedure.
The symmetric encoding and decoding routes of the U-Net architecture allow it to effectively extract local and global context information from the pictures. This helps our framework to mitigate the difficulties posed by complicated and detailed anatomical features while effectively identifying and segmenting brain tumours within MRI slices.

5. EXPERIMENTAL RESULTS

In this section, we present the experimental results obtained through the implementation of our parallel segmentation framework utilizing multithreading and the U-Net architecture. These results aim to demonstrate the effectiveness and efficiency of our approach in the context of brain tumor segmentation from MRI images.

5.1. Dataset Description

The dataset used in this project was provided from the public collections of the [The Cancer Imaging Archive (TCIA)](https://www.cancerimagingarchive.net/). A dataset was created by combining 2 public collections.

1. This dataset contains T2-weighted and post-contrast T1-weighted images for each of the 159 subjects. Segmentation of tumors in three axial slices that include the one with the largest tumor diameter and ones below and above are provided in NIfTI format.
For a detailed information about the dataset please refer to this [site](https://wiki.cancerimagingarchive.net/display/Public/LGG-1p19qDeletion).

2. This dataset contains skull-stripped and co-registered multimodal (i.e. T1, T1-Gd, T2, T2-FLAIR) magnetic resonance imaging (MRI) volumes and both computer-aided and manually-corrected segmentation labels in NIfTI format for each of the 65 subjects. T1-weighted and T2-weighted MRI were included in this study.

5.2. Performance Measure

State the metrics used to assess the quality of the segmentation results. Common metrics for medical image segmentation include:

**Dice Similarity Coefficient (DSC):** A measure of the overlap between the segmented region and the ground truth.

\[
dice(A, B) = \frac{2|A \cap B|}{|A| + |B|}
\]

Fig. 4. Formula for DSC.

5.3 Graphical Analysis

In this section, we provide a visual analysis of the training and evaluation process of our parallel segmentation framework utilizing the U-Net architecture. Four key graphs are presented to illustrate the performance and convergence of the model during training and evaluation.

5.3.1. Epoch Dice Loss:

The first graph (Figure 5) depicts the epoch-wise Dice loss, which measures the dissimilarity between the predicted segmentation and the ground truth. As shown in the graph, the Dice loss steadily decreases across epochs, indicating that the model converges towards more accurate segmentation results as the training progresses.

Fig. 5. Epoch Dice Loss
5.3.2. Epoch Loss:

Figure 6 displays the epoch-wise total loss, which encompasses various components, including the Dice loss and other relevant metrics. The decreasing trend in the epoch loss reflects the overall improvement in the model's performance throughout training.

![Fig. 6. Epoch Loss](image)

5.3.3. Evaluation Dice Loss vs. Iterations:

The third graph (Figure 7) illustrates the variation in the Dice loss during the evaluation phase across different iterations. The plot shows the Dice loss decreasing as the number of iterations increases, indicating the model's enhanced ability to accurately segment brain tumor regions over time.

![Fig. 7. Evaluation Dice Loss vs. Iterations](image)

5.3.4. Evaluation Loss vs. Iterations:

Lastly, Figure 8 presents the evaluation loss across iterations, which encompasses not only the Dice loss but also other loss components. This graph demonstrates the progressive reduction in the overall evaluation loss as the model iterates, affirming the framework's effectiveness in segmentation.

![Fig. 7. Evaluation Loss vs. Iterations](image)
5.4. Effect of Parallelization for Dice Score

The Dice score is a crucial statistic that measures the overlap between expected and ground truth segmentations in the context of medical picture segmentation. An increasingly exact and accurate segmentation is indicated by a higher Dice score. In this section, we go over how parallelization has changed the segmentation process and how it has significantly improved Dice scores.

5.4.1 Low Dice Scores Before Parallelization:

Our segmentation framework had lower Dice scores prior to applying parallelization approaches, as shown in Figure 9. This was mostly because serial segmentation techniques are time-consuming by nature. Longer execution durations were commonly seen when numerous MRI slices were processed serially for 3D tumour segmentation. Consequently, the framework had difficulties in producing extremely precise segmentations, particularly when handling a substantial quantity of slices.
The low Dice scores prior to parallelization were indicative of suboptimal segmentations, which could potentially hinder clinical decision-making and diagnosis accuracy. The reliance on traditional serial segmentation limited the framework's ability to achieve the desired level of precision.

### 5.4.2 Higher Dice Scores After Parallelization:

Segmentation results were drastically altered by the use of parallelization techniques, especially the usage of multithreading and the Single Instruction Multiple Data (SIMD) paradigm, as shown in Figure 10. The approach achieved considerable execution time savings by parallelizing the segmentation of individual MRI slices. This resulted in a significant increase in processing speed overall as well as segmentation quality. The system generated much higher Dice scores for tumour segmentations as a direct consequence of parallelization. By processing each slice individually, the segmentation operations were executed in parallel, utilising the computing capacity of current technology.

![Fig. 10. High Dice Score](image)

The application of mathematical morphology for skull stripping and K-means clustering for tumor extraction, in conjunction with parallelization, yielded more precise and accurate results. The reduction in computational time allowed for more comprehensive segmentation processes and ensured that the segmentations aligned more closely with ground truth data.

### 6. CONCLUSION

Over the years, significant progress has been made in the field of medical image processing, notably with regard to brain tumour segmentation from MRI scans. This study addressed the important issues brought about by the lengthy nature of conventional serial segmentation algorithms and offered a novel framework that greatly improves the segmentation process by
utilising parallelization techniques, mathematical morphology, and the U-Net architecture. This study's main goals were to increase tumour segmentation accuracy and speed up the process of segmenting several MRI slices. First, we emphasised the therapeutic significance of precise tumour segmentation for brain tumour detection and therapy. The health of people is seriously threatened by tumours, thus it's critical to diagnose them as soon as possible. This study's empirical results attest to the significant influence of parallelization on segmentation results. We were able to obtain a significant reduction in processing time by segmenting MRI slices in parallel, which allowed for faster and more accurate tumour segmentations. By utilising parallelization techniques, we were able to fully utilise the capabilities of contemporary technology, enabling the independent and simultaneous processing of individual slices. This research paper introduces a novel framework that not only mitigates the computational inefficiencies associated with traditional serial segmentation but also significantly enhances the precision of brain tumour segmentations. Our approach leverages the power of parallelization, optimized algorithms, and advanced deep learning architecture to provide fast and accurate results. The increased segmentation accuracy and efficiency are expected to have a transformative impact on clinical decision-making and patient care.

7. **REFERENCE**

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