

Study of Manhattan and Region Growing Methods for Brain Tumor Detection

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Abstract—This paper investigates the utilization of region-growing segmentation and Content-Based Image Retrieval (CBIR) techniques to predict brain cancer, particularly focusing on brain tumors. Recent advancements in medical science have brought about promising diagnostic methods and treatments, offering patients renewed hope for recovery. However, the existing problems in diagnosing brain cancer include time inefficiency, inconsistency, inaccuracy, and costly. Hence, this study aims to find an innovative approach to address the predicaments of cancer diagnosis by harnessing the power of artificial intelligence, specifically within the realm of computer vision. The methods of region-growing segmentation and CBIR are particularly employed for this purpose. To predict the presence of brain tumors, these methods are applied to brain CT-scan images. The dataset comprises over 800 images sourced from Kaggle.com and a hospital in Lampung, Indonesia. The effectiveness of the region-growing segmentation method is evaluated using Receiver Operating Characteristics (ROC) analysis, along with an assessment of the quality of affected regions within brain CT-scan images. The study demonstrates that the segmentation methods achieve an accuracy rate of 79% when tested on a dataset consisting of 400 normal brain CT-scan images and 400 brain cancer CT-scan images. Simultaneously, the accuracy of brain image retrieval using CBIR techniques is remarkable, surpassing 96% and 94% with the Manhattan and Euclidean distance metrics, respectively. In conclusion, the findings of this research indicate that the combination of CBIR and segmentation methods can substantially enhance the performance of algorithms designed for brain tumor detection.

Keywords—brain tumor, segmentation, Content-Based Image Retrieval (CBIR), CT-Scan

I. INTRODUCTION

Brain tumor detection using CT-Scan is a complex and crucial task, and addressing these issues will be instrumental in developing accurate and reliable Artificial Intelligent systems to aid healthcare professionals in diagnosis and treatment planning.

The World Health Organization states that generative diseases, including brain cancer and tumors, are the major cause of death in the population aged 65 years and older,

with additional deaths in emerging countries [1]. Furthermore, estimated that 23 of women and 14 of men aged over 65 years suffer from generative diseases, including tumors [2]. Meanwhile stated that based on data collected from 1991 to 2007, generative diseases are the main cause of death as well as disability in the Asian Hospital Association (PERSI) [3].

In 2009, a research investigation indicated that brain cancer stood as the primary factor behind fatalities occurring within hospital environments. Among the cases, 15% were attributed to brain tumors [4]. To concisely recap the details, brain cancer emerges due to the abnormal multiplication of cells within brain tissues. Furthermore, as noted by Zhou *et al.* [5], brain tumors are typically divided into two primary classifications: benign and malignant. The benign variation typically experiences gradual growth and seldom spreads to other locations, while the malignant form demonstrates swift expansion and has a propensity for rapid dissemination.

Garg and Garg [6] explained that depending on where a brain tumor begins, it can be classified as secondary cancer, which can occur in another part of the body and then spread through the bloodstream to the brain. This is acknowledged as secondary cancer or metastasis. The cancers most likely to spread to the brain are melanoma, lung, breast, kidney, and bowel. A metastasis retains the term of original cancer. For instance, bowel cancer that has spread to the brain is still referred to as metastatic bowel cancer, even though the patient may be showing signs because cancer has spread to the brain [7]. The classified tumor images have been passed to the proposed Seg-network segmentation method, where the actually infected region is segmented to analysis the tumor severity level. The outcomes of the reported research have been evaluated on three benchmark datasets, such as Kaggle, 2020-BRATS, and locally collected images. The model achieved greater than 90% detection scores to prove the proposed model's effectiveness [8].

A proposed novel Correlation Learning Mechanism (CLM) for deep neural network architectures that combines Convolutional Neural Networks (CNN) with classic architectures has been introduced by Visa and Salembier [9]. Moreover, they used a neural support network, which helped CNN find the adequate filers for pooling and convolution layers. As a result, the main

neural classifier learns faster and reaches higher efficiency. Results show that our CLM model is able to reach 96% accuracy.

We have described our proposed mechanism and discussed numerical results to draw conclusions and show future work. The aim of this work is to introduce an algorithm into a computer-aided tool so that it can assist in the detection of brain tumors suffered by patients quickly and accurately. The research proposes to build an algorithm that can determine the location of brain tumors from CT-scan images. The benefits obtained from this study are intended to help radiologists diagnose the types of brain tumors suffered by patients rapidly and accurately. Patients in the intensive care unit, and it also becomes one of the references for scientists who focus on computer vision technology in medical imaging.

Biratu *et al.* [10] considered that cancer or brain tumors could influence the central nervous system. When tumor cells invade the brain, then all functions of the body are interrupted, and there is a high risk of death. Additionally, Aboussaleh *et al.* [11] explained that brain tumors can either be malignant or benign. Therefore, this research is aimed at detecting an early stage of a brain tumor so that it does not have time to attack very important parts of the brain and interfere with body functions. Early detection is also needed so that the diagnostic results are precise and accurate. Imaging technology is required to aid in the diagnosis, treatment, and operation of brain surgery. Another proposed of the research is to provide the earliest possible warning to reduce mortality and develop appropriate and rapid methods to treat brain tumors. These works were established by using image region-growing segmentation and Content-Based Image Retrieval (CBIR) with Euclidean and Manhattan distance metrics to produce a better result for brain tumor prediction.

This work also tried to develop applications based on segmentation and Content-Based Image Retrieval (CBIR) techniques. CT-Scan images were collected and deployed from both the hospital and Kaggle.com. According to Venugopalan's study [4], statistical analysis, which includes mean, standard deviation, and variance extracted from object characteristics in the image, can show healthy and sick brain conditions by comparing each of the statistical values of images and detected images. In this work, we tried to diagnose brain conditions using segmentation and CBIR techniques. In addition to diagnose symptoms of disease based on medical photographs (medical images), particularly CT-Scan images. This paper attempts to introduce the fusion of two methods, segmentation and CBIR in order to improve the accuracy of brain tumor detection. Some research has been conducted to try to solve and detect brain tumors as early as possible, such as [11–14] and many other studies; however, their accuracy in medical diagnosis has not been accepted. They used methods such as Support Vector Machine (SVM), Fuzzy C-Means (FCM), and K-Nearest Neighbor (KNN). Considering this, our work tries to introduce an alternative technique to fill the gap left by those studies by using integrated segmentation and CBIR methods.

The primary achievement of this research is an enhancement in the accuracy of brain tumor detection. One of the main goals of applying these methods would be to improve the accuracy of brain tumor detection compared to the works of [15–18], and [8] methods. By leveraging Manhattan distance and region growing, the study might have aimed to better delineate tumor boundaries, minimize false positives or negatives, and enhance the overall detection performance. This could potentially lead to earlier and more accurate diagnoses, improving patient outcomes. Our works might have contributed to the field of medical image analysis by advancing the understanding of how these methods perform compared to other established techniques for brain tumor detection. Comparative analyses with other segmentation methods could help highlight the strengths and limitations of the Manhattan and region growing approaches [19]. Moreover, work also introduces an application of Manhattan Distance (also known as L1 distance) is a distance metric used in various fields to measure the “city-block” distance between two points. In the context of brain tumor detection, the study likely applied the Manhattan distance metric to quantify the dissimilarity or similarity between image pixels or regions within medical images. This application of Manhattan distance might have been used to differentiate between tumor and non-tumor regions based on the intensity or texture characteristics of the image.

The rest of the paper will be structured as follows. Section I explores what is image segmentation and CBIR and describes in detail how it is defined in the context of this paper. It is also explained the proposed method in this work. Section III will give the experiment results and discussion. Section IV describes the conclusion and future works.

II. MATERIALS AND METHODS

The individual images obtained from the CT-Scan are subsequently transformed into digital images using a scanner and the online platform Kaggle (Kaggle.com). In this study, more than 800 CT-Scan images were used. Fig. 1 shows examples of the brain with and without tumors.

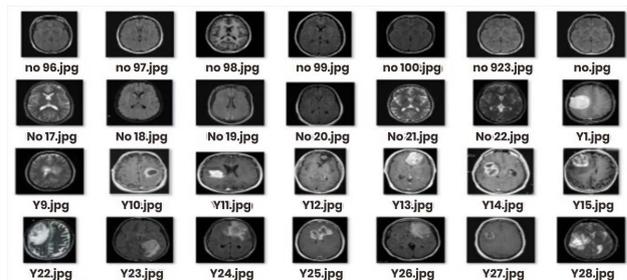


Fig. 1. Examples brain with and without tumors images (Y1...n: brain with tumor, N1...n: Brain without tumor).

A. Segmentation

In this study, segmentation and CBIR methods were used to attempt to separate and retrieve brain image regions or CT-Scan images into regions affected by

generative diseases and those that were not. The research used integrated region-growing segmentation and CBIR methods, which are not been using before in past years. Whilst [15] used region-growing segmentation algorithm to improve image quality, and brain tumor detection method in medical imaging have been presented by some researchers, such as [11, 13, 20, 21]. They stated that region-growing algorithms start from an initial, incomplete segmentation and attempt to aggregate the unlabeled pixels into one of the initial regions. The initial regions are usually called seed regions or seeds. The decision of whether a pixel should join a region or not is based on some fitness function that reveals the similarity between the region and the candidate pixel. As proposed by Morales [22], the order in which the pixel is processed is determined by a global priority queue that sorts all candidate pixels by their fitness values. This approach elegantly mixes local (fitness) and global (pixel order) information. The algorithm can be summarized in Fig. 2.

The process of separating one object from another in an image or between objects and the background contained in an image using certain parameters is known as segmentation. Multi-resolution segmentation also requires parameters such as scale, color, shape, density, and subtlety. The size and shape of the image of an object can be affected by different parameter values; it should also be noted that finding the appropriate object size and shape for classification takes a lot of time and is very subjective [8, 23]. Singh and Hemachandran [24], Hassan *et al.* [25] explained that CBIR is the process of recognizing a digital image, it must use the contents contained in the image. It simplifies the features that can be obtained or used as features into other forms to facilitate computer calculations and produce accurate features. Each image stored in the database has been extracted, and its features have been compared to the features of the query image. In this case, there are two steps to take: first, feature extraction, which is a process to extract the features of the image that can be partially distinguished, and second, matching those features to produce results that are visually similar to the query image.

This work uses region-growing segmentation since it is most widely used by many researchers and more accurate compared to others [26, 27]. Previous research has shown that Region-Growing Segmentation (RGS) has some advantages, including the ability to accurately separate the same properties within a defined region, provide good segmentation results when images have strong edges, require a small number of seed points, perform well against noise, and use images more than one criterion at the same time.

B. Segmentation Accuracy

In assessing the precision of brain image segmentation, this study employed Intersection over Union (IoU) metrics. These metrics determine the proportion of pixels shared between the target and predicted masks, dividing this by the total area of the present crosswise mask in the overall image [28].

$$IoU = \frac{goal\ pixels \cap prediction\ pixels}{goal\ pixels \cup prediction\ pixels} \quad (1)$$

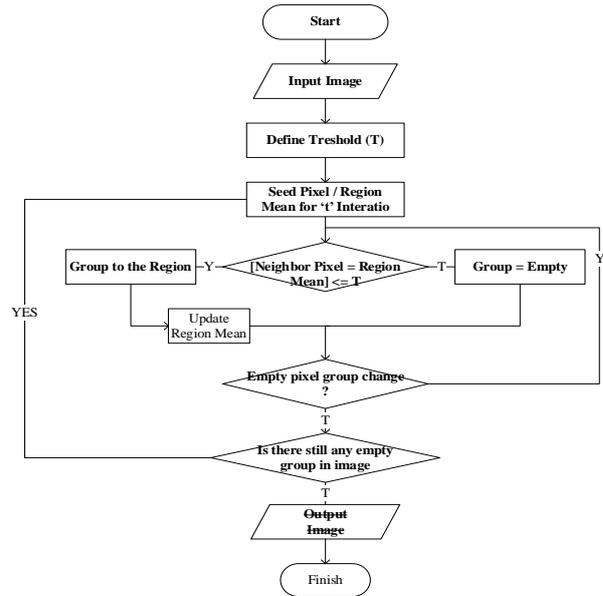


Fig. 2. Utilizing a segmentation algorithm diagram for the identification of brain tumors.

The intersection ($goal\ pixels \cap prediction\ pixels$) is comprised of all pixels found in both the prediction mask and the ground truth mask. All pixels found in either the prediction or goal mask are included where the union ($goal\ pixels \cup prediction\ pixels$) is comprised. Accuracy is considered as a parentage of true prediction, which can be defined as the nearest level between prediction and actual values [10].

C. Content-Based Image Retrieval (CBIR)

CBIR involves the process of exploring a vast collection of images created from an image query. According to Refs. [24, 29–32], the term “CBIR” was introduced. While [29] stated that Content-Based Image Retrieval (CBIR) entails the procedure of examining an extensive array of images derived from an image query.

Mohammed and Taha [33] described CBIR as the visual characteristics of the image in the database being mined and then defined it as a multidimensional feature vector. The vector obtained from the query image will be compared for its similarity with the vector contained in the database. As mentioned by Chu and Liu [34], the preliminary step in the image retrieval scheme is built on content to achieve abstraction and an explanation procedure on an image in the database as a vector feature. Then, the abstraction and explanation were carried out on an image query. The similarity between an image query and images in the database will be indexed and presented as output.

In this paper, segmentation and CBIR systems were proposed to predict brain tumors as early as possible, and Fig. 3 illustrates the systems. In addition, Fig. 3 depicts the CBIR system architecture.

To compute the accuracy of image retrieval, we calculated the distance between two images. Distance is

frequently used to achieve image search, its purpose is to decide the similarity or dissimilarity of two feature vectors. The level of similarity is stated by a score, a lower standing rate is considered a closer match between two vectors. In

this work, the Euclidean and Manhattan distance methods were used to demonstrate a method for measuring the distance between two images.

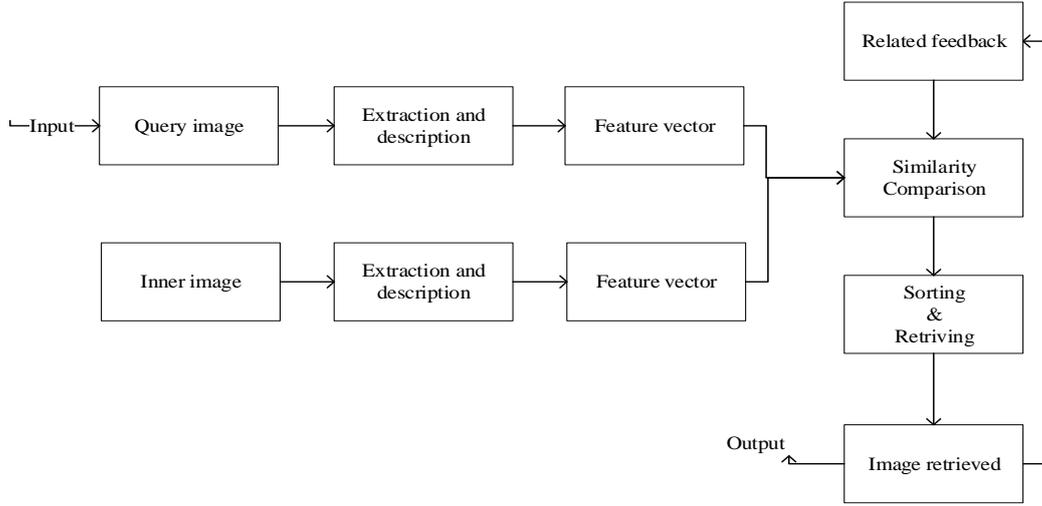


Fig. 3. CBIR system architecture.

D. Euclidean Distance

The most frequently used method to calculate the similarity of two vectors is Euclidean distance [35], see Eq. (2).

$$d(A, B) = \sqrt{\sum_j^n (H_j^A - H_j^B)^2} \quad (2)$$

where A is vector A, B is vector B, and d (A, B) is the Euclidean distance between vectors A and B. In contrast, n and H are considered as the number of vector elements and vector elements, respectively. Essentially, Euclidean distance is the length of the line segment joining a given pair of points in a grid/graph. This is exclusive and is the shortest path between the given pair of points.

E. Manhattan Distance

According to Yasmin *et al.* [36], the Manhattan distance, which is also recognized as the taxicab distance or city block distance, serves as a metric for measuring the separation between two $a(x_1, y_1)$ and $b(x_2, y_2)$ within a grid-based space, such as a Cartesian plane. It is calculated by summing the absolute differences between the coordinates of the two points along each axis. In simpler terms, the Manhattan distance represents the shortest distance that one would travel when moving only along the grid lines to reach from one point to another, much like a car navigating through city blocks. The formulation of Manhattan distance can be defined as:

$$d = \sum_{i=1}^n |x_i - y_i| \quad (3)$$

where “n” is the data dimension, “j” is the test image data, and “i” is the training data. Manhattan distance imposes certain limits on how it can be travelled; this is characteristic of traveling in Manhattan or any other. It can only move in the same number of directions with twice the

magnitude. So, in Manhattan, it can travel to the north, south, east, or west but not, say, the northwest.

F. Precision, Recall, and Accuracy

According to Ref. [30], recall refers to the evaluation of the quantity of relevant images successfully retrieved and presented in response to a specific query, encompassing the entire set of relevant images. Precision can be considered as the accuracy of the retrieval of expected images. According to Refs. [34, 37, 38], the term “recall” in the field of information retrieval systems (information retrieval) is related to the ability to find back information that has been stored. Precision computes the percentage of true positives among all discoveries, whereas recall evaluates the percentage of images based on ground truth observations and is written as:

$$\text{precision} = \frac{TP}{TP+FP} \quad (4)$$

$$\text{recall} = \frac{TP}{TP+FN} \quad (5)$$

$$\text{accuracy} = \frac{TP + TN}{TP + TN + FN + FT} \quad (6)$$

where TP is true positive, FP is false positive, and FN is false negative. Perfectly to precision and recall equivalent to one. In training, a concession occurs between these two measures, as a scheme with a high recall is likely to have false positives, and a scheme with a high precision is likely to fail to make some true observations [9]. At the same time, precision can also be explained as the correctness of the relationship between a query for information and the response to the query. When the system is observing for information and its suggestions closely match the images, then the exactness is principal of relevance. That is, the accuracy with which an image is retrieved is determined by its relevance [39]. The research presents a suggested

approach, depicted in Fig. 4, which combines region growing and CBIR methods.

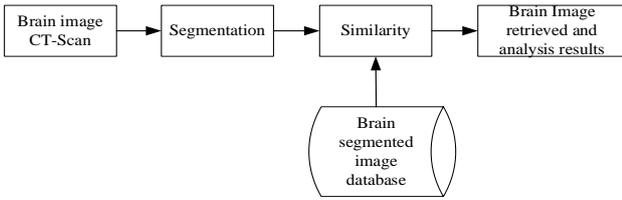


Fig. 4. The proposed methods.

It aims to enhance the accuracy and effectiveness of tumor detection in medical images, specifically in the context of brain tumor detection. Region Growing method is a segmentation technique that involves the iterative expansion of regions based on certain criteria. In the field of medical imaging, this technique is employed to outline specific structures or areas of interest within an image. For brain tumor detection, region growing might be used to identify and segment tumor regions from the surrounding healthy tissue. It begins with selecting one or more seed points within the tumor region and then iteratively adding neighboring pixels that meet certain similarity intensity criteria to grow the tumor region [40].

Meanwhile, Content-Based Image Retrieval (CBIR) is a technique used to retrieve images from a database based on their visual content. In the context of medical imaging, CBIR involves comparing features extracted from an input query image with features of images in a database to find similar images. These features could include texture, shape, color, and other visual attributes. In the case of brain tumor detection, CBIR might involve comparing the features of a suspicious image region (such as the region containing a potential tumor) with features of known tumor images in a database [41]. The proposed method involves blending region growing and CBIR methods, aiming to harness the advantages of both approaches to enhance the precision of tumor detection. One of the advantages of our proposed method was to improved segmentation accuracy where region growing focuses on pixel-level grouping based on similarity criteria. By integrating CBIR, which extracts high-level features to capture visual semantics, the segmentation process can be guided by more meaningful and contextually relevant information. This can lead to more accurate and coherent image segmentation results.

III. RESULT AND DISCUSSION

An example of a segmented brain CT-scan image both with tumor as well as without using region segmentation can be seen in Fig. 5. The observation results, there are variations in the accuracy images for the two types of CT-scans. For CT-scan type Wit, there is a very high accuracy value, reaching 99.91% in the 1st and 9th data. As for the Wot-type CT-scan, the highest value was 99.23% in the 21st data. However, there are also variations in the accuracy value which are quite low in both, especially in the Wit type CT-scan which has low values in some data such as the 4th, 7th, 10th, 12th, 15th, and 10th, 19th data. It can be stated that brain with tumor CT-scan has a higher

accuracy value variation than the brain without tumor CT-scan, but there are some data with low accuracy values on the Wit type CT-scan. The Wit-type CT-scan has a higher accuracy compared to Wot, with an average Wit accuracy of 81.74% and an average Wot accuracy of 80.83%.

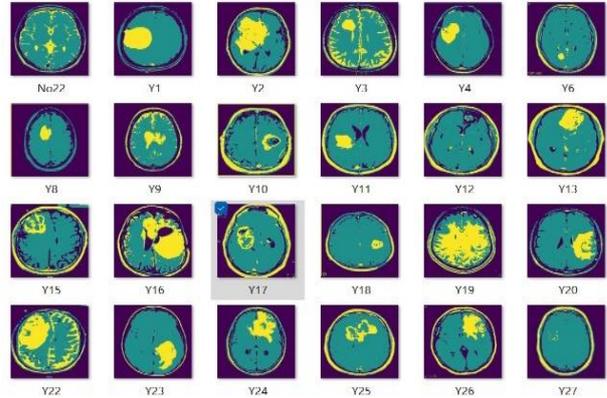


Fig. 5. Brain segmented images.

The experiments show an average segmentation accuracy of 79.57% from 50 CT-scan brain tumors. Furthermore, an analysis of 50 brain CT-scans (comprising both those with tumors and those without. Fig. 6 reveals that brain CT-scans with tumors yield an average accuracy of 79.57%, whereas those without tumors achieve an accuracy of 78.85%. Moreover, Fig. 6 illustrates an accurate region-growing segmentation on the CT-scan brain. The highest accuracy of segmentation reaches up to 99.91% for CT-scan with tumor. Moreover, the lowest accuracy is 65.86% also on CT-brain with tumor.

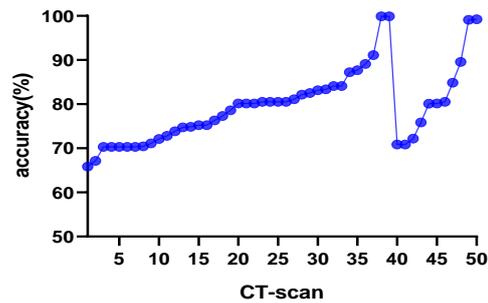


Fig. 6. Region growing segmentation.

Fig. 6 shows that the brain with tumor CT-scan images have a wider accuracy range compared to the Wot CT-scan. For CT-scan type Wit, the accuracy range is between 67.16% to 99.91%. There are some data with accuracy above 80%, but there is also some data with an accuracy below 75%. Meanwhile, for the Wot-type CT-scan, the accuracy range is narrower, specifically between 70.31% and 99.23%. It can also be seen that some CT-Scans have very high accuracy (above 90%), but there are also some CT-scans with very low accuracy (below 70%). This shows that the results of a CT-scan are highly dependent on factors such as the quality of the CT-Scan machine, the skills of the radiologist who performs the examination, and the quality of the resulting image. It can be stated that in

general, CT-scans have a fairly high level of accuracy. However, there are quite large variations in the accuracy values, so further evaluation and validation is necessary to ensure the reliability of the CT-scan results. In addition, it appears that there is no significant difference in the accuracy value between the Wit and Wot CT-scan types. The mean accuracy of 80.43% indicates that on average, the CT-scans have an 80.43% accuracy rate. The median accuracy of 80.34% suggests that the distribution of accuracy rates is relatively symmetrical, with about half the scans having an accuracy rate below 80.34% and half above. The standard deviation of 9.81% indicates that there is some variability in the accuracy rates, with some scans having accuracy rates that are significantly higher or lower than the average.

Furthermore, the experiments yielded an average segmentation accuracy of 79.57% across 50 CT-scan brain tumor images. This indicates how well the algorithm was able to accurately identify and delineate the boundaries of tumor regions in the images. When comparison of Brain CT-scans, the analysis involved a comparison between 50 brain CT-scan images with tumors (brain with tumor) and 50 brain CT-scan images without tumors (brain without tumor). In Fig. 6, it was observed that CT-scan images with tumors had an average segmentation accuracy of 79.57%, while CT-scan images without tumors achieved an average accuracy of 78.85%. This suggests that the algorithm performs slightly better on images with tumors, but the difference in accuracy is not substantial.

In addition, Fig. 6 provides a visual representation of the accurate region-growing segmentation performed on CT-scan brain images. This visualization helps to convey how well the algorithm is able to identify and delineate tumor regions within the brain scans. The works also revealed a range of segmentation accuracy values. The highest accuracy achieved was 99.91% for CT-scan images with tumors, indicating near-perfect segmentation performance in some cases. On the other hand, the lowest accuracy observed was 65.86% for CT-scan brain images with tumors, indicating that there were instances where the segmentation algorithm struggled to accurately identify tumor regions. In summary, the experiments demonstrate the effectiveness of the region-growing segmentation technique in identifying and delineating brain tumor regions in CT-scan images. The results indicate an average segmentation accuracy of 79.57% across the dataset, with higher accuracy achieved in some cases (up to 99.91%) and lower accuracy in others (as low as 65.86%). The analysis also highlights a slight difference in segmentation performance between images with tumors and images without tumors. The provided information sheds light on the algorithm's capabilities and provides insights into its performance across various scenarios in brain CT-scan segmentation.

The proposed methods can be investigated in Fig. 4. In this work, CT-scan brain images were initially segmented before applying the CBIR method. To summarize, all segmented CT-scans collected are saved in a database, which contains CT-scan brain with tumors and without tumors. Consequently, a CT-scan database was deployed

for the CBIR system in order to compute the accuracy of brain tumor detection. The matching similarity in this CBIR was carried out using Euclidean and Manhattan distance matrices.

Our proposed hybrid approach combining region-growing segmentation and Content-Based Image Retrieval (CBIR) can offer several advantages in certain scenarios, such as medical imaging or object recognition tasks. However, like any approach, it also has its limitations. Some of limitations such as: computational complexity, parameter tuning, dependency on initial seed, limited feature representations, sensitivity to image variations, lack of semantic understanding, and overfitting and generalization.

Computational Complexity, since combining region-growing segmentation and CBIR may lead to increased computational complexity, particularly if both techniques are applied exhaustively. The processing time required for segmentation and CBIR might become a significant concern, especially when dealing with large datasets or real-time applications. Computational Complexity, since combining region-growing segmentation and CBIR may lead to increased computational complexity, particularly if both techniques are applied exhaustively. The processing time required for segmentation and CBIR might become a significant concern, especially when dealing with large datasets or real-time applications. Parameter Tuning, both region-growing segmentation and CBIR techniques involve parameter tuning to achieve optimal results.

Hybrid approach may introduce additional parameters that need to be tuned, making the overall process more complex and potentially leading to suboptimal performance if parameters are not chosen carefully. Integrating region-growing segmentation and CBIR methods effectively can be challenging. Ensuring seamless interaction between these two components and avoiding conflicts between their underlying assumptions and methodologies can be complex. Dependency on Initial Seed, region-growing segmentation often relies on initial seed points or regions to start the segmentation process. The quality and location of these seed points can significantly influence the final segmentation results. If the seed points are not chosen properly, the segmentation accuracy might be compromised. Sensitivity to Image variations, both region-growing segmentation and CBIR can be sensitive to variations in lighting, viewpoint, scale, and other image conditions. The hybrid approach may struggle to handle such variations effectively, leading to inaccurate segmentation or retrieval results. Domain dependence, the performance of the hybrid approach might be highly dependent on the specific application domain and the characteristics of the images being processed. However, what works well in one domain may not necessarily translate effectively to another. Lack of Semantic Understanding, while region-growing segmentation can capture spatial coherence, it might not always capture high-level semantic information about the objects present in an image. CBIR, on the other hand, might lack the ability to understand the spatial relationships and context within segmented regions.

Moreover, overfitting and generalization depending on the complexity of the hybrid approach, there could be a risk of overfitting to specific training data and failing to generalize well to new, unseen images.

Considering to these limitations, an analysis with careful design, experimentation, and validation are essential. Therefore, in the near future it's important to thoroughly evaluate the hybrid approach on relevant datasets and compare its performance against other state-of-the-art methods to determine its practical viability in different application scenarios.

The initial data processing step of segmentation is regarded as resource-intensive and tends to lack precision once the necessary dataset has been amassed. The primary goal of this initial data processing is to generate an accurate reference image, which will be utilized in the process of Content-Based Image Retrieval (CBIR) heightened accuracy in the outcomes.

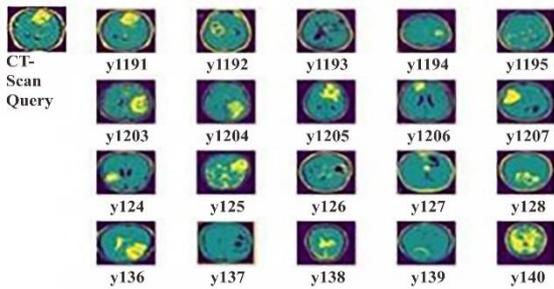


Fig. 7. The 20 most images retrieved using CBIR with Euclidean distance metrics.

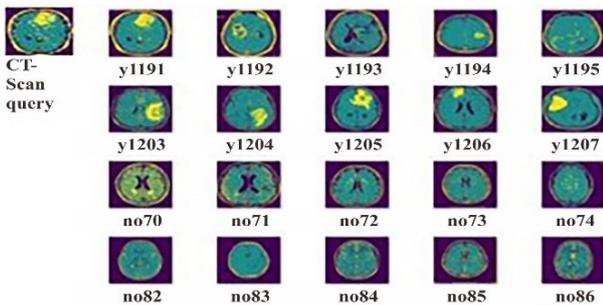


Fig. 8. The 20 images retrieved using CBIR with Manhattan distance.

Figs. 7 and 8 describe the top 20 images with the closest similar obtained from 50 search queries, matched through the utilization of Euclidean distance. According to Fig. 9, the average accuracy of retrieval is 94% and the retrieval time is 1.56 s. While Fig. 10 illustrates retrieval using the Manhattan distance method. In CBIR algorithm, which consists of image matching technique to decide similarity as an essential process, there are some techniques to carry out the similarity process, such as Manhattan, Euclidean Cheeseboard, and Quasi-Euclidean distance metrics [42]. Since Manhattan and Euclidean distance metrics are widely used in CBIR research [30, 31, 39], they are used in this work to match an image query and database. By using the Euclidean distance metric, it shows 94% on average. It takes 1.56 s to achieve a 94% average accuracy of matching using Euclidean distance, Fig. 9 illustrates this state.

Fig. 9 also shows distance metrics for retrieval time of CT-scan brain tumor detection from 50 image queries. The longest time for CT-scan brain tumor detection is 1.95 s, while the fastest image retrieval process is 1.47 s, and the average time needed is 1.56 s. Fig. 10 shows that the accuracy of image retrieval using Manhattan is 96% and time image retrieval process is 1.22 s on average, respectively.

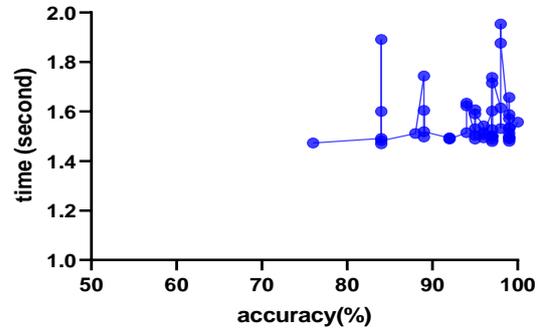


Fig. 9. Accuracy and time of image retrieval with Manhattan distance metrics.

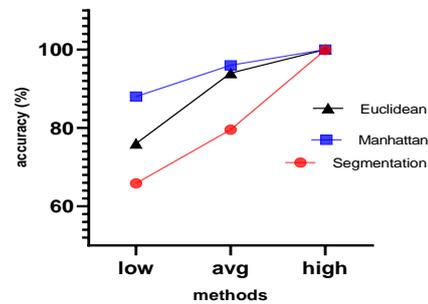


Fig. 10. Accuracy of image segmentation and CBIR.

Fig. 11 shows the fastest retrieving image at 1.11 s and an average time of 1.22 s with Manhattan distance metrics. According to Fig. 6, the average accuracy region-growing segmentation of brain tumor detection is 79.57%, which is quite good for detecting brain tumors using the segmentation method. However, this accuracy can be improved; therefore, in this work, we used hybrid methods such as region-growing and CBIR methods. Moreover, Figs. 9 and 10 demonstrate the affectivity of brain image retrieval.

The accuracy results show that image matching using Manhattan provides better accuracy compared to Euclidean distances, which are nearly 97% and 94%, correspondingly. This is in line with [29], who stated that Manhattan distance metrics perform better than Euclidean distance metrics in the A* algorithm. Subsequently, the accuracy of image retrieval is computed based on similarity, it relies on the calculation of distance metrics. Figs. 7 and 8 shows that varying accuracy from 0.76 to 1.0. The average accuracy of all queries is about 0.95 with an average time of about 1.56 s. The query with the highest accuracy is query number 50 with an accuracy of 1.0 and a time of 1.557 s. While the query with the longest time is

query [36number 39 with a time of 1.954 s. Although there are some differences in accuracy and time between queries, overall system performance can be considered good with high average accuracy and relatively fast time.

Meanwhile, the average computing time for each measurement ranges from 1.47 s to 1.954 s. There are several measurements with a relatively fast average computation time, which is between 1.47 s and 1.6 s, although some measurements require a longer time, specifically between 1.6 s and 1.954 s. Across all measurements, a model that has an accuracy of 1.00 requires an average computing time of about 1.557 s, which is the highest time in Fig. 9. From Figs. 9 and 10, it can be concluded that the resulting accuracy ranges from 0.76 to 1.00. The resulting average accuracy is 0.95. The time needed to run the query ranges from 1.47 s to 1.96 s. The average time needed to run the query is 1.58 s. From these results, it can be said that even though the resulting accuracy is quite high, the time needed to run the query is still quite long. Based on the dataset more than 800 provided, it appears that the accuracy of the experiment is quite high, ranging from 0.76 to 1.00. Moreover, in terms of computational time, if the duration needed for model training or testing is excessively protracted, the model could lack practical efficiency in real-world applications.

In this work the Manhattan distance metric has better performance, this can be examined on Figs. 9 and 10. However, from the two figures can be explained that an accuracy of image retrieval does not rely on retrieval processing time. It means more time needed for retrieving will not continuously improve an accuracy and vice versa. The works also demonstrate that merely region growing segmentation was not adequate to diagnose of brain tumor since only perform 78% of accuracy. This mean that our purposed method improved the accuracy in detecting brain tumor, Fig. 11 illustrates our purposed method. When we compare accuracy image retrieval between Euclidean and Manhattan distances, the last distance performs better which is more than 96%. Furthermore, the utilization of the Manhattan distance resulted in the lowest accuracy at 88%, whereas the application of the Euclidean distance returned only 76%. Therefore, it can be analyzed that Manhattan has superior in retrieval accuracy than Manhattan both of average as well as the lowest.

CBIR using Euclidian distance shows a fairly good accuracy value, which is an average of 0.91, with the lowest value of 0.76 and the highest value of 1. It is relatively fast query execution time, which is an average of 1.56 s, with the fastest time of 1.473 s and the longest time of 1.954 s. However Euclidean distance shows some weakness such as lowest query accuracy value of 0.76 and it is still considered low, and query execution time in some cases is rather slow, such as query numbers 19, 25, and 39 which require an execution time of over 1.8 s. On the other hand, CBIR using Manhattan distance has a better accuracy value than Euclidean which is an average of 0.96, with the lowest value of 0.88 and the highest value of 1. Moreover, query execution time is quite fast, which is an average of 1.21 s, with the fastest time of 1.06 s and the longest time of 1.532 s. Buy Manhattan has the lowest

query accuracy value of 0.88 and query execution time in some cases is rather slow, such as queries number 1, 8, and 9 which require execution time of more than 1.25 s. From Figs. 9 and 10 it can be summarizing that Manhattan has a better accuracy value than Euclidean distance, but in some cases, the query execution time of Manhattan 3 is rather slow compared to Euclidean. Therefore, selecting the best method depends on the needs its use, whether to prioritize accuracy or fast execution time. By considering two factors, an accuracy and time it can be stated that Manhattan is more effective and efficient than Euclidean distance.

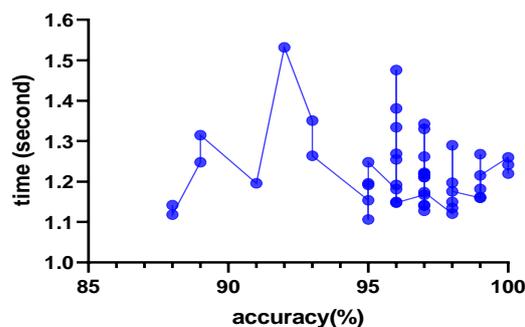


Fig. 11. Time and accuracy of image segmengtation and CBIR.

The experiments using region-growing segmentation to detect brain tumors demonstrate an average accuracy of 79.57%. This result shows that our proposed method, which uses hybrid segmentation and CBIR methods, has already improved the accuracy of brain tumor detection. The improvements in accuracy reach up to 96% and 94% by using CBIR with Manhattan and Euclidean distance metrics, respectively, compared to merely using segmentation. Besides that, our proposed method also provides better accuracy compared to previous works, as illustrated in Fig. 9.

In terms of accuracy, the Manhattan method has the highest performance with the highest accuracy of 100%. The Segmentation method has the lowest accuracy of 65.86%, while the Euclidean method is in between the two with the lowest accuracy of 76%. In terms of time, the Segmentation method is the fastest with an average time of 1.5 s, while the Manhattan method is slightly slower with an average time of 1.22 s. The slowest method is the Euclidean method, with an average time of 1.56 s. The Manhattan and Euclidean methods have the highest accuracy of 100% and 76%, respectively, while the Segmentation method has the highest accuracy of 99.91% and the lowest of 65.86%. Based on Fig. 10 it can be concluded that the Manhattan and Euclidean methods show consistently higher accuracy than the Segmentation method. However, the Segmentation method has a greater accuracy range, indicating that it may have a better ability to deal with variations in data.

From Fig. 10, it can be also seen that the Manhattan method has better highest and lowest accuracy than the Segmentation and Euclidean methods. The Segmentation

method has a higher time which is faster than the Manhattan and Euclidean methods, but the lowest time is slower than the Manhattan method. Whereas the Euclidean method has a slower average and highest time than the Manhattan method and a faster lowest time than the Segmentation method. However, that the figure does not provide information on whether the difference in accuracy and time is statistically. When we calculate the time reliability between Segmentation, Manhattan, and Euclidean methods using the Pearson or Spearman correlation coefficient, the works show that consistency of accuracy between the three methods: 0.6676. However, Time consistency between the three method is negative 0.6625. This negative value indicates a tendency that the longer it takes to process data, the lower the accuracy. However, keep in mind that these results only reflect time consistency in the dataset used, and cannot be generalized to other datasets.

Moreover, Table I shows the performance results of several methods for a certain task, where each method is assigned an accuracy percentage. The proposed method using the Manhattan distance metric achieved the highest accuracy of 96.52%, while the same method using the Euclidean distance metric achieved an accuracy of 94.24%. These results suggest that the choice of distance metric can significantly affect the performance of the proposed method.

TABLE I. COMPARATION OF METHODS DETECTING BRAIN TUMOR

No.	Methods	Accuracy (%)
1a.	Our proposed method (Manhattan)	96.52
1b.	Our proposed method (Euclidean)	94.24
2.	SVM + FCM [3]	92.5
3.	K Means + SVM [45]	92.3
4.	CNN-VGG [46]	66.18
5.	VGG16+MLP [47]	78.59
6.	Multi-Scale CNN [10]	89.10
7.	MRI [8]	93.59
8.	CT-scan [8]	95.6
9.	MRI [48]	91.0
10.	LVQ [40]	85.0

Other methods provided in Table I include SVM+FCM, K Means+SVM, Convolutional Neural Network-Visual Geometry Group Network (CNN-VGG), VGG16+Multi-layer Perceptron (MLP), Multi-Scale CNN, magnetic resonance imaging (MRI), CT-scan, MRI, and Learning Vector Quantization (LVQ). Their accuracies range from 66.18% to 95.6%. However, we can see that the proposed method using Manhattan distance outperformed all the other methods in terms of accuracy. The performance results suggest that SVM+FCM achieved an accuracy of 92.5%, which is lower than the proposed method using Manhattan distance but higher than some other methods listed in the table. This suggests that the combination of SVM and FCM can be effective for certain tasks and data, but may not always outperform other methods.

Fig. 10 shows that accuracy prediction of brain tumor using region growing segmentation was 79.57% in average. Whilst accuracy prediction by deploying CBIR with Euclidean distance and Manhattan are 94% and 96%, respectively. Therefore, it can be said that Semantic Global

Reasoning (SGR) segmentation was deplorable to predict brain tumor using CT-Scan. In Case of CBIR with Manhattan demonstrate better in accuracy compared to Euclidean distance. Besides better accuracy, Manhattan distance also have merits such as simplicity, robustness, Computational efficiency, and cost effective [49]. This better accuracy can be occurred due to computational complexity of the Manhattan distance only depends on the number of features or dimensions in the data being analyzed. In the general case, where each data point has “d” features, the time complexity of computing the Manhattan distance between two data points is $O(d)$. This makes the Manhattan distance a relatively efficient distance metric, especially when compared to more complex distance metrics, such as the Mahalanobis distance or the Makowski, and Euclidean distances.

Ruba *et al.* [8] introduced a CNN-based semantic segmentation network for the classification of CT images. However, our proposed approach achieves a slightly superior performance, with an accuracy of 99.6%. This is because, in their proposed architecture, brain images are first segmented using a semantic segmentation network, which contains a series of convolutional and pooling layers. Then the tumor is classified into three different categories, such as meningioma, glioma, and pituitary tumor, using the GoogLeNet CNN model. Seetha and Raja [46] presented brain tumor classification by applying the CNN and VGG methods, unfortunately, the accuracy is only 66.18%. Consequently, when contrasted with the approach presented in Yasmin *et al.* [36], our method demonstrates enhanced accuracy and proves to be a valuable choice for the early detection of brain tumors. Furthermore, our proposed objective achieves a higher level of accuracy in comparison to Le *et al.* [47], where deep learning is utilized for the classification of brain tumors through the Long Short-Term Memory (LSTM) method. Even though Resa *et al.* [37], utilized deep learning, particularly the LSTM technique, for the classification of brain tumors. Despite the complexity and implementation efforts associated with [37]’s use of the LSTM method, our proposed approach still outperforms it in terms of accuracy. However, that the figure does not provide information on whether the difference in accuracy and time is statistically significant [50], which demonstrated an accuracy of 85% using Learning Vector Quantization (LVQ), ours has better accuracy. Because of their research, they used manual reading as the golden standard and only used 20 images from 40 brain CT-scan images for training and 20 images for image training.

To evaluate the metrics performance, F1-Score was used as a model that combines precision and recall to determine how well the model can re the positive class is very important to identify correctly, and using Eq. (7).

$$F1 - Score = 2 \times \left(\frac{precision \times Recall}{precision + recall} \right) \quad (7)$$

From Eq. (7), F1-Score was calculated and produce 0.76. Its score considered good since The F1-Score is the harmonic mean of precision and recall, where precision is the proportion of true positive results among all positive

results, and recall is the proportion of true positive results among all actual positive cases. F1-Score has a range of values between 0 and 1, where a value of 1 indicates perfect model performance in recognizing positive classes, while a value of 0 indicates poor performance.

Based on the findings of study that explored the application of segmentation and Content-Based Image Retrieval (CBIR) methods for detecting brain tumors in CT-Scan images. Therefore, future research based on the results can be carried out with validation and replication to confirm the results and ensure their generalizability, future research could replicate the study using a larger and diverse dataset. This will help establish the robustness of the findings across different patient populations and imaging conditions. Moreover, future work can be algorithm refinement, feature selection and extraction, metric comparison analysis, clinical impact and implementation the directions for future research based on our works can be carried out such as:

Data diversity and bias analysis: investigate whether algorithm's performance is consistent across different demographic groups (age, gender, ethnicity), scanner types, and imaging protocols. addressing potential biases and ensuring the algorithm's generalizability to diverse populations is crucial.

Clinical utility and workflow integration: evaluate how the improved accuracy translates into better clinical outcomes. Consider factors such as reducing False positives, aiding radiologists in making more accurate diagnoses, and potentially influencing treatment decisions.

Multi-modality fusion: it explores the potential benefits of combining data from multiple imaging modalities, such as CT-Scan and MRI to improve tumor detection accuracy. multi-modal approaches can provide a more comprehensive view of the tumor's characteristics.

Noise and artifact handling: it investigates the algorithm's robustness to noise and artifacts commonly present in medical images. Developing methods to handle these challenges can improve accuracy and real-world applicability.

Transfer learning: it explores the feasibility of transferring knowledge from one dataset (such as a different medical imaging dataset) to improve performance on the current dataset. This could involve pretraining a model on a related task before fine-tuning it for tumor detection.

Ensemble methods: it combines multiple algorithms or models to create an ensemble that leverages their collective strengths. ensemble methods can often provide more robust and accurate results.

Explain ability and interpretability: it develops techniques to explain why the algorithm made a specific decision. this is crucial in medical applications where understanding the rationale behind ai decisions is essential for clinical acceptance.

Longitudinal monitoring: It extends the application to longitudinal monitoring, where the algorithm can track changes in tumor size and characteristics over time. This could be valuable for treatment assessment and patient management.

- Collaboration with medical experts, it collaborates closely with radiologists, neurologists, and other medical experts to ensure the technology aligns with clinical needs, enhances their workflow, and provides meaningful diagnostic information.
- Open-source and collaboration, it considers releasing the algorithm as open-source software to encourage collaboration and further research in the field of medical image analysis.

IV. CONCLUSION

According to the findings, brain tumor detection using only the segmentation method has a 79% accuracy. By applying the CBIR method after segmentation, the accuracy of detection increased up to 96% with Manhattan and 94% using Euclidean distance metrics. Therefore, it can be concluded that CBIR can improve algorithmic performance for detecting brain tumors. Interestingly, in this study, Manhattan distance outperformed Euclidean distance metrics, despite the fact that in previous studies, the second metric outperformed Manhattan. Moreover, compared to other methods, our proposed method performs with better accuracy. Our proposed algorithm can be used to detect other diseases as far as using images as data. In the near future, our algorithm's performance can be improved by using other methods such as different segmentation, different distance metrics, and other image processing methods.

It also can be concluded that the resulting accuracy ranges from 0.76 to 1.00. The resulting average accuracy is 0.95. The time needed to run the query ranges from 1.47 s to 1.96 s. The average time needed to run the query is 1.58 s. From these results, it can be said that even though the resulting accuracy is quite high, the time needed to run the query is still quite long. Therefore, it is necessary to develop more sophisticated and effective technologies so that the time needed to run queries can be accelerated without reducing the accuracy of the query results. In practice, we can evaluate a method by conducting experiments on the same data using various available methods, and comparing the results. In conclusion, choosing the right method for data analysis does not only depend on accuracy, but also on efficiency factors and the purpose of the analysis. Therefore, it is necessary to carry out a careful and careful evaluation before choosing the right method for each different analysis case.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

AUTHOR CONTRIBUTIONS

All the authors in this paper contributed their efforts for implementation of the paper. Suhendro Y. Irianto has done proposed work implementation. Sri Karnila, Dona Yuliawati implemented results part; all authors had approved the final version.

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