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Analysis of the Use of K-Means Clustering Method in Brain Tumor MRI Segmentation

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KEYWORDS
K-Means Clustering, Linear Measurement, MRI Brain, Tumor.

ABSTRACT
Accurate measurement of brain tumor volume in MRI examinations is critical for diagnosis and treatment planning. Traditionally, linear measurement is the gold standard, but it is prone to errors due to subjectivity and fatigue, and only provides a rough estimate of tumor volume. This research aims to compare brain tumor volume calculation on MRI images using linear measurement and k-means clustering method on post-contrast T1WI sequences to evaluate their accuracy and clinical consistency. Using a quasi-experimental design with post-test only and no control group, 32 MRI images of brain tumors were analyzed. Tumor volumes were calculated using both methods, and the results were statistically compared. The average tumor volume was 39,304.55 mm³ for the linear method and 35,374.69 mm³ for the k-means clustering method. Statistical analysis using the Wilcoxon test showed no significant difference between the two methods ($p = 0.082$; $p > 0.05$). The results of this research suggest that although both methods produce comparable volume estimates, k-means clustering offers the advantage of reducing subjectivity, indicating its potential to improve consistency and reliability of measurements in clinical practice. The implication of this research is that the k-means clustering method may be a more reliable alternative in the measurement of brain tumor volume on MRI examinations, especially in reducing the subjectivity bias often present in linear measurement methods. This can help improve the accuracy and consistency of measurement results, which is crucial for more precise treatment planning and evaluation of patient therapy response.

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INTRODUCTION

A tumor is an abnormal growth of intracranial tissue or the meninges, which can be classified into benign and malignant types based on the degree of malignancy (Chaulagain et al., 2021). According to the Global Cancer Observatory (GLOBOCAN), brain tumor cases rank 19th globally among clinical abnormal tissue growths. Each year, approximately 296,851 new cases are reported, accounting for around 1.72% of all new cancer cases annually.

Diagnosis of brain tumors can be achieved through several non-invasive imaging modalities, such as MRI, PET, and SPECT. For MRI scans, gadolinium contrast media is typically administered to enhance image clarity and resolution. Post-contrast MRI images are captured in multiple sequences, including axial T1, sagittal T1, and coronal T1 views (Perkins & Liu, 2016). The resulting images are stored as DICOM (Digital Imaging and Communications in Medicine) files, facilitating standard medical image processing. Traditionally, brain tumor assessments rely on manual measurements by radiologists, a process recognized as the gold standard. However, this manual approach is intricate, subjective, and challenging. Currently, radiologists use linear measurements to estimate tumor size by measuring the largest diameter across two perpendicular slices to capture craniocaudal, anteroposterior, and lateral dimensions (Khalil et al., 2024).

The measurement results using linear measurement are considered a rough and unspecific assessment that cannot show the volume of the tumor. Therefore, an image segmentation system has been developed in the development of medical imaging technology. Image segmentation has an important role in the extraction, analysis, and interpretation of an image that is widely applied in medicine. For example, tissue classification, tumor localization, estimating tumor volume, surgical planning, depiction of blood cells, and image registration (Wadhwa et al., 2019a). Image segmentation aims to separate normal tissue and tumor tissue; in brain tumors, this segmentation can be done in several sequences, namely T1WI, T2WI, FLAIR, and T1WI post-contrast. The T1WI post-contrast sequence is the most commonly used sequence for image classification models (Biratu et al., 2021).

Image segmentation can be applied to 2D and 3D sequences, there are several image segmentation methods, one of which is the K-means clustering method. This method is one of the faster and more sensitive methods than other methods, such as the FCM method. In addition, this method is also a simple method whose working principle is to divide image pixels into several cluster groups according to their characteristics and is able to overcome the fuzziness that comes from grayscale images (Jindal et al., 2022).

This research introduces a post-processing approach in MRI image analysis, specifically employing the K-means clustering segmentation method to measure brain tumor volume (Wadhwa et al., 2019b). This method aims to support radiologists in calculating tumor volume and compares its results with those obtained from traditional linear measurement methods. By contrasting K-means clustering with manual approaches, this research seeks to highlight the potential efficiency and reliability of automated segmentation in brain tumor volume assessment, offering a viable alternative for clinical applications in MRI image analysis.

Conducting tumor volume calculations on MRI brain tumor examinations using both the linear measurement method and the K-means clustering method, with the goal of comparing these approaches (Vishnuvarthanan et al., 2016a). Research hypothesis, Ha: There is a difference in the measurement results of brain tumor volume in MRI images of brain tumors with K-Means clustering method and linear measurement method, and H0: There is no difference in the measurement results of brain tumor volume in MRI images of brain tumors with K-Means Clustering method and linear measurement method.

Based on the above background, this research aims to determine the advantages in efficiency and accuracy offered by K-means clustering over traditional linear measurement, which has the potential to improve MRI reading time and follow-up assessment accuracy for clinical radiology practice. Thus, the benefit of this research is to contribute to the development of a more accurate and consistent method of measuring brain tumor volume on MRI examinations, particularly to improve the work efficiency of radiology specialists and the quality of clinical assessment. The K-means clustering method can be a more reliable alternative to reduce subjectivity and human error, thereby increasing confidence in the results of brain tumor volume measurements.

METHOD

This quasi-experimental research employs a post-test-only design without a control group, analyzing a sample of 32 MRI images from brain tumor patients. Brain tumor volume was measured using K-means clustering segmentation on T1-weighted post-contrast spin echo sequences in axial cuts. Linear measurements were conducted on T1-weighted post-contrast spin echo sequences in both axial and sagittal cuts. For reproducibility, Matlab software was used for the K-means clustering, and the Siemens 1.5T MRI modality was chosen to optimize imaging quality.

RESULT AND DISCUSSION

Analysis of Tumor Volume Calculation Using Linear Measurement Method on 1.5T MRI

The research on brain tumor volume calculation using the linear measurement method on MRI was conducted twice by radiology specialists at separate intervals, employing a quantitative approach. This calculation method uses two perpendicular cross-sectional slices, specifically the axial and sagittal views. The selected slice is the one with the largest tumor dimension. The process for calculating brain tumor volume using the linear measurement method includes the following steps:

1. The workstation display is configured to a 2x1 layout to facilitate comparative imaging.
2. Axial slices are chosen by selecting the T1WI post-contrast axial slice sequence (t1_se_tra CE) and displayed on the left layout, while the right layout is reserved for displaying the T1WI post-contrast sagittal sequence (t1_se_sag CE).
3. Selection of the slice that will be measured to obtain the largest tumor dimension in both cross-sectional cuts. Slice selection is done by scrolling on both images used.
4. Measurement with linear measurement is done through the distance tool available on the view toolbar menu. In axial cut images, tumor diameter measurement is performed by drawing a vertical line from the front edge to the back edge of the tumor area, and then Dap (anterior-posterior diameter) will be obtained. Next, a measurement is made with a horizontal line in the tumor area; then, the Dl (lateral diameter) size will be obtained. An example of measuring the diameter of a brain tumor with linear measurement can be seen in Figure 1.

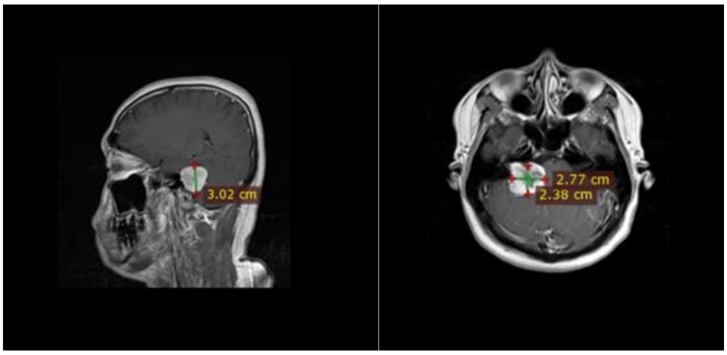

Figure 1. Example of Diameter Measurement Results in a Brain Tumor Using Linear Measurement Method

5. In the image with a sagittal cut, measurements are made by making a vertical line from the top to the base of the tumor; from these measurements will get Dcc (craniocaudal diameter).
6. After all the diameter sizes have been obtained, then proceed with the calculation of the brain tumor volume using the ellipsoid formula, namely:

$$\mathbf{V = DCC \times dl \times dap \times \frac{\pi}{6}}$$

Description:
DCC : craniocaudal diameter
Dap : anteroposterior diameter
Dl : lateral diameter.

7. The procedure is carried out on all samples used so that it will get the results of brain tumor volume in 32 image samples used

Analysis of Tumor Volume Calculation Using K-Means Clustering Method

The research results on the calculation of brain tumor volume using the k-means clustering segmentation method, starting with the creation of machine learning k-means clustering in the Matlab program. Calculation of brain tumor volume with the k-means clustering method is done with several stages, namely:

1. Select patient DICOM data by clicking the browse folder tool. The image used is an axial image with the t1_se_tra CE sequence. The image used is a slice that has an image of a tumor in the brain.
2. The selected image is displayed in box 1 as the original image, then click process to run the image segmentation program. The segmented image will be displayed in box 2 in the form of a ground truth image, while the 3D visualization of the image will be displayed in box 3, and the tumor volume will appear in Vol. The following is the initial appearance of the K-Means Clustering segmentation program in Figure 2.

Figure 2. Initial View of the K-Means Clustering Segmentation Program

Table 1. Window Functions of the Segmentation Program

Window	Function
Window 1	Display the original MRI image
Window 2	Display image of brain tumor segmentation result
Window 3	Display the brain tumor segmentation result in 3D
Button functions in the segmentation program	
Window	**Function**
Browser	Select the MRI image folder
Process	To start brain tumor segmentation
Vol	Display brain tumor volume results
Save	To store the segmented image and volume
Reset	To clear the working window for evaluation on another image

Examples of image segmentation results with the k-means clustering method displaying the original image, segmented image, and 3D visualization of brain tumors. This can be seen in Figure 3.

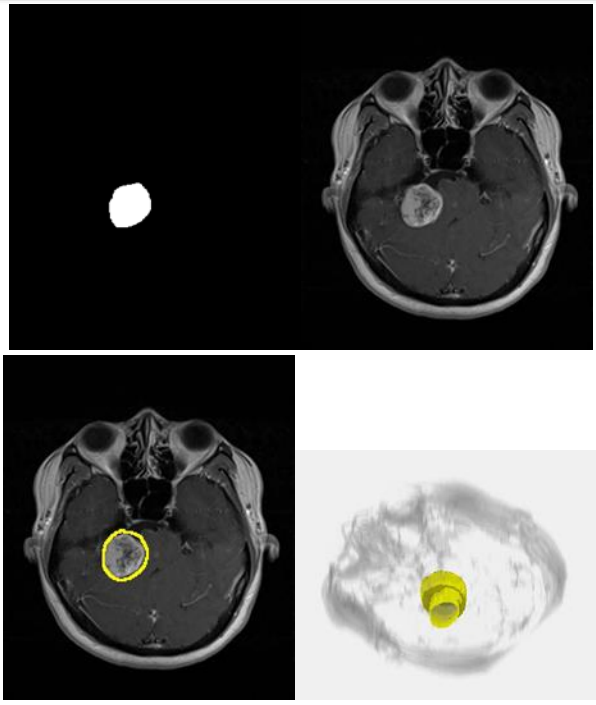

Figure 3. Examples of the original image (a), segmented image (b), ground truth image (c), and 3D visualization of the tumor.

The documentation of the brain tumor volume calculation with the K-means clustering method can be seen in Figure 4.

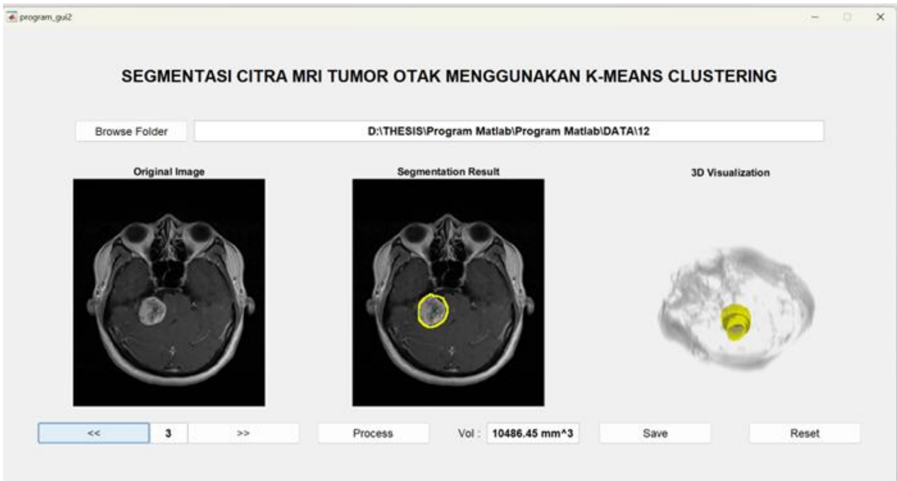

Figure 4. Example of brain tumor volume measurement results with the method k-means clustering

Comparison of Brain Tumor Volume Calculation with Linear Measurement and K-Means Clustering Method

Based on the results of the research that has been obtained regarding the calculation of brain tumor volume with linear measurement and k-means clustering methods, statistical analysis will then be carried out to determine whether or not there is a difference in the results of calculating brain tumor volume in the two methods. A comparison of brain tumor volume measurement results with linear measurement and k-means clustering methods can be seen in Table 1.

Table 2. Comparison of Brain Tumor Volume by Linear Measurement Method and K-means Clustering

Sample	Linear measurement (mm)^3	K-means clustering (mm)^3
Sample 1	8008.00	7146.61
Sample 2	1464.32	2698.24
Sample 3	48971.89	44096.79
Sample 4	21508.76	25057.01
Sample 5	22959.30	1678.96
Sample 6	60950.92	47928.96
Sample 7	74020.13	31694.46
Sample 8	19777.87	17322.3
Sample 9	1856.40	1509.45
Sample 10	30850.56	14315.19
Sample 11	105963.00	127709.47
Sample 12	10284.46	10486.45
Sample 13	37619.40	34800.99
Sample 14	3871.39	2696.01
Sample 15	26208.00	29243.48
Sample 16	144144.00	139351.68
Sample 17	5304.87	7210.22
Sample 18	7960.68	2292.85
Sample 19	66664.00	75991.33
Sample 20	30476.16	23259.18
Sample 21	131459.33	105737.85
Sample 22	87207.99	76018.8
Sample 23	38012.46	41542.6
Sample 24	19068.40	17322.3
Sample 25	2365.54	2279.66
Sample 26	3556.80	1509.45
Sample 27	11982.48	18344.97
Sample 28	25828.29	22963.62
Sample 29	43056.00	45995.36
Sample 30	80886.00	70909.62
Sample 31	18230.11	30574.95
Sample 32	67228.20	52301.51

Calculation of brain tumor volume by linear measurement method obtained the largest result in sample 16 with a volume of 144144.00 mm3, while the smallest value in sample 2 with a volume of 1464.32 mm3. Calculation of brain tumor volume with this method obtained an average value of 39304.53 mm3. For the calculation of brain tumor volume with the k-means clustering method, the largest volume was obtained in sample 16 with a volume of 139351.68 mm3 and the smallest volume in sample 26 with a volume of 1509.45 mm3. The average value in the k-means clustering method is 35374.69 mm.3

This research shows the analysis of differences in the calculation of brain tumor volume performed using manual methods, namely linear measurement and segmentation methods, namely k-means clustering (Kaya et al., 2017). This research used 32 research samples, namely the results of MRI images of brain tumors from 32 patients. After collecting images in accordance with the inclusion criteria that have been set, then the calculation of brain tumor volume is carried out using the linear measurement method on the Siemens 1.5 Tesla MRI modality and the Matlab-based k-means clustering method. Measurement of brain tumor volume was performed by one observer, a radiology specialist who has more than 5 years of work experience.

Data were collected from patients with clinical brain tumors who performed MRI examinations using routine brain MRI examination sequences. Routine brain MRI examinations in clinical brain tumors use spin echo sequences T1 weighting sagittal cuts, spin echo sequences T1 weighting axial cuts, spin echo sequences T2 weighting axial cuts, TIRM sequences T2 weighting axial cuts, blade sequences T2 weighting coronal cuts, spin echo sequences T1 weighting coronal cuts. After that, contrast media was injected into the patient, and image acquisition was performed with spin echo sequences of T1 weighting of sagittal section + contrast media, spin echo sequences of T1 weighting of axial section + contrast media, and spin echo sequences of T1 weighting of coronal section + contrast media.

For the measurement of brain tumor volume, the linear measurement method used T1 post-contrast weighted spin echo sequence images on axial and sagittal sections with t1_se_tra CE and t1_se_sag CE sequences. The use of contrast media has the benefit of clarifying the image of the brain tumor in the image used for tumor volume calculation. In addition, in image segmentation, the T1WI post-contrast sequence is the most commonly used sequence because it is able to visualize the lesion well and does not show edema areas. Thus, the resulting image and segmentation focus on the tumor area (Biratu et al., 2021).

The results of this research are quantitative data in the form of brain tumor volume calculations that have been carried out by radiology specialists who act as observers. An observer performed the volume calculation method with linear measurement on 1.5 Tesla MRI modality. The calculation of brain tumor volume with this method was performed on T1WI post-contrast weighted spin echo sequences in axial and sagittal sections. The use of T1WI post-contrast sequences is because these sequences can make the tumor image clearer due to the use of contrast media given to patients through intravenous injections. The contrast media used was Gd-DTPA.

Calculation of brain tumor volume with linear measurement method is done by several steps, namely opening the MRI image file of the patient's brain tumor and selecting the SE T1WI post-contrast axial slice sequence, then the radiologist will select one slice that displays the largest tumor area, and continue by measuring the diameter of the tumor. The diameter measurement is done using the distance tools menu located on the view toolbar. Measurements on the axial slice will obtain the lateral diameter (Dl) and anterior-posterior diameter (Dap). Tumor diameter measurements were also taken on the t1_se_sag CE sagittal slice sequence by selecting one sagittal slice that displays the largest tumor area. The tumor diameter was then measured to obtain the cranio-caudal diameter (Dcc). The final results of these measurements are Dap, Dcc, and Dl. To calculate the tumor volume, the ellipsoid formula is used, namely $V = Dap \times Dcc \times Dl \times \pi/6$.

The stages that have been carried out to measure the volume of brain tumors using the linear measurement method are in accordance with the research conducted the research explained that the calculation of tumor volume could be done by measuring the diameter of the tumor using linear measurement and continued with the calculation of tumor volume with the ellipsoid formula where $V = Dcc \times Dl \times Dap \times \pi/6$ or can also be called diameter-based volume (Choi et al., 2024).

Calculation of brain tumor volume with k-means clustering segmentation method using post-contrast MRI images; this is because the algorithm used for tumor detection performs analysis based on the contrast in MRI images. The post-contrast MRI image shows a hyperintense image of the tumor compared to the normal area (Sarris et al., 2023). K-means clustering segmentation requires information related to the image, such as spatial resolution and slice thickness. The slice thickness information in the image is used to calculate the tumor volume, while the spatial resolution information is related to the tumor area. The next step is to segment the tumor area using the k-means clustering method. In the image segmentation process, several stages are carried out, starting with pre-processing; in this stage, several processes are carried out, including image denoising to reduce noise, intensity inhomogeneity correction, edge detection in the image, and also skull striping, which removes all tissues that are not brain tissue in MRI images. The second stage is ROI extraction, which aims to get the tumor area and separate it from the normal area. The next stage is the classification stage, which aims to classify tumors; at this stage, starting to use the selected segmentation method (Biratu et al., 2021). The segmentation stage with k-means clustering begins by separating the tumor area from the surrounding normal area and continues with the calculation of the tumor area by counting the pixels in the tumor area in the segmented image or binary image. Then, the tumor area in each slice is multiplied by the slice thickness used, which is 5mm; this is done on all existing slices so that the volume of each slice is known (mm3), and then all the results of the volume of each slice are accumulated to determine the total volume. So as to obtain the final volume in the brain tumour area and also visualize the brain tumor in 3D view (Li et al., 2021).

In this research, the segmentation method and the K-Means clustering segmentation stages are in accordance with research conducted by Sabaghian S (2020), in which it is explained that the stages in image segmentation begin with preparing the automatic detection module to be used and also the image to be tested. Furthermore, anisotropic filters were provided to the image with the aim of removing noise in the image and performing the skull stripping process. Then, proceed with the application of the k-means clustering algorithm on the image and determine the number of clusters to be used. In this research, the number of clusters used is 3 clusters, so K = 3. The MRI image section is divided into 3 clusters, namely the tumor area, the normal area, and also the background area (Sabaghian et al., 2020).

Calculation of brain tumor volume using linear measurement method and k-means clustering method yielded different volume results. The comparison of the volume calculation results was obtained because of the different ways of calculating the volume used. In the linear measurement method, the tumor volume calculation is done by measuring the diameter of one axial slice image that has the largest tumor dimensions to obtain the length (p) x width (l) of the tumor, while the height (t) of the tumor is measured through one of the sagittal slice images that have the largest tumor dimensions. From the measurements on the two perpendicular slices, the size of p x l x t or Dap x Dcc x Dl of the tumor is obtained, and then the tumor volume calculation will be carried out with the ellipsoid formula. Furthermore, the calculation of tumor volume with the k-means clustering segmentation method is carried out on axial slice images on all slices that have tumor images. This is in accordance with the research, the k-means clustering segmentation method, the calculation of tumor volume is obtained from the thickness of the slice thickness used, namely using a 5 mm slice thickness in MRI examination of brain tumors. Thus, to obtain brain volume results, each tumor area is multiplied by the slice thickness used and then accumulated.

The Wilcoxon test showed that there was no significant difference in the calculation of brain tumor volume with linear measurement and k-means clustering methods with a p-value > 0.05, namely 0.082. The results of the calculation of brain tumor volume with the two methods are not significantly different, although the measurement principles of the two methods used are different. Measurement of brain tumor volume with linear measurement is only performed on one slice that visualizes the largest tumor area on two perpendicular cross-sectional pieces. Measurements are taken to obtain the length, width, and height of the tumor or Dcc x Dl x Dap. The results of these measurements are multiplied by a constant 0.52, according to the ellipsoids formula, which is Dcc x Dl x Dap x 0.52. This step is in accordance with the research of regarding the calculation of tumor volume using linear measurement (Choi et al., 2024).

In calculating the volume of brain tumors with both methods, there are several samples with relatively small differences in brain tumor volume results or <5000mm3. One example is in sample 1, where the volume result with linear measurement is 8008.00mm3, while with k-means clustering is 7146.61mm3, the difference in tumor volume calculation results is 861.39mm3. The MRI image of sample 1 can be seen in Figure 5. The image of sample 1 shows a tumor that is regular or close to a round shape and has almost the same shape in each slice. So, the results of calculating tumor volume with the ellipsoid formula and the results of calculating tumor volume with k-means clustering tend to be the same.

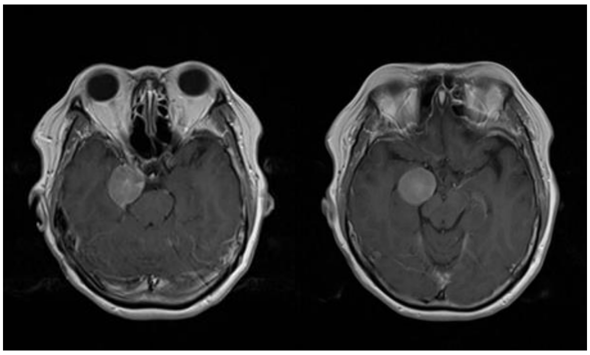

Figure 5. MRI Image of Sample 1 Brain Tumor Showing Regular Tumor Shape

The results of this research show that the calculation of brain tumor volume with the linear measurement method is generally greater than the k-means clustering method. The comparison of brain tumor volume calculations using linear measurement and segmentation methods showed that the results of tumor volume calculations with linear measurement were greater than the results of volume calculations with image segmentation. This is due to the difference in the size of t or lateral diameter (Dl), in the calculation with linear measurement, the value of t is obtained from the largest diameter of the sagittal slice, while in the image segmentation method, the value of t is the result of the number of slices that have tumor images with the slice thickness used (Putri et al., 2022).

One example of a brain tumor volume result with a large difference is in sample 21, where the volume result with linear measurement is 131459.33mm3, while with k-means clustering is 105737.85mm3 with a difference of up to 25721.48 mm3. This is because the method of measuring the volume of brain tumors with linear measurement uses the ellipsoid formula, where the object measured or the tumor measured is the tumor with the largest area that is considered to represent the shape of the tumor as a whole and is assumed to be in the form of an ellipse that can be calculated volume. The k-means clustering method does not measure the volume of the object based on the shape of the space but calculates the tumor area in each slice based on the image pixel. Therefore, the shape of the segmentation results follows the intensity of the image or the shape of the tumor based on the enhancement of the image. So, the difference in the results of measuring the volume of brain tumors in the two methods can be explained by the difference in volume calculation principles in the two methods used, namely linear measurement techniques that refer to the shape of an elliptical space and k-means clustering which does not refer to a specific space shape but by measuring the segmentation area of each object and visualized in 3D (Li et al., 2021).

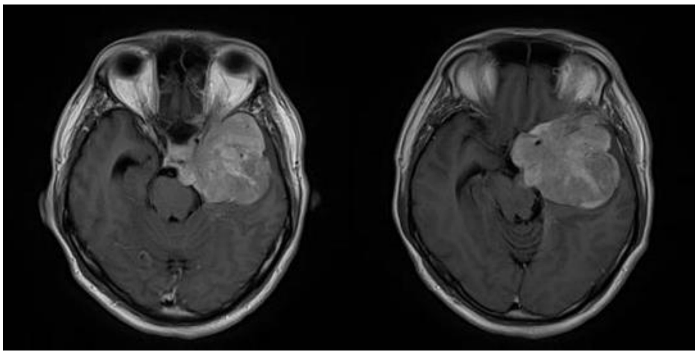

Figure 6. MRI Image of Brain Tumor Sample 21 Showing Irregular Tumor Shape

In 11 samples used, the results of brain tumor volume with the K-means clustering method are greater than the results of tumor volume with linear measurement. For example, in sample 11, the volume result with the k-means clustering method is 127709.47mm3, and the linear measurement method is 105963.00mm3. The difference between the two methods reached 21746.47mm.3 The magnitude of the results of measuring the volume of brain tumors with k-means clustering can be caused by tumors that have spread to the brain area; this is the nature of neoplasms from tumors, so the segmentation area needed is wider.

Segmentation of brain tumor MRI images with K-means clustering has many benefits in tumor segmentation. In addition, the use of K-means clustering can still be developed to get more accurate segmentation results, such as the use of K-means clustering combined with Convolutional Neural Network (CNN) or deep learning for more specific brain tumor detection to classify the level of tumor malignancy (benign or malignant tumors). K-means clustering can also be developed using the iterative Co-Clustering and K-Means (ICCK) algorithm. The working principle of Co-Clustering is clustering the rows and columns of the matrix. This ICCK segmentation method obtained better results on more complex images and also has high sensitivity, specificity, and accuracy values of 82.41%, 99.74%, and 99.28% in brain tumor MRI image detection (Nasor & Obaid, 2020).

The advantage of the linear measurement method in the MRI examination of brain tumors is that it uses linear measurement as a gold standard to determine the size of the tumor performed by radiology specialists (Biratu et al., 2021). In clinical practice, 2D measurement with linear measurement to determine the size of the tumor is fast and simple because it does not require additional software. Volume calculation with this method can use the ellipsoid formula (V = Dap x Dl x Dcc x 0.52), where the tumor is depicted in an oval shape. This formula requires linear measurements in three orthogonal planes (Dap, Dl, and Dcc) to calculate the volume (Sreenivasan et al., 2016). The shortcomings of the linear measurement method are that it only uses one representative slice, not all slices that show the brain tumor. so the resulting volume measurement results cannot provide information on the volume of the brain tumor as a whole, so the resulting tumor volume is a rough volume estimate (Mohammadi et al., 2023).

The advantage of the k-means clustering segmentation method is unsupervised learning, which has a function to divide the pixel intensity in the image; besides that, this method is an automatic segmentation method (Chouhan et al., 2019). The working principle of this segmentation is to divide the image into several clusters based on the centroid distance set. Pixel grouping will be carried out until there is no significant change in centroid distance so that the shape of the segmentation results will follow a homogeneous pixel shape. MRI image segmentation is an important and effective step in the diagnosis and treatment of tumors because proper detection determines patient treatment (Nasor & Obaid, 2020). Image segmentation with k-means clustering is able to produce 3D image reconstruction derived from 2D tumor contours. This is done by connecting and stacking the segmentation results obtained on each slice (Li et al., 2021). The shortcomings of the k-means clustering method are several things that can affect the use of segmentation methods, such as the existence of partial volume effects that can reduce image accuracy because each image pixel can represent several types of tissue. In addition, image segmentation needs to prepare the automatic detection module that will be used (Sabaghian et al., 2020). The k-means clustering method can produce different segmentation results based on the number of clusters specified. The more clusters used, the more image segmentation results. In addition, the placement of the initial centroid point will also affect the segmentation results (Dhanachandra et al., 2015).

Digital image processing is an important part of efforts to enforce diagnoses on patients, such as in measuring the volume of brain tumors owned by patients. In this research, the digital image processing method used, especially in the image segmentation method, produces an effective tumor volume calculation that can help radiology specialists, although the application of this segmentation method is still limited to images with post-contrast T1WI weighting in the spin echo sequence. The resulting image segmentation is able to reduce subjectivity because the segmentation is done based on pixel intensity. In addition, the use of k-means clustering segmentation is able to improve patient diagnosis information and can be an alternative in calculating brain tumor volume (Dhanachandra et al., 2015).

In this research, there are several limitations in the application of the k-means clustering segmentation method, which is only applied to one modality of MRI aircraft, namely Siemens 1.5T MRI (Vishnuvarthanan et al., 2016b). Therefore, the results of this research still cannot be generalized to images produced by other MRI modalities. In addition, this k-means clustering segmentation method is proposed as an additional method that can be used for brain tumor volume measurement, not as a substitute method in brain tumor measurement.

CONCLUSION

In analyzing the application of the K-means clustering method in MRI segmentation of brain tumors, a comparison was made between the linear measurement method and K-means clustering for calculating tumor volume. The linear measurement method estimates the volume using the largest single slice from the axial and sagittal views, while K-means clustering considers the entire set of slices. Although these methods yielded different volume estimates, the Wilcoxon statistical test indicated that the difference was not statistically significant. The linear measurement method generally provided slightly higher volume estimates than the K-means clustering method, but this difference lacked statistical significance. For further development, it is recommended to optimize the K-means clustering method, especially in the segmentation of brain tumors with irregular edges, in order to more accurately distinguish tumors from surrounding normal tissues.

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