

Received June 28, 2021, accepted July 8, 2021, date of publication July 13, 2021, date of current version July 21, 2021.

Digital Object Identifier 10.1109/ACCESS.2021.3096790

# Visualization of Medical Volume Data Based on Improved K-Means Clustering and Segmentation Rules

JI MA<sup>1</sup>, YAZAN AHMAD MUAD<sup>1</sup>, AND JINJIN CHEN<sup>2</sup>

<sup>1</sup>School of Computer Science and Technology, Zhejiang University of Technology, Hangzhou 310014, China

<sup>2</sup>School of Design and Art, Communication University of Zhejiang, Hangzhou 310019, China

Corresponding authors: Yazan Ahmad Muad (yazanawm@hotmail.com) and Jinjin Chen (chenjinj@cuz.edu.cn)

This work was supported in part by the National Natural Science Foundation of China under Grant 61902350, and in part by the Open Project Program of the State Key Laboratory of CAD&CG of Zhejiang University under Grant A2111.

**ABSTRACT** Accurate extraction and visualization of the target features are important in medical visualization, allowing the user to get a meaningful view of their targets. The traditional way to generate visualization results is 1D TF-based volume visualization, which uses a 1D -TF to determine the optical properties of each voxel. However, it is difficult to distinguish multiple targets by using the 1D TF-based volume visualization. It is also challenging to distinguish accurate targets when the objects' intensity values are similar in volume. Using the traditional transfer function usually fails to extract important target features and generates less accurate results. In this paper, we proposed extracting and segmentation techniques based on K-means algorithm that allows the users to segment and enhances single or multiple targets by a single point to view the features in 3D view. We have applied it to various univariate or multivariate volume datasets from the medical field to demonstrate its effectiveness. Moreover, we have performed both qualitative and quantitative experiments to compare its results against the results from two state-of-the-art techniques and the ground truths. The experimental results showed that our method is able to generate the closest results to the ground truth.

**INDEX TERMS** Medical visualization, volume segmentation, K-means, transfer function.

## I. INTRODUCTION

Medical visualization is the process of delivering a visual impression of the interior segments of a person for further examination of clinical jobs and medicinal purposes. Likewise, it tends to be seen for picking up information on the elements of the organs and tissues in a human body. Medical visualization refers to techniques that project 3D volumetric datasets to 2D screens and can free the users to view the volume data slice-by-slice and view them to present a more intuitive and informative view [1]. The challenge in medical visualization is to detect and enhance the visualization of the important features of interesting targets.

This usually achieved by image segmentation functions using the Transfer function (TF), which maps voxels to various optical properties. Much research has been conducted in designing meaningful and robust TFs for volume

visualization. References [2]–[5] TF for volume visualization is classically created by exploring data properties of the given volume. The TF space is usually created and visualized as a 1D or 2D histogram for more instinctive manipulation clustering or segmentation techniques in the TF space to help detect and select interesting regions. In the medical data, the objects with similar properties or overlapping data values could be projected to the same or nearby regions of the TF space, making it difficult for an image segmentation function to distinguish them. More sophisticated methods are needed to separate and highlight essential structures in these kinds of datasets.

Using volume attributes like the intensity and the gradient is very important for the image segmentation process to detect the user's interesting targets. The intensity attribute is a data matrix whose values represent the intensities of the objects in the volumetric data within some range. The gradient is a directional change in the intensity or colour of an image. In the image segmentation functions, the local

The associate editor coordinating the review of this manuscript and approving it for publication was Gianmaria Silvello<sup>1</sup>.

frequency distribution used to pre-process the data to give the voxels of the dataset a value to allow the functions to detect them or extract features from them to segment the interesting targets. Our system used the intensity and gradient attribute in different segmentation steps to extract the features based on the attribute voxels value.

We have addressed the problem of extracting the targets that have similar value with other tissues and connecting to them by using the extracting and segmentation techniques that work as follows.

First, we have designed the target segmentation technique based on K-means clustering algorithm that can segment the targets which have a similar value to the user's interesting target in the volume. We also have improved the k-means algorithm to make it able to give the same result every time the user will test the dataset by using the extracted features from the user-selected slice and point as the centroid center value rather than the traditional k-means algorithm that works by random centroid center value to classify the targets in the volumetric data.

Second, we have designed the segmentation rules technique that works to improve the result of the k-means segmentation technique and extract accurate features which used to create the intensity mask range (IMR) based on the intensity attribute and create the gradient mask range (GMR) based on gradient attribute to classify the interesting targets from other tissues in the volume.

Third, we designed target extracting and segmentation techniques that can detect and segment the user's interesting targets from the other tissues that do not have a boundary with the interesting target and from the targets that have a similar value to it. Also, it will ensure that the interesting target has thoroughly segmented using extracted features based on the features mask.

Finally, we have designed a visualization technique and modulated the opacity values of the voxels Based on the features mask that generated using previous techniques to enhance the visualization of the interesting target in the volume. Moreover, we utilized Dynamic Parallelism to speed up the segmentation process of the volumetric data.

## II. RELATED WORK

In recent years many efforts have been devoted to the image segmentation functions. Segmentation is a commonly used technique and also a longstanding challenge in volume visualization. It can be performed in the 2D TF space or the 3D volume space compared to the 2D TF space. 3D volume space segmentation can take advantage of spatial information to separate objects of interest, but it is usually more time-consuming to ensure the efficiency of volume exploration.

Levoy [6] proposed volume rendering based on the classical ray casting, which implements a simple physical light emission and absorption model without scattering effects. Bruckner and Groller [7] their general approach is to shoot rays through the pixels into the field volume and accumulate

the colour and opacity contributions at discrete locations to produce the final pixel colour. The GPU-based ray-casting is denoted as VolumeShop. It is an interactive system that features advanced manipulation techniques and illustrative rendering techniques to generate interactive illustrations directly from the volumetric data. The system is using latest-generation texture-mapping hardware to perform interactive rendering applying various kinds of rendering styles. It implements a multi-volume concept to enable individual manipulations of each volume part. The segmentation of the volumetric objects can be done directly via 3D painting. Apart from importance-driven visualization resulting into cut-away and ghosted views, VolumeShop features label management to introduce basic descriptions for the visualized data.

To focus on a particular feature, this feature can be moved from its original spatial position. To indicate its original spatial position, it is possible to display a ghost or add additional markers such as fanning or arrows. It has demonstrated the capability to manage in GPU moderate-size datasets and efficiently provide the user with insights about volumetric data.

Huang and Ma [8] applied partial region growing to a subset of the volume and derived a 2D TF-based on the partial region growing results by leveraging on the parallel processing capabilities of programmable graphics cards and automatic generation of a TF for the user by making use of the result of partial region growing. Enhancing TFs with computed or acquired values often results in an even more complex feature space. However, they had a disadvantage with the data size because it is large hampering interactive rendering. The volume data is noisy, and the user needs to point to the region of interest.

Cheuk *et al.* [4] converted a 3D intensity field to a 2D intensity-gradient histogram and applied the normalized cut algorithm to segment the IGM histogram hierarchically. They have shown the idea of using computational visual segmentation to mimic user interaction and classify intuitive volumetric regions effectively. By iteratively partitioning the histogram, they created the hierarchy and stored it in a tree structure. The resulting hierarchy of segments was used to guide the user interactively explores and visualize the volume data.

Xiang *et al.* [9] proposed the skeleton cuts to segment interesting structures of a volume and to visualize the segmented structures by using a combination of segmentation and local TFs to visualize complex medical datasets where they archive the volume data with high-quality results. The segmentation provides better localization of TFs and better feature separation, but it was slow Recognizing and partitioning an object with boundaries from the image.

Sherbondy *et al.* [10] implemented region-growing-based volume segmentation with simultaneous volume visualization their advantage is the segmentation method that allows interactive visualization and control because of its computation speed and coordination with a hardware-accelerated

volume renderer, but the process slows down by using the CPUs for general computation.

Burget *et al.* [11] Presents an innovative algorithm combining the theory of artificial intelligence and knowledge of human eye anatomy. Bhanumurthy and Anne [12] proposed an ABC algorithm that gives an efficient fitness function that improves the segmentation quality. Clustering is done after the transition of the input data into a higher dimensional feature space. This proposed technique has accomplished automated detection.

Neethu and Shruti [13] proposed a reliable tumor detection method based on CNN that reduces the operators and the errors. The system is divided into two phases: firstly learning and training phase. Secondly recognition and testing phase. CNN is used in convolving a signal or an image with kernels to obtain feature maps. Their results gave more information about brain tumors and helped the doctors with diagnosis, treatment plan-making, and tumor monitoring. However, the software taking a long time to train and having some limitations, i.e. it can only provide accurate results for a limited number of images. Therefore, trusted and automatic detection of brain tumour is essential to decrease the death rate.

Yang *et al.* [14] identified landmarks on the distal femur surface by processing three independent sets of 2D MRI slices (one for each plane) with regular CNNs. The 3D position of the landmark was defined as the intersection of the three 2D slices with the highest classification outputs.

Kindlmann and Durkin [3] have considered the 3D histogram volume defined by attribute value, first and second directional derivative. In this space, they have defined a model with classified boundaries and then used this model for automatic opacity function generation. Those distinguished boundaries appeared as arches in the derived histogram with axes representing scalar value and gradient magnitude. Although using this histogram can improve the selection of boundaries, intersection or overlapping of two arches caused by different feature voxels sharing the same scalar value and gradient magnitude may result in ambiguities in the classification of boundaries. The gradient magnitude histogram did not correctly measure the soft boundary between the dendrite and the background.

Sereda *et al.* [15] proposed the LH (Low-High) histogram as the TF space, where boundaries appear as blobs instead of arches in the intensity-gradient magnitude (IGM) histogram, which are also more robust to noise and bias. Despite their popularity and ease of implementation, these approaches cannot capture spatial information that may provide better visibility of features of interest. Their approach has failed with the two boundaries because they could not be separated as they overlap in the TF domain.

Bajaj *et al.* [2] introduced the contour spectrum, which plots several contour properties, i.e., surface area, volume, and gradient integral of the contour, to guide the user in selecting significant values. They showed that measures such as

contour length, area, volume, etc. are piecewise polynomial since they are piecewise polynomial in each cell

Pereira *et al.* [16] performed a thorough evaluation of data augmentation strategies for brain lesion segmentation to combat class imbalance using a hybrid intelligent fuzzy Hopfield neural network. They used small kernels, a more profound architecture, intensity normalization and data augmentation. Different CNN architectures were used for low and high-grade tumors. The error is minimized in Artificial Intelligence, and with greater precision, the accuracy is achieved; it has also carried out repetitive and time-consuming jobs efficiently. They attained top results on a 2013 public challenge dataset and second place in an on-site 2015 challenge.

Zhao and Kaufman [17] and Pinto and Freitas [18] proposed Machine learning methods, such as neural networks and support vector machines, have been applied to classify high-dimensional data this design of multi-dimensional TF that uses self-organizing maps to perform the dimensional reduction of the voxel attributes and allows building multidimensional TFs through the exploration of a simplified (reduced) space where traditional interaction techniques can be employed. However, it is losing the information caused by the dimensional reduction process, and it performs a non-discrete classification which can represent uncertainty.

Purohit and Joshi [19] introduced a new approach to K-means clustering algorithm. They proposed a new method for generating the cluster center by reducing the mean square error of the final cluster without increasing the execution time. Their proposed methods reduced the means square error without sacrificing the execution time.

Jose *et al.* [20] who is engaged in the health sector, discuss brain tumours' segmentation in patients using the Fuzzy C-Means and K-Way algorithms. The results obtained are that Fuzzy C-Means have better K-Means performance because the resulting segmentation is more precisely identified. They divide their proposed methods into three parts, pre-processing, advanced k-means and fuzzy c-means and feature extraction. In the pre-processing, they implemented it by using the filter to improve the quality of the image. Then they proposed an advanced K-means algorithm followed by Fuzzy c-means to cluster the image. Then they have used the resulted segment image for the feature extraction for the region of interest. Their proposed method is simple, fast and understandable. Easy to determine which clusters are neighbouring, but all the cluster boundaries are either horizontal or vertical, and no diagonal boundary is detected. Kniss and Wang [21] presented a simple and robust method that treats the volume as a 3D manifold and performs segmentation based on manifold distance metrics. References [22]–[25] alternatively dimension reduction is first performed on the high-dimensional data followed by clustering or classification in the low-dimensional space.

Yedla *et al.* [26] proposed a new method to determine better initial centroids and provide an efficient way to assign the

data points to proper clusters with lower time complexity. Any additional input like threshold values is not considered in this method. Finding the initial centroid is introduced, and it provides an effective way of assigning the data points to suitable clusters with reduced time complexity. They proved their proposed algorithm is accurate with less computational time than the original k-means clustering algorithm, and their proposed algorithm does not require any additional input like threshold value, but the algorithm still initializes the number of clusters.

Selver [27] applied the Brushlet to increase the volumetric information in order to identify low and high frequency texture. Nazeer and Sebastian [28] proposed an enhanced algorithm to improve the accuracy and efficiency of the K-means clustering algorithm that combines a systematic method consisting of two approaches. The first one is finding the initial centroid, and another is assigning the data point to the clusters. They have chosen different initial centroid and tested execution time and accuracy. From the result, the proposed algorithm reduced the time complexity without sacrificing the accuracy of clusters. In original k-means, initial centroids are selected randomly, affecting the operational time and accuracy of the cluster directly. For different initial centroids, selection resulting clusters will be different. Also, the operational complexity of the basic k-means algorithm is high.

Klinker *et al.* [29] they observed Physical Approach to colour Image understanding with additional example through opposed to k means and Anil Z Chitade evaluated the Colour-based image segmentation using k-means clustering. The colour of each pixel in the object can be described as a linear combination of the object's colour and its reflection. The object's colour is a diffuse reflection from the body of the material, and the specular reflection is a stronger reflection (a brighter spot) in one viewing direction from the object's surface.

Lundström *et al.* [30] proposed the Probabilistic Animation technique. This technique is used to visualize uncertainty caused by the material classifications and automatically shows all possible appearances for each material's regarding an explicitly probabilistic TF. However, this technique has one main drawback: when the intensity of the interesting target and other materials is similar or overlapping, and/or the interesting target is occluded by other materials, it would be difficult or even impossible to reveal the interesting target and its associated uncertainties. In comparison, our proposed uncertainty visualization technique could overcome this drawback and thus provides a better uncertainty visualization service. The parallel coordinate plot is a widely used method to display high-dimensional data on a 2D plane, where the TF is designed by selecting a certain range in one dimension or selecting line segments with similar slopes between two neighboring axes [17], [31].

Conze *et al.* [32] utilized cascaded pretrained convolutional encoder-decoders as generators of cGAN for

abdominal multi organ segmentation. Raidou *et al.* [33] presented a visualization method that overlays black circle-type glyphs on top of the colours to indicate the radiation dose uncertainties used to irradiate tumors. The drawback of this method is that the colours could be occluded by the black circle-type glyphs on top of them and thus causes difficulties for perception.

Cai *et al.* [34] proposed the Rule-Enhanced Transfer Function (Rule-Enhanced) that utilizes the rules obtained from user-labelled interesting target on a few slices to automatically and intellectually segment the user interesting target in the entire medical volume data. Ma *et al.* [35] refined this approach and proposed the Dynamic Visualization of Uncertainties (Dynamic Visualization) that allows the users to express the feature of interest via transfer functions. Comparing to [34] Single-attribute rule-based Segmentation method, here the author has approach a segmentation method consisting of multiattribute-rule to produce more accurate segmentation result. These methods [34], [35] have used the genetic algorithm to find the best rule that can segment more accurate target which in some cases is time-consuming. We have performed both qualitative and quantitative experiments to compare our method results against the results from the Rule Enhanced and the Dynamic Visualization to show that our method is able to generate the closest results to the ground truth.

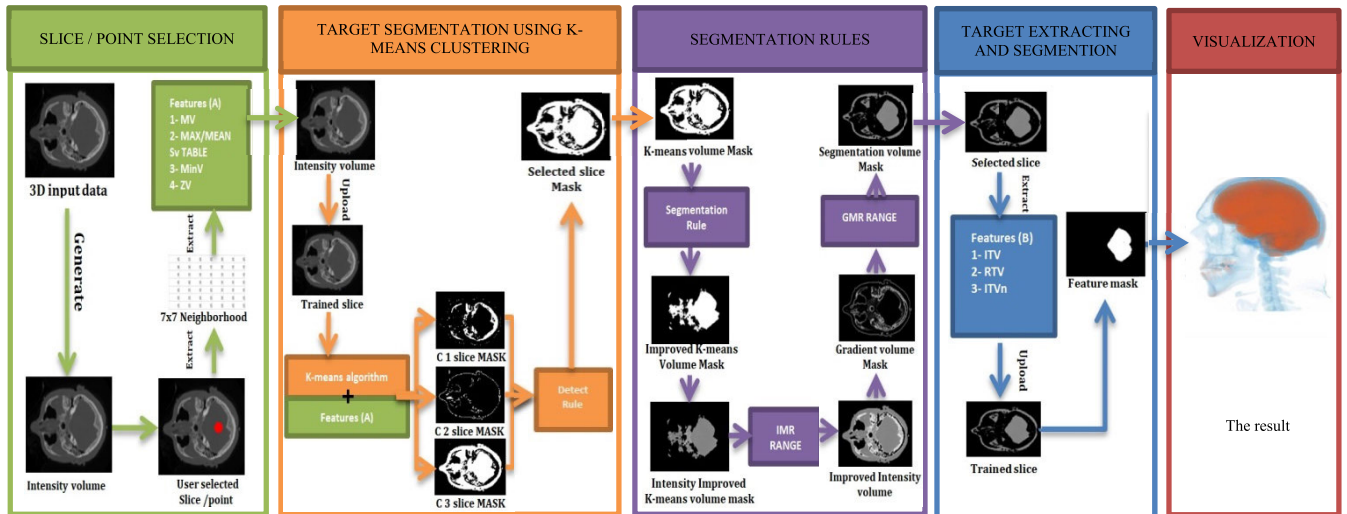
### III. METHODS

#### A. OVERVIEW OF WORKFLOW

The framework of the proposed method is presented in Fig. 1. The system will start by generating the intensity attribute for the original data. And as an input, the user will select a slice that contains the target and select a point on each target that needs to segment then the system will extract the features based on it. Second, the system will input the intensity attribute and the extracted features to the target segmentation technique based on the k-means algorithm to segment the masks generated from the k-means algorithm which contains the targets that have similar intensity values or are connected to user interesting target in the volume. Third, the system will use the k-means mask as input to the segmentation rule to improve the k-means mask. Based on the original intensity attribute the system will give each voxel in the improved k-means mask an intensity value.

The system will use the modified mask with the selected slice and point to extract new features from the mask, and based on the features; the system will generate the IMR. Using IMR, the system will distinguish the voxels that will not meet the range from the improved mask. Using the selected slice and point, the system will extract new features to generate GMR and will distinguish the voxels that will not meet with it from the mask to generate the segmentation rules mask that has the interesting target classified from the other tissues.





**FIGURE 1.** The workflow of this paper: (MV) is the mean value, (min) is the min in the feature table, (max/mean) is the maximum value in Sv table, (ZV) is the zero value, (C1,C2,C3) is the clusters value, (IMR) is the intensity mask range, (GMR) is the gradient mask range, ITV is the intensity target voxels, RTV is the rest targets voxels and (ITVn) is the intensity target voxels number.

Fourth, the system will input the segmentation rules mask to the target extracting and segmentation technique to detect the user’s interesting target from the other tissues and segment it. This technique can classify the interesting user target from the other tissues that are connected to it and have similar value in some slices.

Fifth, the system will use the features mask voxels to modify each voxel intensity value in the original image. Using the modulate opacity technique will view the result on a 3D view which is meaningful and accurate results. Moreover, we utilized Dynamic Parallelism to speed up the segmentation process of the volumetric data.

**B. SLICE/POINT SELECTION**

**1) PREPROCESSING**

The medical data is partitioned into several regions based on its intensity. The intensity attribute is a data matrix whose values represent the intensities of the objects in the medical data within some range, and it is commonly used in image segmentation.

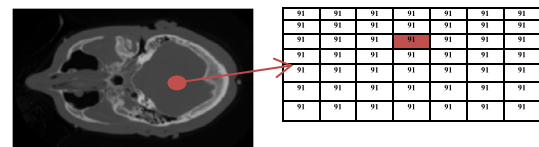
The main aim of segmentation is to differentiate the regions of the interesting target in an image and then label it as one target. While the medical datasets contain different bits of raw data, the system will start by checking the voxels bits size of the input data and changing the data to 8-bits which will help the system use the same rules on all the inputs datasets. The system will generate the intensity attribute to the original data and present a 3D view to it to allow the user to explore the data and select a slice and point on their interesting target. The user can select single or multiple targets that need to segment the data using a single point on each interesting target. We used the modified pointer function to allow the user to see the pointer from the other targets.

The system will extract the location of each point the has user made to get the position of the selected target in the

data, which based on it, the system will use to extract the features.

**C. FEATURES EXTRACTION**

In the medical data, the objects with similar intensity values will stand out and visible as one object, making them difficult to be segmented from each other. The feature is a piece of information about the content of an image and its specific structures in the image, such as points, edges or objects. Our system has used three types of features to extract and segment the user’s interesting targets. The first one is for the target segmentation technique using k-means clustering. The second one is for the segmentation rules technique. The third one is for the target extracting and segmentation technique. The system will use the location of each point the user has input and, for each point, will generate a  $7 \times 7$  neighbourhood table that will contain the values of the voxels around the selecting point in the selected user slice. We define the neighbourhood table H around voxel v as a set of voxels Vi surrounding V (fig.2). H serves as a sample space, and each Vi is an elementary event in space H.



**FIGURE 2.** The extracted  $7 \times 7$  neighbourhood table from the user-selected point.

The simplest and default neighbourhood is the set of all voxels within a Euclidean distance (d) which is  $7 \times 7$  of v. The system will generate a new volumetric data based on the intensity attribute that will use in the target segmentation technique based on k-means clustering algorithm, and it will

have unit-8 size. The system will generate the new volume data using the following algorithm:-

**Algorithm 1** New Mask Generation

1. for  $i = 1$  : slice size of  $IV$
2.  $IV_s = IV(:, :, i)$ ;
3.  $NV_{sv} = \max(\max(IV_s))$ ;
4.  $NV_s = IV_s \times (255/NV_{sv})$ ;
5.  $NV_s = \text{unit8}(NV_s)$ ;
6.  $NV(:, :, i) = NV_s$ ;
7. end

where (IV) is the intensity volume, (IV<sub>s</sub>) is the intensity slice value, (NV<sub>sv</sub>) is the new volume slice value, (NV<sub>s</sub>) is the new volume slice, and the (NV) is the new volume. After generating the new volume, the system will distinguish the non-target voxels, which are mostly the air values, by finding these voxels based on the clear rule that takes the form:-

$$\begin{aligned}
 f &= \text{find}(USs > 0.1); \\
 v &= \text{Uss}(f(1)); \\
 C_v &= v + 0.01;
 \end{aligned}
 \tag{1}$$

where (USs) is the user selected slice, (v) is the first value that is bigger than the average air value in the medical volume data, and (C<sub>v</sub>) is the clear rule value.

The system will distinguish all the values that are less than C<sub>v</sub> values in the data to ensure that the air values will not be detected while extracting the features. To extract the features, the system will use the extracted table from the selected slice on the new volume on the same slice to get the new values of each voxel in the table. First, the system will find the mean value from the table and based on it; the system will extract the features.

We have separated the features into two branches based on the mean value while some of the objects in the data will have high-intensity and others will have low-intensity value using conditional statement rule that takes the form:-

where (MV) is the mean value, (USs) is the user selected slice, (Sv) is the first value in the selected slice that has match the range, (Sv table) is the neighbourhood table 7\*7 around the Sv, (MinV) is the minimum value in the neighbourhood table.

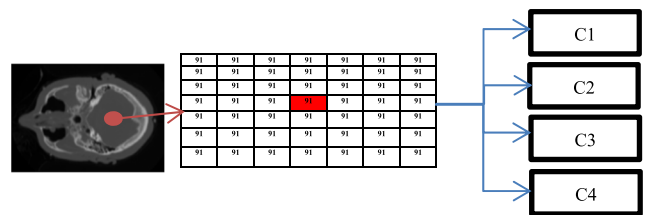
Using this rule, the system will generate four features and will use them as the inputs to the k-means clustering as centroids center. The system will forward the new volume with new values with these features to the target segmentation based on k-means clustering to segment the targets that have similar value to the user’s interesting target.

**D. TARGET SEGMENTATION BASED ON K-MEANS CLUSTERING**

K-Means is one of the simplest unsupervised learning algorithms that solve the well-known clustering problem. A data-partitioning algorithm assigns n observations to exactly one of k clusters defined by centroids, where k is chosen before the algorithm star. The k-means algorithm

**Algorithm 2** Features Extraction

1. if  $MV < 128$
2.  $\rightarrow S = \text{find}(USs > MV)$ ;
3.  $S_v = S(1)$ ;
4.  $S_v \text{ table} = USs(S_v(x) - 3 : S_v(x) + 3, S_v(y) - 3 : S_v(y) + 3)$ ;
5.  $MinV = \min(S_v \text{ table})$ ;
6.  $\max S_v \text{ table} = \max(S_v \text{ table})$ ;
7.  $C1 = MV$
8.  $C2 = \max S_v \text{ table}$
9.  $C3 = MinV$
10.  $C4 = 0$
11. if  $MV > 128$
12.  $\rightarrow S = \text{find}(USs > 0)$ ;
13.  $S_v = S(1)$ ;
14.  $S_v \text{ table} = USs(S_v(x) - 3 : S_v(x) + 3, S_v(y) - 3 : S_v(y) + 3)$ ;
15.  $\text{mean } S_v \text{ table} = \text{mean}(S_v \text{ table})$ ;
16.  $MinV = \min(S_v \text{ table})$ ;
17.  $C1 = MV$
18.  $C2 = \text{mean } S_v \text{ table}$
19.  $C3 = MinV$
20.  $C4 = 0$



**FIGURE 3.** The extracted features from the user-selected slice and point.

chooses seeds as follows, assuming the number of clusters is k. It will select an observation uniformly at random from the data set. The chosen observation is the first centroid and is denoted (C<sub>1</sub>). Then it will compute distances from each observation to C<sub>1</sub>. Denote the distance between (C<sub>j</sub>) and the observation m as d(X<sub>m</sub>, C<sub>j</sub>), and then it will select the next centroid, C<sub>2</sub>, at random from the dataset with probability using this rule

$$\frac{d^2(x_m, c_1)}{\sum_{j=1}^n d^2(x_j, c_1)}
 \tag{2}$$

where (x) is the dataset, (C) is the cluster or the centroid center. Then to choose the center (j), it will compute the distances from each observation to each centroid and assign each observation to its closest centroid. Using the center rule: -

For  $m = 1, \dots, n$  and  $p = 1, \dots, j - 1$ ,  
 select centroid  $j$  at random from  $X$  with probability

$$\frac{d^2(x_m, c_p)}{\sum_{h: h \in C_p} d^2(x_h, c_p)}
 \tag{3}$$

where  $(C_p)$  is the set of all observations closest to the centroid  $(C_p)$  and  $(X_m)$  belongs to  $(C_p)$ .

The algorithm then will select each subsequent center with a probability proportional to the distance from itself to the closest center that already chose. And it will repeat until  $k$  centroids are chosen.

So these centroids should be placed attentively because of different location causes different result and that shows how these centroids values are important in the K-means clustering. In our system, we have improved the K-means clustering algorithm by assigned these centroids from the extracted feature in the previous section rather than let the algorithm choose random centroids center to ensure that one of the centroids will be in the interesting user target and to make the results be the same every time the system test the dataset.

Using this way, the user interesting target will be clustered with the tissues that have similar value to it. We have added these features to the k-means algorithm as following, first assign the centroids using our features to be:-

---

#### Algorithm 3 K-Means Centroids Extraction

---

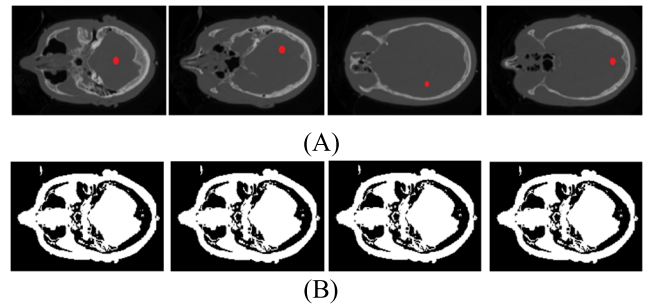
1. *If*  $MV < 128$
  2.  $C1 = MV$
  3.  $C2 = \max S \text{ table}$
  4.  $C3 = \min V$
  5.  $C4 = 0$
  6. *if*  $MV > 128$
  7.  $C1 = MV$
  8.  $C2 = \text{mean } S \text{ table}$
  9.  $C3 = \min V$
  10.  $C4 = 0$
- 

where  $(C1 \dots C4)$  are the centroid center values. Moreover, according to the weighted average value of objects in the cluster, each object is assigned to the lowest cluster dissimilarly, then updates the weighted average values of cluster, i.e. compute the weighted average values of objects in each cluster. It will assign each object to the group that has the closest centroid.

The results of figure 4 show the effectiveness of our technique that can present the same results with the different selected points in different selected slices too by changing the inputs of the k-means based on the extracted features.

After the k-means has clustered each voxel to one centroid, the algorithm will present a slice that has voxels value from (1- 4), and each value is called responding to one cluster. After generating the k-means slice, the system will use the matching function to check which cluster is matching with the neighbourhood table (H) to segment it from the other values. After segmenting the value of the voxel that matches the (H), the system will save each voxel's location and assign it to one table called K-means segmentation target (KST).

After extracting the KST, the system will upload the next slice from the new volume to the k-means algorithm. After generating the slice that has values from (1-4), the system will



**FIGURE 4.** Shows the results of using different points and slices as an input to k-means clustering where (A) is showing different choosing points in different slices (B) is the generated C1 mask from k-means clustering using our technique.

match it with the extracted KST from the previous slice then will save the new KST to use for the next slice.

At the end of this step, the algorithm will present a new volume data called k-means segmentation mask that contains the user's interesting target and the tissues that have a similar value to it. The system will forward this data to the segmentation rules with the features to improve the user k-means segmentation mask and generate the IMR and GMR to generate the segmentation rule mask.

#### E. SEGMENTATION RULES

In the previous section, the system using the k-means algorithm has segment a mask that contains the user's interesting target and the tissues that have similar value to it.

This section will describe the segmentation rules that work to improve the k-means segmentation mask based on features extracted from the intensity and the gradient attribute of the k-means segmentation mask. In some slices of the medical data, the user target will not be connected to other tissues and classified alone. So to improve the k-means segmentation mask, the system will view it to the user to select a slice where their interesting target is not connected to other tissues and based on the selected slice and point the system will do the following steps:

##### 1) IMPROVE K-MEANS SEGMENTATION MASK

Using the user-selected slice and point, the system will use the matching function to distinguish the tissues which are not connected to the user interesting target in some slices. The system will start by extract the user's interesting target from the selected slice and save it in one slice called test slice (TS).

To ensure that the system has extracted only the user interesting target from the selected slice, the system will generate a  $7 \times 7$  neighbourhood table around each voxel equal to 1 in the selected slice and assigned each voxel as a trained voxel.

Then will check this table in TS to find how many cells in the table are equal to 1. Based on how many cells are equal to 1, the system will classify the trained voxel as matched one or not matched. If the trained voxel table has less than three cells equal to 1, then the system will classify it as not matched voxel and save the voxel to one table containing all the voxels

that did not match the voxels in TS, we assigned this table as Non-Matched Voxel (NMV).

After testing all the trained voxels, the system will distinguish all the voxels in the NMV table from the TS and will present new target that is improved, and all its voxel is related to the user interesting target we assigned the new target as Main Extracted Target (MET). The system will save the MET to a new mask called an improved k-means segmentation mask.

Next, the system will distinguish the MET from the selected slice. Then using the 2D connected component, it will extract the location of the voxels of each target rest in the selected slice and assigned the outputs of the 2D connected component as the Main Rest Target (MRT).

The system will upload the next slice from the k-means segmentation mask and will check the extracted MET voxels in the uploaded slice for any of the voxels equal to zero to modify the MET by removing these voxels from it.

Then the system will distinguish the MET from the uploaded slice and test each voxel in it equal to 1 as follows.

First, it will generate a 7\*7 neighbourhood table around the trained voxel, then will test it on MET to see how many cells in the table of the trained slice will have a voxel value equal to 1.

Second, if the table contains a voxel with value 1, the system will use the matching function to find if the table voxels match any target in MRT.

If the generated table has a cell with value 1 when the system has tested it on MET and it will not match with any target from the MRT, then the system will save the trained voxel to a table containing the target voxel in the uploaded slice.

After the system is done from testing each voxel in the uploaded slice, it will generate a new MET from the table that containing the target voxels and then distinguish the MET from the uploaded slice to generate a new MRT.

The system will repeat the segmentation steps for each uploaded slice. At the end of the segmentation, the system will generate the improved k-means segmentation mask that contains the user interesting target with the tissues connected to it and has similar value with it.

### F. FEATURES EXTRACTION

In previous sections, the system has segmented the user's interesting target with the tissues connected to it and has similar value with it. To classify the user's interesting target, features that are related to the interesting target need to be extracted. As pre-processing to extract the features, the system will need to give the voxels in the improved k-means segmentation mask a value while all the voxels in it are equal to 1.

The system will check each voxel in the improved k-means segmentation mask on the intensity attribute to get the value of the voxel from it. Based on the improved k-means segmentation mask with intensity values, the user selected slice, and the user selected point, the system will extract the features.

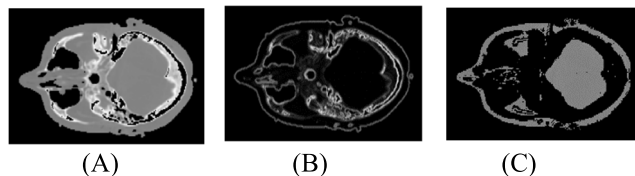


FIGURE 5. Show the results of the segmentation rules where (A) is showing the IMR mask, (B) is showing the GMR mask, and (C) is showing the segmentations rules mask.

We have extracted two features that will be inputted to the segmentation rules to generate the segmentation rules mask.

The system will start by finding the maximum value in the improved k-means segmentation mask. In contrast, the improved k-means segmentation contains the interesting user target and will assign it as Max Mask Value (Max MV), and this value will be the first feature.

Then from the selected point and slice, the system will generate an 11\*11 neighbourhoods table around the selected point and will extract the mean value from the table and assigned it as Mean Table Value (MTV) and based on the MTV and MaxMV, the system will generate the second feature which is the Minimum Mask Value (MinMV) using the minimum rule that takes the form: -

$$MinMV = MTV - ((MTV \times 3) - MaxMV) / 8 \quad (4)$$

where (MinMV) is the minimum mask value, (MTV) is the mean table value, (MaxMV) is the maximum mask value.

We have multiplied the MTV by three while the datasets are 3D and divided them by eight while the dataset voxels are 8-bits. After extracting these features, the system will use it to generate the segmentation rule mask containing the user's interesting target classified from the other tissues that are connected to it.

### 1) SEGMENTATION RULE MASK GENERATION

This section will describe the segmentation rules based on the intensity, the gradient attributes, and the extracted feature from the previous methods.

As input to the segmentation rules, the system will input the original intensity of the dataset and using the extracted features will create an intensity range we called intensity mask range IMR to distinguish the voxels in the data that has bigger or less value than the IMR and the IMR will set as following: -

$$\begin{aligned} IM(IM < MinMV) &= 0; \\ IM(IM > MaxMV) &= 0; \end{aligned} \quad (5)$$

where (IM) is the intensity mask of the original dataset.

After the system has distinguished the voxels that do not match the IMR, the system will assign the result as an IMR mask and generate the gradient magnitude mask to it.

Based on the generated gradient magnitude mask, user-selected slice and the user-selected point, the system will generate another 11\*11 neighbourhood table around the selected



point and extracted the maximum value of it to create a Gradient Magnitude Range GMR.

We have used this range to find all the voxels in the gradient magnitude that are bigger than the maximum value of the extracted table and assigned them in one table we called gradient magnitude values (GMV). The system will remove all these values from the IMR mask that has generated using IMR.

At the end of this section, the rule will output the feature mask based on segmentation rules that contained classified user interesting target from other tissues.

### G. TARGET EXTRACTING AND SEGMENTATION

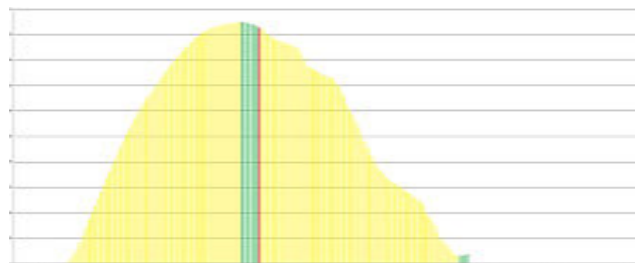
The previous steps will present volumetric data that contains the user interesting target classified from the other targets in the original data. In the medical data, some tissues will not have a boundary between them, presenting them as one object. After the system has used the gradient magnitude mask to segment the user's interesting target, some targets will still be connected to it because they do not have a boundary between each other at that point, which will present them as one target at that slice. To classify and segment only the user interesting target, we have designed extracting and segmentation technique that could detect and extract only the user interesting target based on the segmentation rules mask, user-selected slice and user slice point.

The system will start using the selected slice and point to extract the first Extracted Main Target while the user has chosen a point and slice where the target is not connecting to other tissues. Using this point, the system will generate an  $11 \times 11$  neighbourhood table around the selected point and assign the table as a point table (PT). Then the system will extract each tissue location voxels in the selected slice using the 2D connected component and save it in one table called selected slice target (SsT).

Using the matching function, the system will find the PT is matching with which tissue from the SsT. The matched tissue will be the user's interesting target in the selected slice. The system will save the voxel location in a table we called interesting target voxel (ITV). After extracting the ITV, the system will distinguish it from the selected slice then, by using the 2D connected component, the system will generate a table that will contain each target voxels rest in the selected slice and assign it as rest targets voxel (RTV).

The system will include the ITV to RTV as the last tissue and save the place number of it as an interesting target voxel Place (ITVp). These extracted features will be the input to the extracting and the segmentation technique to detect and segment the user interesting target from the segmentation rule mask.

The system will upload the first slice after the user selects a slice as a trained slice to segment the interesting target using the extracted features. It will start by extracting each object voxels in the trained slice using the 2D connected component and assign it as a trained slice table (TST) then, by using the matching function, will do the next steps:



**FIGURE 6.** Shows the target size of each slice where (red) is the user-selected slice (green) representing the target when it has a bigger size than the previously trained slice (yellow) is representing the target when it is a smaller size than the previously trained slice.

First will check which target in TST is matching with ITV. If the ITV has a match with one target, it will assign the matched targets as matched targets (MT).

Second, the system will check which target in the RTV is matching with the MT. If there is only one matched target and it matches ITVp, then the MT is related to the user's interesting target, and the system will segment it and save it in the feature mask. After saving the MT, the system will assign its voxels as ITV then generate a new RTV and ITVp based on the extracted target.

In cases where the MT is not equal to ITVp or when the ITV is matching with more than one target from the RTV, we have designed our system to find if all these matched objects are related to the user interesting target using checking rules that can detect the right target that needs to segment.

In the beginning, the system will test the ITV voxels in the trained slice to distinguish any voxel value will equal to zero then will generate a new ITV and RTV from the trained slice. The system will test each voxel of each target in RTV by generating a  $7 \times 7$  neighbourhood around the trained voxel and assign it as a trained voxel table (TVT). Then it will generate a slice for the ITV voxel values and assign it as an interesting target voxel slice (ITVs).

The system will test the TST on the ITVs. If one cell in the table will equal one, then the system will assign the trained voxel to one table that will contain all the trained voxels that have matched with this rule, and we call it matched voxels table (MVT). After testing all the voxels, the system will assign all the voxels in MVT to ITV, generate a new RTV from the trained slice, and upload the next trained slice to segment the user's interesting target from it the extracted features from the trained slice.

In the medical data, the objects first appear as small objects and then grow their size with the slices until it reaches the biggest size of it then it will start to go back small until it disappears.

In some cases, the medical data will contain a large object that will separate into few parts and all of these parts represent one object in the data. We have designed the system to find out if these objects that have separated from the main object are still related to it or have been connected to other objects and become part of it.

To check if the user interesting target has separated, the system will check the extracted target from the trained slice to find if it is more than one part by using the 2D connected component, which will present a table of each connected object in the extracted target. If the 2D connected component result shows that the target has separated and becomes more than part, the system will check the separated parts using the following steps.

First, the system will distinguish the object with the biggest size from the 2D connected component while the biggest object in it is the main part and the small ones are the separated parts.

Second, the system will test each small object in the table and assign each object as a trained object (TO). The system will upload the next five trained slices and, using the matching function, will find the object that will match the TO. After finding the object that has matched the TO, the system will test the size of it and compared it to TO size to find if the TO is growing after it has separated from the main part because while the main object is going small, then any object related to it should go small too.

After the system has tested the TO in the next five slices, if the system finds that it has gone small, the system will be assigned as a user interesting target. But if the system finds that TO is growing in the next slices, then the system will distinguish it from the ITV and generate a new RTV because the TO is growing, possibly becoming a part of another object.

Using this fact that the objects are starting as small objects and end as small objects. To avoid having the wrong result that will contain some part of other objects that are not related to the user interesting target we designed a stop function to let the system stop extracting the interesting target after it has finished.

The stop function is working by checking the ITV size of each extracting target from a trained slice to find which side of the dataset the user interesting target is growing. If the size of the extracted target has become bigger in the next trained slices, the stop function will keep the system in the extracting process until it detects that the target size has got smaller. Here, the system will first ensure that the target is getting small by finding in the next trained slice if the extracted target is getting small.

When the target has got small after it was big in the previously trained slice, then the stop function will work and repeat checking the size of the extracting target until the target size gets bigger again to stop the system from extracting the user interesting target.

The system will repeat the steps of segmentation for each slice to segment the user's interesting target. At the end of this step, the system will generate the feature mask with only the user's interesting target.

After generating the feature mask, a post-processing step might be desirable to extend or improve the results. Some of the extracted user target slices will mess some voxels between, and while the extract target voxels will have the

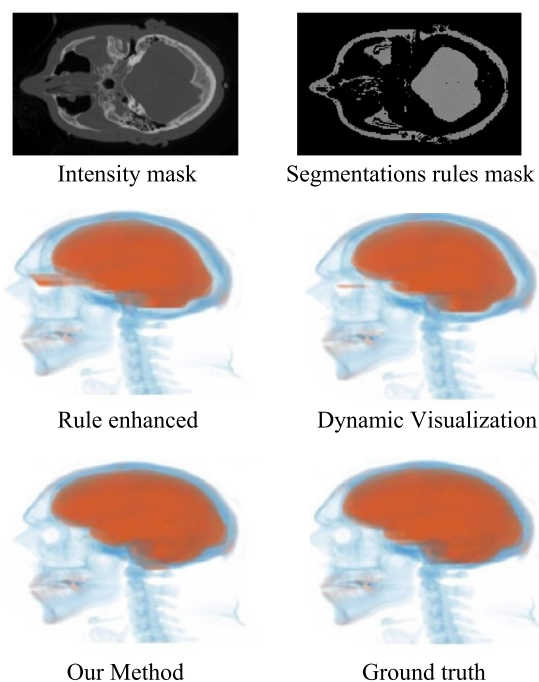


FIGURE 7. Visible Male Head dataset (VisMale). Red denotes the human brain.

same value, they will be visible as one white object. To ensure that all the voxels of the user interesting target are extracted, the system will use as input the original data and will test each voxel in it on the features mask.

The system will start by uploading the same slice from the features mask, and the original data mask then will distinguish the target that in the features mask from the original data slice and will test each voxel rest in it by generating a  $3 \times 3$  neighbourhood table around the trained voxel and check the table on the features mask slice.

If the trained voxel table has more than 3 voxels connected to the target, the system will assign the trained voxel to the feature mask slice.

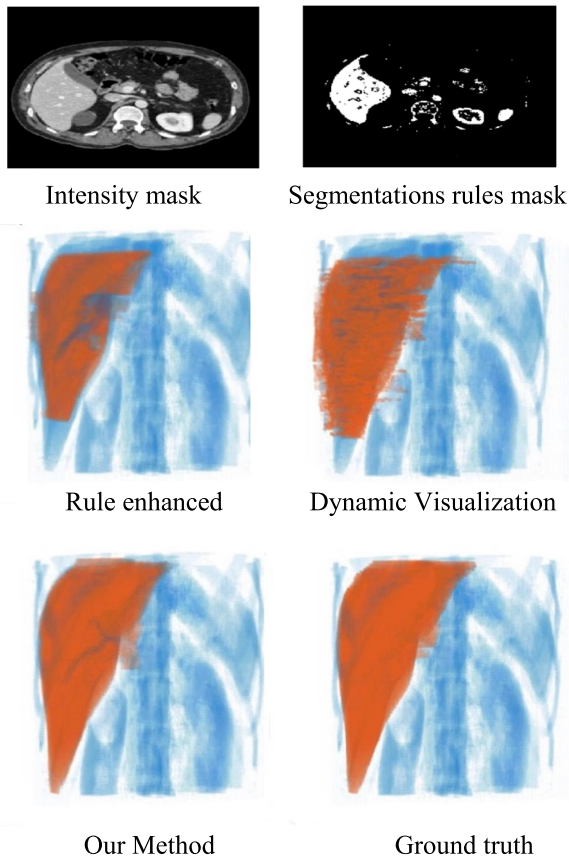
The system will repeat this technique with each slice from the original data and test its rest voxels after distinguishing the target.

The result of this step will present a new volumetric data which contain extracted user object.

#### H. VISUALIZATION

This section will describe our visualization technique that can view the result of the previously proposed method with a meaningful view and highlight the important features of the interesting user target. The system will use the features mask to generate a TF that can enhance the user's interesting target visualization. In TF design, higher opacity is usually assigned to important structures to be visible from other objects.

We modified the default intensity of each voxel ( $v$ ) from the feature volume by finding the maximum intensity value in the original data and add it to each voxel value in the



**FIGURE 8.** Combined (CT-MR) Healthy Abdominal Organ Segmentation (CHAOS) Challenge Dataset. Red denotes the human liver.

feature volume then we combined it with the original data so the interesting target voxels will stand out and be more visible which will enhance the user interesting targets because all its voxels will have a high-opacity value. We also modulated the opacity of each voxel  $v$ , and the modulation is described by:

$$opacity_e(v) = opacity_m(v) \cdot (enhanceVal, opacity_m(v)) \quad (6)$$

where  $opacity_e(v)$  is the enhanced opacity of voxel  $v$ ,  $opacity_m(v)$  is the main opacity of voxel  $v$ , and  $enhanceVal$  is a user-controlled value to decide the extent to which enhanced effect should be applied.

#### IV. IMPLEMENTATION

The system is tested on an ASUS ZX63 laptop with an I7-7700HQ 2.80MHz CPU, with 32GB Memory and an NVidia GTX 1050 graphics card with 4GB video memory. The system is implemented with MATLAB and uses parallel computing for further acceleration. We viewed and explored the volumetric data in MATLAB C using the 3Dimshow function. The 2D connected components function has been used to extract the voxels' location using the local neighbourhood

table. All the volumetric input data has been modified through our system to 8-bits. The run-time performance of the system is fast for user interactions.

#### V. RESULTS

In this section, we demonstrate the effectiveness of our method by applying it to different volumetric datasets and performed both qualitative and quantitative experiments to compare our method results against the results from two state-of-the-art techniques, known as the Rule Enhanced and the Dynamic Visualization.

We highlight one slice from the Segmentation rules mask generated for each dataset to show how it helps segment the interesting features. For each dataset, we generated the Intensity mask, the Segmentations rules mask, the Rule enhance, the Dynamic Visualization, the ground truth and the result of our method.

##### A. VISIBLE MALE HEAD DATASET (VisMale) (128 × 256 × 256, 16-BIT CT)

This dataset consists of the CT scan of a male head [36]. Traditional functions usually fail to detect and segment the brain due to the occlusion of the skull and the similar intensity range of the brain and other soft tissues because the intensity of the brain and other soft tissues is overlapped, and the brain is occluded by the skull. Second, it is manual rather than automatic to obtain these TFs which can clearly show the structure of this dataset, and thus could be time-consuming.

Third, even if it can reveal the hidden brain, it is still impossible to reveal all uncertainties of the brain, as its TF adjustment is performed in an uncontrollable way. This could lead to some important uncertainty visualization results of the brain are missing, and thus may cause medical experts to make inappropriate decisions using the extracting and segmentation techniques, our system has classified the human brain from the skull, and we have archived an accurate result with 0.9803 dice.

##### B. COMBINED (CT-MR) HEALTHY ABDOMINAL ORGAN SEGMENTATION (CHAOS) CHALLENGE DATASET (256 × 256 × 81, 32-BIT)

This dataset is a healthy abdominal liver of the human body [37]. Understanding the medical image is an important key to successful operations. It is difficult to classify the liver from other organs and detect its important features using the traditional transfer function technique. This is because the intensity of the liver and the other organs are partially overlapped and it is manual rather than automatic to obtain these TFs which can clearly show the structure of this dataset, the lack of contrast at the borders between the organs makes them hard to understand. This problem has been solved using our extracting and segmentation techniques that could detect more accurate result and classify the liver from the other organs with 0.9443 dice.



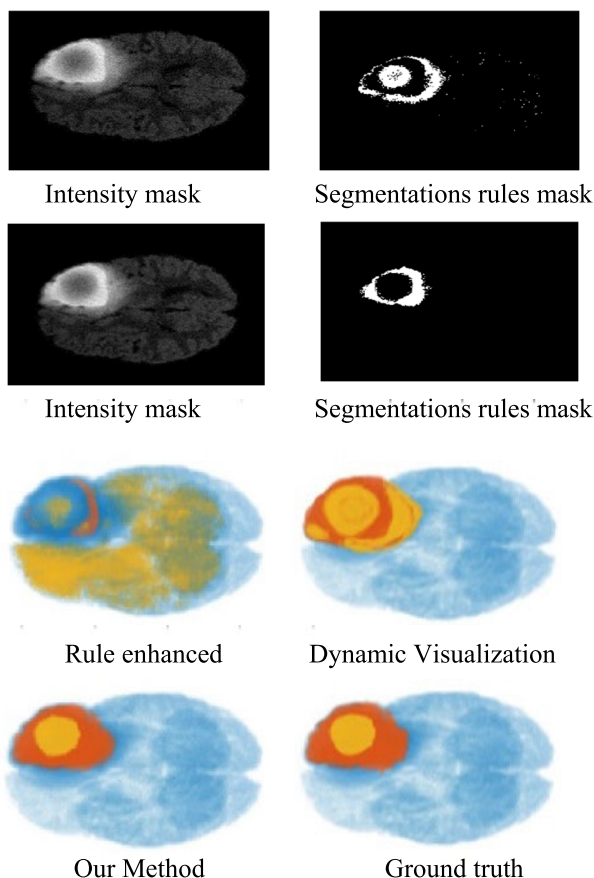


FIGURE 9. Brain Tumor Segmentation (BraTS) Challenge dataset. Orange denotes the edema, and Yellow denotes the tumor.

**C. BRAIN TUMOR SEGMENTATION (BraTS) CHALLENGE DATASET (256 × 256 × 181, 16-BIT)**

This dataset is an MRI brain glioma tumor and edema [38]. Brain tumors grow in different shapes and textures, manual predictions require anatomical knowledge, and it is time-consuming. While the Tumor and Edema has similar intensity values and lack of contrast at the borders between them, making them difficult to segment. Because it is difficult to clearly reveal the brain tumor and its uncertainties.

This is because the intensity of the brain tumor and the brain is partially overlapped, and the brain tumor is occluded by the brain. Second, it is manual rather than automatic to obtain these TFs which can clearly show the structure of this dataset and thus could be time-consuming.

Third, it is never possible to reveal all uncertainties of the brain tumor, as its TF adjustment is performed in an uncontrollable manner. This could lead to some important uncertainty visualization results of the brain tumor are missing, and thus may cause medical experts to make inappropriate decisions.

Using the proposed techniques we have segmented the edema and the tumor from the other organs with 0.89 dice for edema and 0.92 for the tumor.

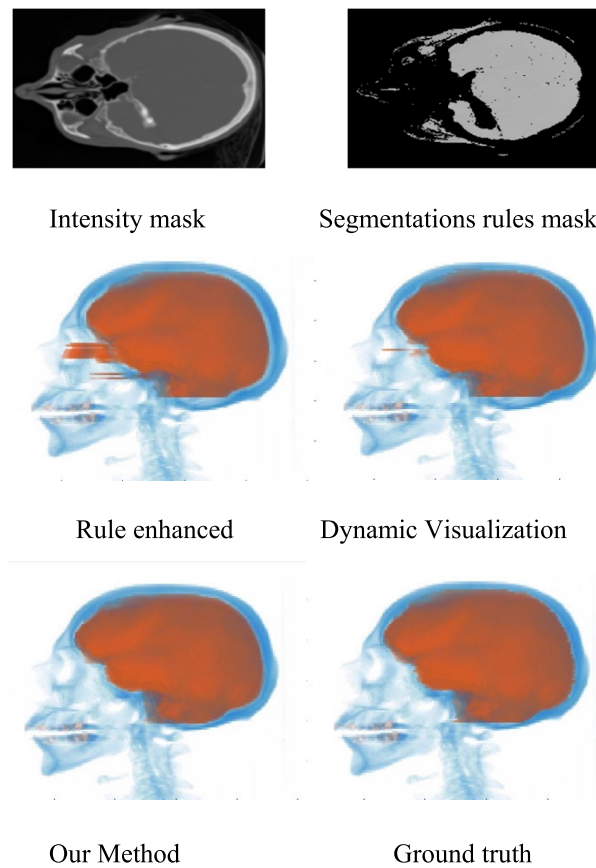


FIGURE 10. CT male head dataset (CT-HEAD). Red denotes the human brain.

CT Head dataset (256 × 256 × 113, 16 bit CT): This dataset consists of the CT scan of a male head [36]. Traditional transfer functions usually fail to separate and segment the brain while the brain is connected to some other tissues like the eyes or the skull at some slices also because the brain has different shapes and gets separated into few parts when it goes small.

As the intensity of the brain and other soft tissues is overlapped, and the brain is occluded by the skull which makes it impossible for the Traditional transfer functions technique to classify the brain and reveal it and its important features that are hidden in this dataset.

Using our extracting and segmentation techniques, our system could detect the human brain from the tissues that are connected to it and generate the closest results to the ground truth with 0.9755 dice.

**VI. DISCUSSION**

In the medical data, correct results and time are required for better diagnoses. In now time, there are large datasets that are time-consuming to get the results from it. The similarity value issue between the objects makes it difficult to detect and extract an accurate result.



Some important features of the interesting target will be missing, or the result of the interesting target will contain some parts that are not related to it.

The k-means clustering algorithm has shown a good effort in image segmentation, but it has a disadvantage with some results it gives. The K-means algorithm uses as input random centroid center value, which makes the algorithm, give different results in each test, which makes it unreliable to use in the medical data.

Using our technique of modifying the K-means algorithm’s input, we have allowed the algorithm to output the same wanted result in each test.

Using our segmentation methods, we have addressed the similarity value issue between the object and could finally detect more accurate results for the user’s interesting target. Also, we have designed our system using parallel computing to speed up the segmentation process and segment multiple targets in a short time.

Johnson and Huang’s work [39] shows that using the local distribution as the basis for feature identification not only produces results that agree with enhanced traditional feature detection methods but also reveal new features that were previously inaccessible to be visualized or not easily specified by the user.

Some datasets using the local distribution showed not accrued target and a slow process while some objects not fully visible because it has a similar value to other objects and other issues that require many methods to segment the user interesting targets.

We have compared our method results, the Rule Enhanced and the Dynamic Visualization result (Table 1) with the ground truth and supervised segmentation results by using the Dice coefficient, which is a standard similarity index in the range of 0 to 1 to measure the volumetric overlap of two binary segmentation masks, the sensitivity and specificity coefficient.

$$\text{Dice equation} = \frac{2 \times |A \cap B|}{2 \times |A \cap B| + |B \setminus A| + |A \setminus B|} \quad (7)$$

where (A) is the Ground truth mask and (B) is the generated result.

$$\text{Specificity equation} = \frac{TN}{TN + FN} \quad (8)$$

$$\text{Sensitivity equation} = \frac{TP}{TP + FN} \quad (9)$$

where (TN) is true negative, (FN) is false positive and (TP) is true positive.

The system automatically learned from a single point on the user interesting object in the selected slice to extract the features and feed the information to the rules and algorithm to get the result. It provides a more intuitive manner to present and highlight the important structures of the user’s interesting target.

**TABLE 1. Segmentation results and computing times comparison among our proposed method, the Dynamic Visualization and the Rule Enhanced.**

Data set	target	Segmentation Technique	Dice	sensitivity	Specificity	Comparison time (seconds)
VisMale	Brain	Our method	<b>0.9803</b>	<b>0.9849</b>	<b>0.9995</b>	<b>64.6</b>
		Dynamic Visualization	0.9206	0.8594	0.9992	1219.8
		Rule Enhanced	0.8661	0.7775	0.9981	17.4
CHAOS	Liver	Our method	<b>0.9443</b>	<b>0.9937</b>	<b>0.9997</b>	<b>35.5</b>
		Dynamic Visualization	0.7245	0.8192	0.9917	2313.7
		Rule Enhanced	0.7263	0.9940	0.9998	70.1
BraTS	Tumor	Our method	<b>0.9219</b>	<b>0.9692</b>	<b>0.9999</b>	<b>45.2</b>
		Dynamic Visualization	0.4744	0.3540	0.9976	679.9
		Rule Enhanced	0.0304	0.0157	0.9365	59.1
	Edema	Our method	<b>0.8937</b>	<b>0.8876</b>	<b>0.9988</b>	<b>41.2</b>
		Dynamic Visualization	0.7887	0.8057	0.9980	687.4
		Rule Enhanced	0.3697	0.5670	0.9978	58.8
CT head	Brain	Our method	<b>0.9755</b>	<b>0.9949</b>	<b>0.9995</b>	<b>79.7</b>
		Dynamic Visualization	0.9452	0.9090	0.9985	752.1
		Rule Enhanced	0.7731	0.6851	0.9911	21.5

**TABLE 2. The program’s total run time (in seconds) and visualization performance (in Frames per Second).**

Dataset	Target tissue	Data size	Rule Enhanced (Fps)	Dynamic Visualization	Our method (Fps)
VisMale	Brain	128 X 256 X 256	8.6	6.3	<b>9.2</b>
CHAOS	liver	256 X 256 X 81	8.5	8.7	<b>8.9</b>
BraTS	Edema	230 X 230 X 181	8.3	8.5	<b>8.9</b>
	Tumor		8.7	8.9	<b>8.6</b>
CT head	Brain	256 X 256 X 113	8.6	9.4	<b>9.1</b>

**VII. CONCLUSION AND FUTURE WORK**

Generating meaningful 3D visualizations from acquired medical image data is a challenging problem. We have presented a contribution to that field by introducing the segmentation techniques. In this paper, we proposed a Simi auto technique that allows the users to extract and view more than one target with accurate results and in a short time. We have designed a target segmentation technique based on the K-means clustering algorithm that could classify the user’s interesting targets with targets with similar value to it in the volume.

We also designed the segmentation rules that work to improve the result of the target segmentation technique and classify the interesting target from the other targets that have a similar value to it. We also designed the extracting and segmentation technique that represents a few steps of segmentation to detect and segment the important structures of the user's interesting target and classify it from the targets that do not have a boundary with them in some slice. We proposed a visualization technique to enhance the feature mask in the original data and give the user a meaningful 3D view of their interesting targets with high accuracy results.

The effectiveness of our method has been demonstrated on a large variety of volumetric datasets. The fast generation of the results with good accuracy makes it also be usable for clinicians. In future work, we are plan to use artificial intelligence methods that will speed up the extraction features steps and will be able to train and work with other datasets which have the similar user interesting target features and find more features that can be used to detect the user object in the volumetric data, which will help to extract more accurate features and reduce the time of generating the results.

Also, we would like to improve our rules and algorithm to let them have the ability to segment and classify each object in the volumetric data without user input information to have a volumetric data that contains classified objects to allow the users to explore all the volumetric data and enhance any object in it.

## REFERENCES

- [1] F. Fischer, M. A. Selver, W. Hillen, and C. Guzelis, "Integrating segmentation methods from different tools into a visualization program using an object-based plug-in interface," *IEEE Trans. Inf. Technol. Biomed.*, vol. 14, no. 4, pp. 923–934, Jul. 2010.
- [2] C. Bajaj, V. Pascucci, and D. Schikore, "The contour spectrum," in *Proc. Vis.*, 1997, pp. 167–173.
- [3] G. Kindlmann and J. W. Durkin, "Semi-automatic generation of transfer functions for direct volume rendering," in *Proc. IEEE Symp. Volume Vis.*, Oct. 1998, pp. 79–86.
- [4] C. Y. Ip, A. Varshney, and J. Jaja, "Hierarchical exploration of volumes using multilevel segmentation of the intensity-gradient histograms," *IEEE Trans. Vis. Comput. Graphics*, vol. 18, no. 12, pp. 2355–2363, Dec. 2012.
- [5] L. Cai, W.-L. Tay, B. P. Nguyen, C.-K. Chui, and S.-H. Ong, "Automatic transfer function design for medical visualization using visibility distributions and projective color mapping," *Comput. Med. Imag. Graph.*, vol. 37, nos. 7–8, pp. 450–458, Oct. 2013.
- [6] M. Levoy, "Display of surfaces from volume data," *IEEE Comput. Graphics Appl.*, vol. 8, no. 3, pp. 29–37, May 1988.
- [7] S. Bruckner and M. E. Groller, "Volumeshop: An interactive system for direct volume illustration," in *Proc. IEEE Vis.*, Minneapolis, MN, USA, Oct. 2005, pp. 671–678.
- [8] R. Huang and K.-L. Ma, "RGVis: Region growing based techniques for volume visualization," in *Proc. Pacific Conf. Comput. Graph. Appl.*, Oct. 2003, pp. 355–363.
- [9] D. Xiang, J. Tian, F. Yang, Q. Yang, X. Zhang, Q. Li, and X. Liu, "Skeleton cuts—An efficient segmentation method for volume rendering," *IEEE Trans. Vis. Comput. Graphics*, vol. 17, no. 9, pp. 1295–1306, Sep. 2011.
- [10] A. Sherbondy, M. Houston, and S. Napel, "Fast volume segmentation with simultaneous visualization using programmable graphics hardware," in *Proc. IEEE Vis.*, Oct. 2003, pp. 171–176.
- [11] R. Burget, V. Uher, and J. Masek, "Biology inspired image segmentation using methods of artificial intelligence," *J. Softw. Eng. Appl.*, vol. 05, no. 12, pp. 172–174, 2012.
- [12] M. Y. Bhanumurthy and K. Anne, "An automated detection and segmentation of tumor in brain MRI using artificial intelligence," in *Proc. IEEE Int. Conf. Comput. Intell. Comput. Res.*, Dec. 2014, pp. 1–6.
- [13] O. C. Neethu and K. Shruti, "A reliable method for brain tumor detection using CNN technique," *IOSR J. Elect. Electron. Eng.*, vol. 1, pp. 64–68, Oct. 2016.
- [14] D. Yang, S. Zhang, Z. Yan, C. Tan, K. Li, and D. Metaxas, "Automated anatomical landmark detection on distal femur surface using convolutional neural network," in *Proc. IEEE 12th Int. Symp. Biomed. Imag. (ISBI)*, Apr. 2015, pp. 17–21.
- [15] P. Sereida, A. V. Bartroli, I. W. O. Serlie, and F. A. Gerritsen, "Visualization of boundaries in volumetric data sets using LH histograms," *IEEE Trans. Vis. Comput. Graphics*, vol. 12, no. 2, pp. 208–218, Mar. 2006.
- [16] S. Pereira, A. Pinto, V. Alves, and C. A. Silva, "Brain tumor segmentation using convolutional neural networks in MRI images," *IEEE Trans. Med. Imag.*, vol. 35, no. 5, pp. 1240–1251, May 2016.
- [17] X. Zhao and A. Kaufman, "Multi-dimensional reduction and transfer function design using parallel coordinates," in *Proc. 8th Int. Conf. Graph. Norrköping, Sweden: Eurographics Association*, 2010, pp. 69–76.
- [18] F. D. M. Pinto and C. M. Freitas, "Design of multidimensional transfer functions using dimensional reduction," in *Proc. 9th Joint Eurograph./IEEE VGTC Conf. Vis. Norrköping, Sweden: Eurographics Association*, pp. 131–138.
- [19] P. Purohit and R. Joshi, "A new efficient approach towards K-means clustering algorithm," *Int. J. Comput. Appl.*, vol. 65, no. 11, pp. 7–10, Mar. 2013.
- [20] A. Jose, S. Ravi, and M. Sambath, "Brain tumor segmentation using K-means clustering and fuzzy C-means algorithms and its area calculation," in *Int. J. Innov. Res. Comput. Commun. Eng.*, vol. 2, no. 2, Mar. 2014.
- [21] J. Kniss and G. Wang, "Supervised manifold distance segmentation," *IEEE Trans. Vis. Comput. Graphics*, vol. 17, no. 11, pp. 1637–1649, Nov. 2011.
- [22] L. Wang, X. Zhao, and A. E. Kaufman, "Modified dendrogram of attribute space for multidimensional transfer function design," *IEEE Trans. Vis. Comput. Graphics*, vol. 18, no. 1, pp. 121–131, Jan. 2012.
- [23] J. J. Caban and P. Rheingans, "Texture-based transfer functions for direct volume rendering," *IEEE Trans. Vis. Comput. Graphics*, vol. 14, no. 6, pp. 1364–1371, Nov. 2008.
- [24] F.-Y. Tzeng and K.-L. Ma, "A cluster-space visual interface for arbitrary dimensional classification of volume data," *Proc. IEEE/Eurograph. Symp. Vis.*, Jun. 2004, pp. 17–24.
- [25] L. Linsen, T. Van Long, P. Rosenthal, and S. Rosswog, "Surface extraction from multi-field particle volume data using multi-dimensional cluster visualization," *IEEE Trans. Vis. Comput. Graphics*, vol. 14, no. 6, pp. 1483–1490, Nov. 2008.
- [26] M. Yedla, S. R. Pathakota, and T. M. Srinivasa, "Enhanced K-means clustering algorithm with improved initial center," *Int. J. Sci. Inf. Technol.*, vol. 1, no. 2, pp. 121–125, 2010.
- [27] M. A. Selver, "Exploring brushlet based 3D textures in transfer function specification for direct volume rendering of abdominal organs," *IEEE Trans. Vis. Comput. Graphics*, vol. 21, no. 2, pp. 174–187, Feb. 2015.
- [28] K. A. A. Nazeer and M. P. Sebastian, "Improving the accuracy and efficiency of the K-means clustering algorithm," in *Proc. World Congr. Eng.*, vol. 1, London, U.K.: WCE, Jul. 2001, pp. 1–3.
- [29] J. G. Klinker, A. S. Shafer, and T. Kanade, "A physical approach to colour image understanding," *Int. J. Comput. Vis.*, vol. 4, no. 1, p. 738, 1990.
- [30] C. Lundström, P. Ljung, A. Persson, and A. Ynnerman, "Uncertainty visualization in medical volume rendering using probabilistic animation," *IEEE Trans. Vis. Comput. Graphics*, vol. 13, no. 6, pp. 1648–1655, Nov. 2007.
- [31] H. Guo, H. Xiao, and X. Yuan, "Multi-dimensional transfer function design based on flexible dimension projection embedded in parallel coordinates," in *Proc. IEEE Pacific Vis. Symp.*, Mar. 2011, pp. 19–26.
- [32] P.-H. Conze, A. E. Kavur, E. C.-L. Gall, N. S. Gezer, Y. L. Meur, M. A. Selver, and F. Rousseau, "Abdominal multi-organ segmentation with cascaded convolutional and adversarial deep networks," 2020, *arXiv:2001.09521*. [Online]. Available: <http://arxiv.org/abs/2001.09521>
- [33] R. G. Raidou, O. Casares-Magaz, L. P. Muren, U. A. van der Heide, J. Rørvik, M. Breeuwer, and A. Vilanova, "Visual analysis of tumor control models for prediction of radiotherapy response," *Comput. Graph. Forum*, vol. 35, no. 3, pp. 231–240, Jun. 2016.
- [34] L.-L. Cai, B. P. Nguyen, C.-K. Chui, and S.-H. Ong, "Rule-enhanced transfer function generation for medical volume visualization," *Comput. Graph. Forum*, vol. 34, no. 3, pp. 121–130, Jun. 2015.

- [35] J. Ma, J. Chen, L. Chen, L. Jin, and X. Qin, "Dynamic visualization of uncertainties in medical feature of interest," *IEEE Access*, vol. 8, pp. 119170–119183, 2020.
- [36] *The Volume Library*. Accessed: Jun. 28, 2020. [Online]. Available: <http://schorsch.efi.fh-nuernberg.de/data/volume/>
- [37] A. E. Kavur, M. A. Selver, O. Dicle, M. Bari, and N. S. Gezer, "CHAOS challenge-combined (CT-MR) healthy abdominal organ segmentation," *Med. Image Anal.*, vol. 69, Apr. 2021, Art. no. 101950.
- [38] B. H. Menze, A. Jakab, S. Bauer, J. Kalpathy-Cramer, K. Farahani, J. Kirby, and Y. Burren, "The multimodal brain tumor image segmentation benchmark (BRATS)," *IEEE Trans. Med. Imag.*, vol. 34, no. 10, pp. 1993–2024, Oct. 2015.
- [39] C. R. Johnson and J. Huang, "Distribution-driven visualization of volume data," *IEEE Trans. Vis. Comput. Graphics*, vol. 15, no. 5, pp. 734–746, Sep. 2009.



**JI MA** received the master's and Ph.D. degrees from University College Cork (UCC), Ireland. He is currently a Lecturer with the School of Computer Science and Technology, Zhejiang University of Technology. His research interest includes data visualization.



**YAZAN AHMAD MUAD** received the bachelor's degree from the Department of Computer Science and Technology, Zhejiang University of Technology, Hangzhou, China, where he is currently pursuing the degree with the College of Computer and Software. His research interests include image processing and data visualization.



**JINJIN CHEN** received the bachelor's and master's degrees from Jiangnan University. She is currently a Lecturer with the School of Design and Art, Communication University of Zhejiang. Her major research interests include virtual reality and interactive design.

...