

# Lung Tumor Segmentation and Classification in 3D CT Images

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**ABSTRACT** This report presents a methodology for the segmentation and classification of lung tumors. The proposed approach integrates segmentation of the 3D computed tomography (CT) scans and K-Means clustering to accurately delineate tumor regions within the lung volume. Initially, the CT data are segmented using thresholding and morphological operations to remove background and noise in order to isolate the lung region. Subsequently, K-Means clustering is employed to segment tumor regions within the lung volume. In both procedures, neighborhood and connectivity properties are used, for the segmentation of the right and left lung, and to isolate the tumor from the airways. Following segmentation, a classification scheme based on tumor diameter is implemented to determine the stage of the tumor. The stage detection is crucial in medical context because it may lead to an increase in patient's survival rates. This system is implemented in MATLAB.

**KEYWORDS** 3D Segmentation, Computed Tomography, Connectivity, K-Means Clustering, Morphological Operations, Thresholding, Tumor Classification,

## I. INTRODUCTION

Lung cancer presents a significant global health challenge, standing as one of the most serious cancer in the world, with an increase in mortality rates every year. According to a study conducted by the European Cancer Information System (ECIS), in the EU-27 countries in 2020, lung cancer accounted for 20.4% of all cancer. This statistic positions lung cancer as the fourth most common cancer (after prostate cancer, breast and colorectal cancers) and the leading cause of death from cancer. [1]

In recent years, advancements in medical imaging technologies with the integration of machine learning tools were developed to improve patient outcomes in the management of lung cancer.

This report focuses on the segmentation and classification of lung tumors using computed tomography (CT) imaging data. It combines image processing techniques with the K-means clustering algorithm for tumor segmentation and the TNM staging system for classification.

Image processing techniques play a key role in distinguishing lung tissue from the background. Global thresholding, morphological operations such as dilation and erosion, and the pixel connectivity properties are employed to an accurate lung segmentation.

K-means clustering, a fundamental unsupervised learning

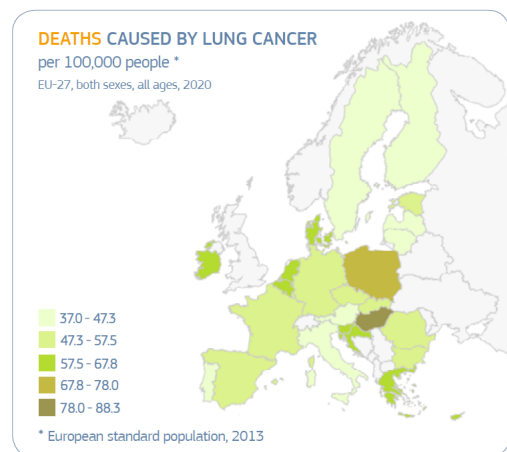


FIGURE 1. Deaths Estimates in 2020 for Lung Cancer

algorithm, iteratively assigns data points to clusters based on their proximity to cluster centroids. In the context of lung tumor segmentation, with the computation of coverage area for each cluster, the image is partitioned into clusters representing tumor and non-tumor regions.

Following segmentation, the TNM staging system enables the classification of tumor based on the extent of the primary tumor (T), regional lymph node involvement (N), and distant metastases (M). In this report, there is a focus on the T

classifier, which evaluates the stage based on the diameter of the nodule.

The structure of this report is organized as follows: Section 2 reviews relevant literature and related work in the field. Section 3 provides a detailed explanation of the methodology employed, including the image processing techniques and K-means clustering algorithm, Fig 2 shows the methodology flowchart used. Finally, Section 4 presents and discusses the results obtained from the application of this methodology.

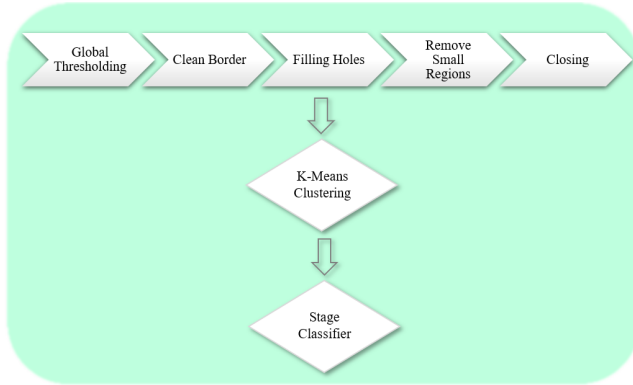


FIGURE 2. Methodology Flowchart

## II. RELATED WORK

In recent years, researchers have proposed different methods aimed at enhancing the accuracy and efficiency of tumor segmentation. This section provides an overview of the related work in this field, highlighting their strengths and limitations. One commonly employed technique is region-based segmentation, which includes algorithms like region growing and active contours. While these methods provide a good accuracy, they tend to be computationally expensive.

Machine learning techniques, such as support vector machines (SVMs), have also been applied to lung tumor segmentation. For instance, in [2], researchers combined lung segmentation using standard image processing techniques and feature extraction, with the tumor classification using SVM and backpropagation networks. However, these classifiers are limited to binary classification as cancerous or non-cancerous.

The rise of deep learning has introduced many new techniques for lung tumor analysis, focusing on convolutional neural networks (CNNs). In [3], an improved hybrid neural network integrating two architectures demonstrated enhanced classification performance, achieving a precision of 0.93. Despite their effectiveness, deep learning models require sufficient training data.

In contrast to supervised learning approaches, Sarker [4] proposed a method using the K-Means Algorithm for 3D CT image segmentation. Researchers in [5] suggest that K-means is better than other techniques like Fuzzy C Means, making it the choice for lung tumor segmentation in this report.

## III. MATERIALS AND METHODS

### A. DATASET

The dataset was obtained from the Medical Segmentation Decathlon (MSD), sourced from The Cancer Imaging Archive (TCIA). It contains 96 3D volumes, 64 of these are designated for training purposes, each of them related to the corresponding ground truth.

Each CT scan volume has dimensions of  $512 \times 512 \times X$ , where  $X$  represents the variability in voxel size of each CT scan. To optimize memory usage, the volumes were resized to  $256 \times 256 \times X$ . To enable lung segmentation, each 3D scan was processed by splitting it into 2D images. Figure 3 and 4 illustrates various 2D slices extracted from the 3D CT scans.

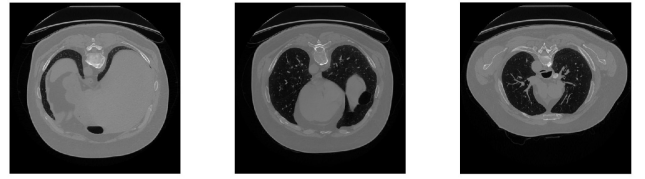


FIGURE 3. CT Image Training 006



FIGURE 4. CT Image Training 014

### B. THRESHOLDING

Global Thresholding is used for the segmentation of lung from background. It is based on the assumption that the image has a bimodal histogram, in particular the object and background pixels have gray levels grouped into two dominant modes [6]. In this way, the object can be extracted from the background by a simple operation that compares image values with a threshold value  $T$ . The threshold can be automatically computed from the gray level histogram of an image, to be specific, the threshold is chosen to minimize the intraclass variance of the thresholded black and white pixels. Then the global threshold  $T$  can be used to convert a grayscale image to a binary image. The resulted image  $g(x, y)$  is defined:

$$g(x, y) = \begin{cases} 1 & \text{if } (x, y) > T \\ 0 & \text{if } (x, y) \leq T \end{cases}$$

### C. MORPHOLOGICAL OPERATIONS

Morphology is a set of image processing operations that process images based on shapes. In a morphological operation, each pixel in the image is adjusted based on the value of other pixels in its neighborhood [7].

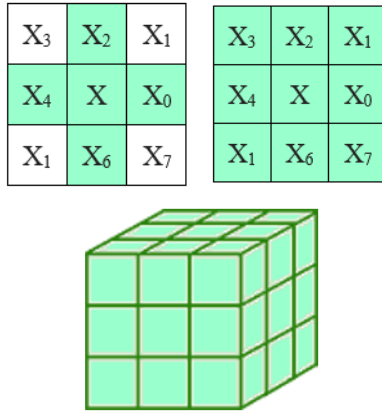


FIGURE 5. 4-Connectivity, 8-Connectivity, 26-Connectivity

### 1) PIXEL CONNECTIVITY

In order to identify objects in a binary image, there is a need to locate groups of pixels that are connected to each other. These objects are defined as the connected components. Pixel connectivity defines how one pixel  $X$  is connected to other pixels.

In particular, in two dimension, there are 2 types of connectivity: 4-connectivity and 8-connectivity.

A pixel is 4-connected if it touches the edges of the other pixels, in other words if  $X$  is logical 1 and  $X_0, X_2, X_4, X_6$  are logical 1, as shows Fig. 5.

A pixel is 8-connected if it touches the edges or corners of the other pixels, so if  $X$  is logical 1 and  $X_0, X_1, X_2, X_3, X_4, X_5, X_6, X_7$  are logical 1, as shown in Fig. 5.

In three dimension case, there are three type of connectivity: 6, 18, 26-connectivity. By default MATLAB uses a 26-connectivity in which pixels are connected if their faces, edges, or corners touch.

This property is used to label the connected regions in the image. Specifically, the 2D pixel connectivity is used for the segmentation of the left and right lung, in order to remove the background, while the 3D pixel connectivity is used after the clustering to calculate volume, diameter and centroid of each nodule.

### 2) DILATION AND EROSION

Dilation and erosion are the most basic morphological operations. They are used for the segmentation of lung from background and to remove airways after the k-means clustering. Dilation adds pixels to the boundaries of objects in an image, while erosion removes pixels on object boundaries. The number of pixels added or removed from the objects in an image depends on the size and shape of the structuring element used to process the image. In particular, erosion removes the regions with 1s, defined by the structuring element, while dilation removes regions with 0s.

Referring to binary image, in dilation a pixel is set to 1 if any of the neighboring pixels have the value 1. This make objects

more visible and fills in small holes in objects. In erosion, a pixel is set to 0 if any of the neighboring pixels have the value 0. This allows to remove floating pixels and thin lines so that only substantive objects remain. Dilation and erosion are respectively defined as:

$$D(j, k) = B(j, k) \oplus S(j, k)$$

$$D(j, k) = B(j, k) \odot S(j, k)$$

X-OR operation between the binary image and the structuring element for dilation, and for erosion X-NOR operation.

### 3) OPENING AND CLOSING

Closing is the operation of dilation followed by erosion, using the same structuring element for both operations. It is used for the segmentation of lung from background since it allows to close small gaps and smooth the boundaries of objects. Closing removes small-connected regions with logical 0 (background) defined by the structuring element.

Opening is the operation of erosion followed by dilation. It is used to remove airways from the segmented image, indeed it removes small objects while preserving the larger structures. Opening removes the small connected regions with logical 1 (foreground), defined by the structuring element.

### D. K-MEANS CLUSTERING

K-means clustering is a unsupervised machine learning algorithm used for partitioning a dataset into a fixed number of clusters. The goal is to group similar data points together, indeed, in this case it is used to extract the datapoints belonging to the tumor region. In detail:

- 1) **Initialization** : Choose the number of clusters  $k$  and randomly initialize  $k$  centroids
- 2) **Assignment** : Assign each data point to the nearest centroid. This can be done using different metrics, the most common is the Euclidean distance between each point and each centroid.
- 3) **Update** : After all data points have been assigned to clusters, recompute centroids as the mean of all data points assigned to each cluster.
- 4) **Repeat** : Repeat steps 2 and 3 until convergence, so until the centroids no longer change.

In this case, the number of clusters is set to 3 since the segmented lung contains background, soft tissue and tumors bronchioles. Then the cluster with the least coverage aerea is chosen as tumor feature.

### E. TNM CLASSIFICATION

The TNM Classification is a system for classifying a malignancy. It is based on three elements:

- **T** - Tumor: describe the size of the primary tumor. T0 indicates that no evidence of tumor is present, while T1-T4 are used to identify the size and extension of the tumor progressively.
- **N** - Nodes: describe regional lymph node involvement of the tumor

- **M** - Metastasis: identify the presence of distant metastases of the primary tumor

In this method, only the **T** classifier is used, so based on the diameter of the nodule, the stage of the tumor is obtained. Table 1 shows in detail the staging based on **T**.

**TABLE 1.** T Classification

T Stage	Diameter
T0	Tumor not Present
T1a	$\leq 1\text{cm}$
T1b	$> 1\text{cm and } \leq 2\text{cm}$
T1c	$> 2\text{cm and } \leq 3\text{cm}$
T2a	$> 3\text{cm and } \leq 4\text{cm}$
T2b	$> 4\text{cm and } \leq 5\text{cm}$
T3	$> 5\text{cm and } \leq 7\text{cm}$
T4	$> 7\text{cm}$

#### IV. RESULT ANALYSIS AND DISCUSSION

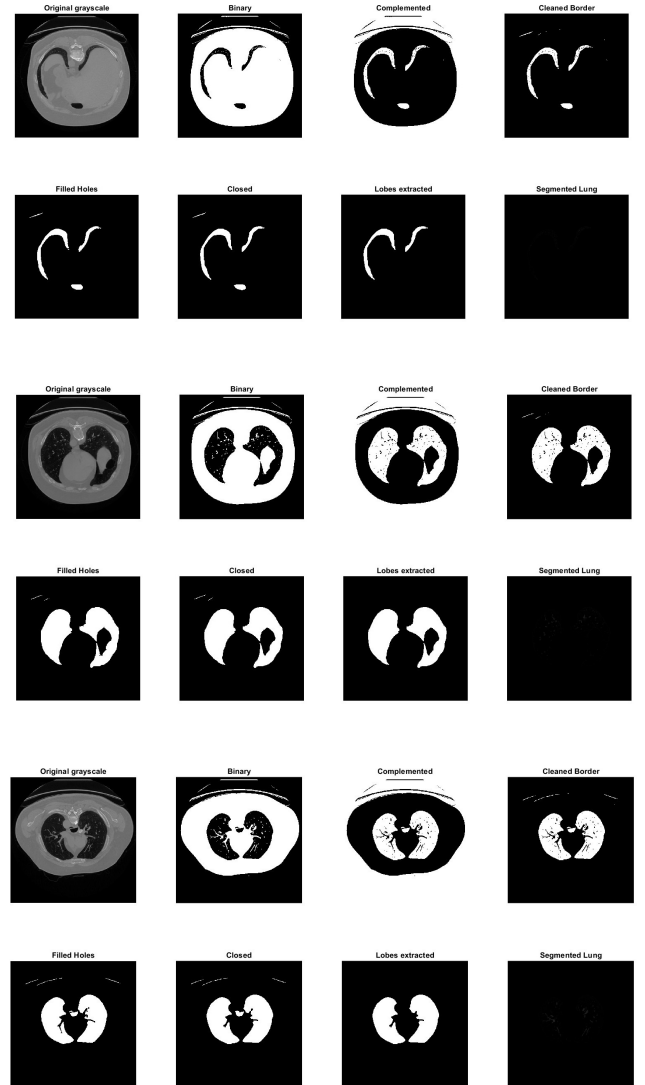
This method of tumor segmentation and classification begins by normalizing the lung CT 3D image. Subsequently, the image is divided into slices and for each slice, the lung is extracted using global thresholding and morphological operations. Then, clustering is applied and the cluster with the lowest probability is identified as the tumor feature. Following this, the volumes and diameters of 3D lung nodules are computed to perform classification. In following subsections, the detailed results of each step are discussed.

##### A. LUNG SEGMENTATION

The goal is to delineate the lung region from the surrounding background. Initially, 2D CT slices are segmented with a global thresholding technique. With MATLAB functions, binary images are obtained using Otsu's method to determine the optimal threshold. Then, the binary images are complemented. To enhance the segmentation quality, pixels connected to the image border are deleted, resulting in border-cleaned images. Employing connectivity properties, connected regions with less than 10 pixels are deleted too. A morphological closing operation, using a disk-shaped structuring element with a radius of 3mm, is then applied. Following this, holes are filled. Lastly, unwanted regions are discarded by extracting the two major lobes through connectivity property. The final mask is obtained and lung segmentation from background is performed. Figure 6 shows the results obtained from the different steps of the segmentation procedure related to three slices of a 3D image.

##### B. TUMOR SEGMENTATION

The 2D slices are reconstructed to form the 3D segmented lung as shown in Fig. 7. Subsequently, K-means clustering is applied with three clusters, representing soft tissue, background regions, and tumor bronchioles within the segmented lung. The coverage area of each cluster is computed, and the cluster covering the least space is selected as the tumor feature, given that soft tissue and background typically



**FIGURE 6.** Lung Segmentation of three slices of 006 CT Image

occupy larger areas. Then, the K-means segmented images are opened using a sphere-shaped structuring element with a radius of 5mm. This step is crucial as it helps eliminate unwanted objects such as airways, which may be included in the chosen cluster. Finally, the 3D lung tumor segmentation is achieved. Some examples of the tumor detected in 3D images of segmented lung are shown in Fig. 8 with the corresponding truth in Fig. 9.

##### C. STAGING CLASSIFICATION

Following the segmentation of lung tumors, volumes, diameters, and centers of the nodules are computed. Initially, the meta-data information of the image is analyzed to extract the pixel dimensions necessary for calculating the volume of each voxel. For instance, in a given image, the pixel dimen-



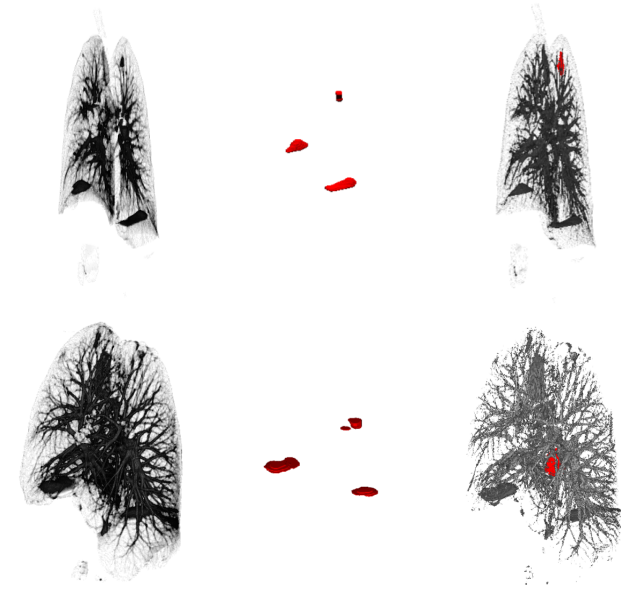


FIGURE 7. 3D Lung Segmentation

FIGURE 8. Tumor Segmentation

FIGURE 9. Labeled Image

sions are represented as [0.7 0.7 1]. Using the connectivity property, connected regions are identified, and the volume of each tumor is determined by multiplying the volume in voxel with the volume of a single voxel. Subsequently, diameters are computed along both the XY and YZ planes, and the maximum diameter is selected as the nodule's diameter. Then, centroids are computed with the connectivity property, and their coordinates are displayed as (rows, columns, slice number). These information about the volume and diameter are crucial to determine the stage of the tumor and centers are useful to determine the position of the tumor in the lung. In Table 2 are shown volumes, diameters and centers of detected tumors in some images. After obtaining the information about the diameter, the stage is computed with respect to T Classifier.

CT Image	Nodules Number	Volume (mm <sup>3</sup> )	Diameter (cm)	Center	Tumor Stage
006	3	3195	4.44	(120,175,212)	T2b
		3671	3.38	(130, 76, 253)	T2a
		856	1.61	(112, 155, 359)	T1b
014	4	2561	3.33	(127,60,188)	T2a
		520	1.19	(109, 162, 333)	T1b
		1236	1.67	(86, 64, 350)	T1b
		4739	2.69	(87, 63, 376)	T1c

TABLE 2. Tumor size calculation and classification

Finally, Table 3 shows the performance of this method by computing two metrics, the Accuracy and the Dice Similarity Coefficient in a restricted dataset of 10 3D CT images. Accuracy is the most common metric in classification tasks, which measures the proportion of correctly classified instances among the total number of instances. It is computed

as:

$$\text{Accuracy} = \frac{TP + TN}{TP + FP + TN + FN}$$

where

- True Positives (TP) is the number of correctly predicted positive instances
- False Positives (FP) is the number of instances that were predicted as positive but are actually negative
- True Negatives (TN) is the number of correctly predicted negative instances
- False Negatives (FN) is the number of instances that were predicted as negative but are actually positive.

The Sørensen–Dice coefficient is commonly used in image segmentation tasks. In general it is a measure of the similarity between two sets of data, in the specific case of image segmentation, it can be used to evaluate the similarity between the predicted and ground truth segmentation masks. The Dice Score ranges from 0 to 1, where a score of 1 means that the segmentations in the two images are a perfect match. Given two sets  $A$  and  $B$ , the formula for calculating the Dice Coefficient is:

$$\text{Dice Score} = \frac{2 \times \text{Intersection}(A,B)}{\text{Area of Set A} + \text{Area of Set B}}$$

where

- 'Intersection' refers to the number of common elements between the predicted segmentation (Set A) and the ground truth segmentation (Set B)
- 'Area of Set A' represents the total number of elements in the predicted segmentation.
- 'Area of Set B' represents the total number of elements in the ground truth segmentation.

Metric	Result
Accuracy	0.99
Dice Score	0.12

TABLE 3. Performance Analysis

Lastly, Fig 10 and Fig 11 represent the graphs of the accuracy and Dice scores respectively for 10 images.

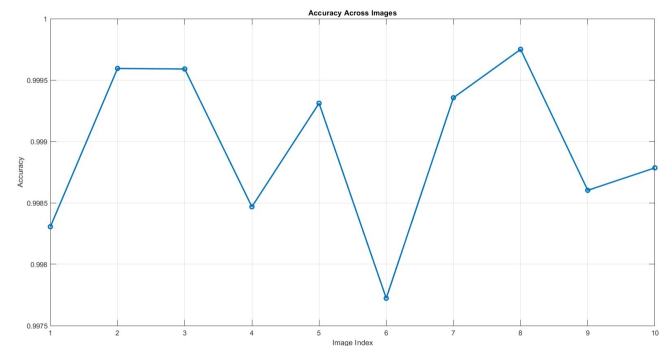


FIGURE 10. Accuracy Score

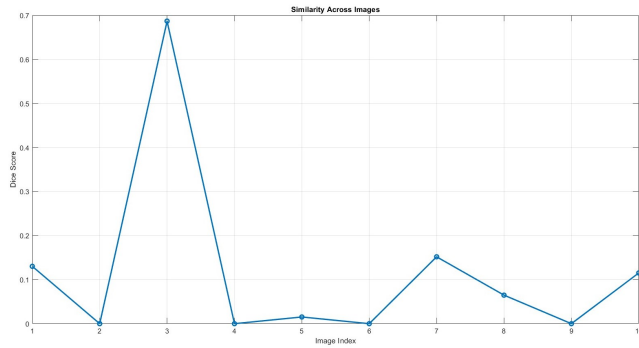


FIGURE 11. Similarity Score

## V. CONCLUSIONS

The results obtained clearly demonstrate that this method fails to achieve satisfactory outcomes, as evidenced by the Dice score close to zero. The problem may come from the lung segmentation process, where non-relevant areas are erroneously extracted and subsequently misidentified as nodules. A possible solution may be represented by the use of an alternative thresholding method, instead of the global one adopted in this method which does not offer satisfactory results. Adjusting the threshold value individually for each image could effectively solve this issue by eliminating non-relevant areas and consequently enhancing the accuracy of segmentation. Regarding the choice of K-means, it represents a good strategy for detecting all tumor-related points.

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