3D Medical Imaging by using Point Cloud Generation

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Abstract—Three-dimensional (3D) reconstruction of anatomical structures from medical images represents a significant advancement in the healthcare field—a topic already explored in various studies. Traditional methods often rely on contrastenhanced computed tomography (CT), which is contraindicated for certain patients. To address this limitation, this work proposes a new methodology for 3D lung modeling. The method consists in generating a unified point cloud from segmented CT slices, followed by the construction of a polygonal mesh using Poisson surface reconstruction. To enhance result visualization, a graphical user interface was developed to simultaneously display the reconstructed 3D model and the original DICOM slices. The results of this new approach confirm the feasibility of the project, establishing an alternative method for the 3D representation of lungs.

Index Terms—3D Representation, Computed Tomography, Point Clouds, Polygonal Mesh.

I. Introduction

The three-dimensional (3D) reconstruction of anatomical structures from medical images represents a significant advancement in the field of healthcare. It is fundamental for tumor and nodule detection, as well as for improving anatomical understanding during complex surgical procedures [1]. Following Wilhelm Conrad Roentgen's discovery of X-rays in 1895, researchers have continuously developed non-invasive methods for examining the human body.

In this context, computed tomography (CT), introduced in 1972 by Cormack and Hounsfield, has been largely responsible for the these methods. Unlike ultrasound images, CT scans can be stored and analyzed by multiple specialists, making them particularly valuable for clinical diagnosis [2].

Despite its benefits, the two-dimensional and monochromatic nature of conventional CT images limits their interpretability. Initial efforts to generate 3D renderings of tomographic data began in the 1970s, but technological constraints delayed progress. With recent advances in computing power, 3D reconstruction techniques have evolved significantly. Nevertheless, accurately isolating individual anatomical structures remains a challenging task.

To address this issue, this work proposes a novel method for 3D reconstruction from CT scans. The proposed approach generates a unified point cloud from all segmented tomographic slices. This cloud is then converted into a polygonal mesh,

in which its points serve as the vertices of a graph used to model the surface of anatomical structures. The resulting model enables precise visualization and facilitates in-depth analysis by medical professionals.

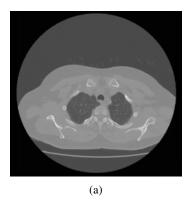
This paper is organized as follows: Section II reviews existing 3D reconstruction methods for medical imaging. Section III details the proposed methodology, including point cloud generation and mesh construction. Section IV presents the reconstruction outcomes. Finally, Section V concludes the study and outlines directions for future research.

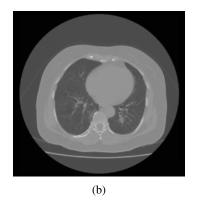
II. RELATED WORK

Three-dimensional visualization of medical images is an indispensable tool in modern medicine, especially in thoracic surgeries. Computed Tomography (CT) stands out as the primary modality for data acquisition, enabling detailed internal visualization of the human body and the 3D reconstruction of complex anatomical structures [3].

CT's ability to generate suitable data for 3D reconstruction has been widely leveraged in various clinical applications. For example, multislice computed tomography angiography (CTCA) with 3D reconstruction is employed in evaluation of coronary artery anomalies, proving crucial for surgical planning and recognized as the most accurate modality for identifying anomalous vascular courses [4]. Additionally, CT plays a fundamental role in the identification and monitoring of tumor growth, such as cardiac myxomas [5], as well as in the diagnosis and follow-up of aortic dissections. However, 3D reconstruction is typically performed using contrast-enhanced CT scans, which require the administration of injectable or ingested contrast agents - usually iodine-based - to highlight specific anatomical structures. This dependency presents a significant limitation for patients with contrast allergies or impaired renal function, for whom contrast agents are contraindicated [6].

In this context, the method proposed in this work seeks to address the challenge of working with non-contrast-enhanced CT images. The approach involves generating a unified point cloud from all segmented slices, followed by the construction of a polygonal mesh to enhance visualization and facilitate analysis. The importance of generating polygonal meshes from point clouds for creating solid 3D models is supported by





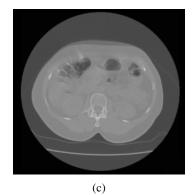


Figure 1: Computed tomography slices of the thorax from the same patient.

other studies. Dinesh [7] describes a technique for constructing triangular meshes from low-resolution point clouds to achieve super-resolution, inserting new points at the centroids of local triangles. Similarly, Wenju et al. [8] proposes a lightweight network based on "graph walking" for 3D point cloud analysis, which extracts long-range features and geometric structure from the point cloud by using graph-based connections to filter and relate neighboring points based on their similarities.

III. 3D MEDICAL IMAGING

The proposed method is structured around the main pillars of the tree, which are detailed in this section: processing and segmentation, polygonal mesh construction of point cloud generation. To illustrate each step of the process, we use a real CT scan as an example; three representative slices are shown in Figure 1.

A. Preprocessing and Segmentation

Computed Tomography (CT) scans, as illustrated in Figure 1, display various shades of gray. In these images, the intensity of the gray tone is directly related to tissue density: the lighter the shade, the denser the represented tissue. In a chest CT scan, such as the one shown in the figure, the brighter areas correspond to the spinal column and muscles, while the darker region, surrounded by the lighter structure, represents the lungs — the region of interest in this project.

The similarity between shades of gray can hinder segmentation, as the contrast between different structures is not always clear, as can be observed in Figures 2(a) and 2(b). To mitigate this issue, contrast enhancement is applied as a preprocessing step to increase the visibility of specific structures. Implemented using the ImageEnhance.Contrast function from the PIL (Pillow) library, this method performs a transformation on the image histogram. This transformation expands the dynamic range of pixel intensity values, amplifying the differences between light and dark areas, shown in Figures 2(c) and 2(d). As a result, this process facilitates both the identification and subsequent processing of the information contained in the image.

With the transformed image, the next step is segmentation, aimed at isolating the region of interest in the CT scan

while discarding irrelevant areas. For this purpose, the DISF (Dynamic and Iterative Spanning Forest) algorithm [9] is applied to each slice of the image. DISF operates based on user-defined parameters, including the number of initial seeds, the number of iterations, and the number of objects to be segmented. Starting from these initial seeds, the algorithm iteratively groups pixels with similar intensity characteristics until it converges to the desired number of superpixels, the method is bounded by the complexity $O(N \log N)$, where N is the number of pixels.

Following the initial segmentation generated by DISF, the resulting mask undergoes a refinement process. First, the regions labeled as background by DISF are excluded. Then, to remove potential isolated components and refine the contours of the segmented areas, a binary morphological erosion operation is applied to the mask. Finally, a post-processing step selectively sets the highest-intensity pixels in the segmented image to zero. This approach ensures the preservation of high-density structures essential for analysis—such as pulmonary blood vessels—which, while dense, do not reach the maximum intensity values in the spectrum, thus remaining visible for three-dimensional reconstruction, obtaining as a final result Figures 2(e) and 2(f).

B. Point Clouds

Point clouds are collections of 3D coordinates that represent discrete geometric samples of an object's 2D surfaces [7]. Although they are defined as a 3D data structure that accurately reflects the real world, processing point clouds presents significant challenges due to their disorganized, sparse, and unstructured nature [8]. To improve the analysis of such irregular data, the use of graph-based approaches has been increasingly applied to point cloud processing.

After preprocessing and segmentation, each tomographic slice is projected into 3D space. During this transformation, the Z-axis dimension is adjusted to eliminate the artificial thickness that would otherwise be introduced by the point cloud, resulting in a "paper-thin" effect. Each of these "sheets" are then stacked sequentially to form create a unified point cloud. Although this cloud represents the 3D structure of the object from the CT scan, it still consists of sparse voxels, which

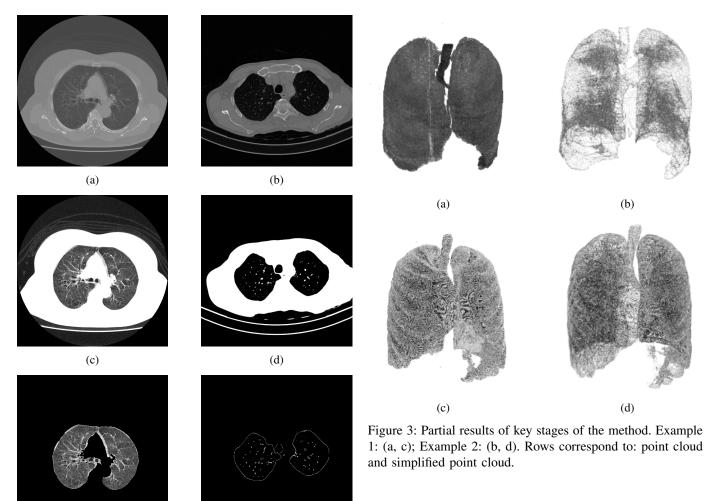


Figure 2: Segmentation phases for point cloud creation. Example 1: (a, c, e); Example 2: (b, d, f). Rows correspond to: real histogram slice, slice with histogram transformation, and final region of interest.

is suboptimal for the precise analyses required in medical contexts, as illustrated in Figure 3. Therefore, covering the point cloud with a polygonal mesh becomes an essential step.

C. Polygonal Mesh

One of the most well-known algorithms for surface reconstruction from points in computer graphics is the Poisson method. It creates smooth surfaces and is minimally affected by noise in the data. This is possible because the method is a global solution, considering all points at once, without relying on heuristic partitioning, which reduces the solution to a sparse and well-conditioned linear system, according to [10]. This is the method that will be used to transform the point cloud into a robust 3D model. However, before applying the Poisson method, clustering is performed using the K-means algorithm. This step is crucial for separate the right and left sides of

the lung from the bronchus, making them more manageable and avoiding possible shape distortions that could occur due to the short distance between these parts. After clustering, the Poisson method is applied to each of the regions separately.

In the end, we obtain a structure similar to a graph. In this model, the voxels from the point cloud are used as vertices. The oriented normals function as implicit edges, ultimately forming the 3D model shown in Figure 4.

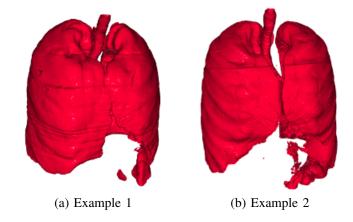


Figure 4: 3D lung model formed by a point cloud enclosed by a polygonal mesh.

IV. RESULTS

The results obtained confirmed the initial expectations, demonstrating the feasibility of a new approach to the three-dimensional representation of organs. Although the generated model is an early prototype compared to more complex existing 3D representations, this work establishes an alternative method for modeling anatomical structures from CT scan data.

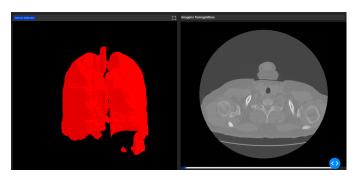


Figure 5: Graphical interface for viewing lung representations.

To optimize visualization and facilitate comparison between the reconstructed 3D model and the original CT slices, a graphical user interface was developed. It allows simultaneous viewing of both lung representations, as illustrated in Figure 5. On the left side is the three-dimensional image, and on the right side, the original DICOM images are displayed, which—due to their specific format—typically require heavy software for viewing.

Below the CT images is a scrollbar that allows users to navigate through the slices sequentially and at their desired speed. This dynamic scrolling of images was designed to resemble the frame-by-frame progression of a film, as this approach helps users perceive spatial continuity and depth—features that are not easily observed when images are simply displayed side by side. This aids the user in understanding how the two-dimensional images were used to construct the final three-dimensional model.

V. CONCLUSION AND FUTURE WORKS

In conclusion, the initial objective of this work was fully achieved: to successfully demonstrate a new methodology for three-dimensional lung modeling. Unlike some existing approaches that rely on contrast-enhanced images, the method is capable of analyzing CT data without the need for iodinated contrast agents. This feature represents a key advantage of the project, as contrast-enhanced CT scans are contraindicated for patients with certain conditions, such as allergies or impaired kidney function.

As a next step, the goal is to improve the integration between DICOM images and the reconstructed 3D model. To this end, an interactive feature is proposed, in which clicking on a specific area of a tomographic slice will automatically highlight the corresponding part of the 3D model.

The implementation of this feature aims to further improve the visualization of the lung model, creating a way for any user, including non-specialists, to clearly understand what is happening inside their own body. This aligns with the central goal of the proposed method: to facilitate understanding and increase the educational value of 3D representation in healthcare.

After the completion of this last feature, the next step is to perform validation with healthcare professionals and a usability study with patients and potential system users. For future versions, it's possible to consider integrating other imaging modalities, such as magnetic resonance imaging, in addition to conducting tests with CT scans of other human organs, such as the brain.

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