3D RECONSTRUCTION AND VOLUME COMPUTING IN MEDICAL IMAGING

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<u>Abstract:</u> Medical imaging domain is a field of interest which concentrates great efforts to offer software tools for the assisted diagnosis. Segmentation, 3D reconstruction and visualization are techniques that allow physicians to observe possible pathological structure inside of the human body. Computing the volume of such a structure offers critical information in the evaluation of the disease gravity. In this paper we present a method for 3D reconstruction of the pathological zone and propose a method for volume computing. We consider this as a start for developing a complex software tool for Deep Brain Stimulation procedure in the neurosurgery domain.

Keywords: volume/ surface rendering, multi-planar reformatting, DICOM files, segmentation

I. INTRODUCTION

Medical imaging is a set of techniques and methodologies used to process images of the human body for clinical purposes. Some branches may be used for surgical planning, monitorization and navigation of different diseases.

Every year, millions of images of patients are taken, in different dimensions and sizes. Most of them are 3D images of patients in order to assist in therapy and diagnosis. To process this large set of data, fast and accurate visualization methods are needed. For this, we need to provide dedicated computer support and it is necessary to have an in-depth understanding of the computer graphics field and visualization.

In Webster's Ninth New Collegiate Dictionary the term visualization is defined as the act or process of interpreting in visual terms or of putting into visual form. This implies vision, which is the primary human sensory apparatus, and the power to process of the human mind. Three terms are defined in this way, [1]:

Scientific visualization is a field of computer science that includes the user interface, data representation and processing algorithms.

Data visualization refers to representation of data sources in different domains.

Information visualization is specific for computer vision and deals with abstract information that exists in a computer.

As we can see, the base of the visualization process is the *data*. First, the data is acquired from some source, then it is transformed using various methods, and then mapped to a form appropriate for presentation to the user. Finally, the data is rendered or displayed, completing the process. This process can be repeated and new models can be developed.

Medical image data are usually represented as a stack

of individual images, stored in many medical formats, the common one being the DICOM format. When we develop an application it is important to study how this format is processed by the tools that application is based, because in this way we can guarantee the accuracy of the data. Many tools can store the DICOM format slices in other formats to be viewed, and in this case the files can be compressed, so we can lose important information.

Using the best suited format for the files, we can render the graphical data into images and if we want, to reconstruct a 3D volume from these slices. In the context of medical volumetric data we can use either direct or indirect volume rendering. Starting from the rendered image data, we can outline regions of interest from each slice. Using these selections, a 3D model may be obtained. It is important to numerically calculate the surface of the region of interest (ROI) on each slice and the volume of the obtained 3D structure, to allow a quantitative evaluation of the structure, which can be a tumor.

In neurosurgery domain, dependent to medical visualization, the problem of predicting behavior from the brain activity has attracted considerable attention over the past decades. If we are referring especially to brain activity, two main types of signals are most considered: *the spikes* (extracted from a single neural cell) and the *local field potentials* (*LFPs*) (viewed as a sum of multiple neurons activity).

LFPs refer to the low frequency component of the recorded neural activity, and have been shown to carry a lot of useful information. These signals are extracted within human brain using Deep Brain Stimulation (DBS), an invasive neurosurgical procedure used in the treatment of severe forms of epilepsy, Parkinson's disease, obsessive-compulsive disorder and depression.

Combining medical visualization with signal

processing is a domain which concentrates special efforts from researchers.

II. 3D VISUALIZATION SYSTEMS

In 3D medical image modeling and visualization there are many systems and software tools which can be used. Visualization Toolkit (VTK) and the Insight Segmentation and Registration Toolkit (ITK) are frequently used in 3D medical image visualization, they being also used as a solid foundation for many other systems. These two software tools are Kitware company products, and besides these, they also have some good visualization tools that include powerful interfaces: ActiViz, VolView, MIDAS, CDashPro, ParaView and IGSTK. Other tools, which are not belonging to Kitware, and need to be mentioned, are: MIPAS, VolumePro100, Vizard II, SepINRIA, VisTools, SciRun, Amira, MeVisLab, MITK, VolV, BioImageSuite and 3D Slicer.

The most of these tools include powerful interface and interactive systems for volume visualization and are designed to be flexible for different purposes. Some of them are briefly described in this chapter.

The *MIPAS* system produces a photo realistic face skin surface model by using texture mapping. Thus, it is possible to see the whole human head on 3D surface models completely with outer face and inner brain tissues, [2].

Another system, *VolumePro1000* is an accelerator based system that uses its hardware-implemented raycasting algorithm. The system is based on a typical graphics accelerator that uses "volume texture" feature and pixels shaders.

Vizard II is a volume rendering system based on a reconfigurable ray casting implementation. The high image quality is guaranteed by enabling the use of different gradient filters, pre-integration to avoid common slicing artifacts, and high precision color and opacity accumulation, [3].

SepINRIA is a free software dedicated to Multiple Sclerosis (MS) patient brain MRI analysis. The aim of the product is to provide to clinicians tools that allow analyzing MS (Multiple Sclerosis) brain images, [4].

VisTools is a suite of cross-platform interoperable toolkits for analyzing, rendering, visualizing, and interacting with very large data sets from a variety of scientific disciplines, [5].

3D Slicer is a tool widely used in clinical research, especially for image-guided therapy, because of its ability to visualize collections of MRI data. It has also some segmentation options.

ParaView – is an instrument built using VTK libraries. The main feature is that it is able to analyze extremely large datasets due to its power to distribute memory computing resources. If it is used on supercomputers it can analyze datasets of terascale, [5].

BioImageSuite – it belongs to *National Institutes of Health (NIH) from Yale* and it comes with a great support for the beginners in medical visualization field using VTK and Tcl. It offers image analysis in different domains and supports manual segmentation and registration, [6].

Most of the presented software instruments were developed for general 3D visualization. They also include the most used image processing techniques in the field of medical visualization, like: zooming, padding, contour extraction, and the interaction with the volume. Many of these software tools are developed under the VTK (Visualization Toolkit) software package, able to implement visualization data structures, algorithms and image processing, [5].

III. SEGMENTATION OF SLICE IMAGES

Segmentation of medical images is used in all medical domains, being a great tool for identifying and outlining relevant anatomical structures.

The main task of the segmentation is to compute a map, called *label volume*, which classifies pixels in an image or voxels in a volume. Based on this purpose, different algorithms and methods for segmentation have been implemented in recent years. Even if we are talking about manual-interactive or semi-automated segmentation methods, there exist different techniques used to improve the segmentation process.

The most general and robust method for image segmentation is the *manual* selection of the relevant structure, on each slice of the radiological data. This type of segmentation is commonly used when we deal with low contrast images and hard-to-select shapes. Its drawbacks: time-consumption and non-reproducibility make semi-automatic segmentation methods to be preferred, but sometimes tumor segmentation is preferred to be done manually.

A very common approach of image segmentation is based on *region growing* algorithms, [7]. The principle is to select seed pixels from the target structure, and then aggregate successively neighboring pixels to obtain a connected volumetric region. We can include pixels in the volumetric region by verifying if the intensity values of the pixels remain in a specific threshold interval. The most common application of region growing is the segmentation of the vascular structures, having the capability for improved vessel segmentation. There were developed advanced region growing methods, by considering a second criterion for obtaining the volumetric region, or by developing adaptive threshold intervals.

Threshold-based segmentation, [3] is a simplified method of region growing, implying the generation of a binary image based on a threshold or an interval of a lower and upper threshold applied to the image intensity. The most typical application of this type of segmentation is the bones extraction in the CT data, but for an accurate detection of the bones, the method must be improved using a connected component analysis (CCA) approach.

Another important region-based segmentation method is *watershed segmentation*, [3] based on the idea of considering an image as a landscape topology with water flowing into low collecting basins. As the water fills these low basins, they will merge together into larger basins (called *catchment basins*), which form the regions. Watersheds are the border lines that separate basins from each other. A watershed transform decomposes the entire image and assign each pixel either to a region or a watershed. The drawback of this method is oversegmentation, encountered in the noisy medical image data, but there exist different techniques (criteria for merging regions) for avoiding this problem.

A special segmentation method is *livewire method*, because instead of directly generating a target region (as in the region growing methods), it performs edge detection. This method extracts the contours of interest from each slice of the medical dataset. Livewire uses Dijkstra's graph search algorithm to compute the minimal cost paths and based on these paths, it selects the edges of the region of interest. In order to apply the search algorithm, each slice must be represented as a graph, where the vertices represent the image pixels and the edges represent the costs between neighboring pixels. Because of the graph representation of each slice, the livewire method is not suited for larger 3D dataset, being time-consuming even for a minimum cost function. Then, it can be imprecise in defining the contours in each slice. In order to eliminate these drawbacks, some interpolation methods were developed for this segmentation algorithm.

Besides traditional segmentation methods, there exist also methods used for specific segmentation tasks, called *model-based segmentation* methods. In order to be implemented, we need to have information about the size and the shape of the region to be segmented. One approach of the model-based segmentation is the active contour models, being a deformable model, where the initial contours are deformed towards edges in the image, [3]. The most common application is to approximate the boundary shape of a region of interest, under the assumption that the boundaries are smooth.

We must pay attention that in segmentation not only the development of strong and fast algorithms must be considered. The interaction aspects, referring to the accuracy and the simplicity in using a segmentation application, must be taken into account. They take into account the strength and the weaknesses of human beings and allow human-computer collaboration for a given application. Interaction methods were developed for every segmentation method, being a support for developing advanced segmentation applications. Then, we must consider also some postprocessing methods in order to correct the small errors that may appear and enhance the visualization of the result.

In order to perform segmentation, there exist several open source software tools. The ITK (Insight ToolKit) includes a basic set of algorithms implemented in C++ programming language that can be used to develop a segmentation application, based on its segmentation filters; MITK – used for manual segmentation; ITK-SNAP – use level-set methods to combine manual and semi-automatic segmentation, [7].

IV. VISUALIZATION IN MEDICAL IMAGING

Medical visualization is primarily based on 3D volume data. The interaction facilities must be focused on 3D interaction techniques which allow the immediate exploration of 3D data.

The volumetric visualization methods can be divided in two categories: *surface rendering* and *volume rendering*. If we consider surface rendering, the most common method is marching cubes. This method produces polygonal approximations of the real edges, known as isosurface. On the other hand, the volume rendering techniques display the volumetric data as a colored semi-transparent fog, [9].

Volume rendering visualization methods make possible obtaining of a 3D good perception, by integrating the 2D slices in a volume. That volume can be seen from any angle and with shadows effects, with small variations in density and opacity. There exists a variety of modes for presentation of the volumetric data on the display which will be discussed in the following.

The first step in medical imaging is the visualization of the data. This step is very important in obtaining the results of an experiment and in testing different methods that can be beneficial for a patient. The volumetric data is composed of a very large number of individual voxels. There exist two main methods of volume rendering in medical visualization, [8]: *indirect volume rendering* and *direct volume rendering*.

1. Indirect volume visualization

Two methods are common used in indirect volume visualization:

- *Plane-based volume rendering*: we can easily visualize a plan aligned with the cuboid of the volume, and we obtain the three views: axial, coronal and sagittal.

- *Surface-based volume rendering*: to represent a material surface of the object. The resulting surface is called an isosurface and the value used for extraction of this surface is called isovalue. The common methods used for contour extraction are the contour tracing and marching cubes.

2. Direct volume visualization

The method consists in the visualization of the volume using all the voxels. Despite there exist many volume rendering algorithms, classified as image space approaches and object-space approaches, four techniques are the most common ones, [8]:

- The classic direct volume rendering technique is *ray casting*, in which the rays are casted from the eye or viewpoint through the image-plane and through the dataset. The ray samples the volumetric dataset along its path and depending on the specified properties, makes parts of the volume visible or not.

- In *splatting*, a voxel can be discarded if the voxels surrounding it in the direction of the viewing ray have "high" opacity. Splatting methods for volume rendering are substantially faster than ray-casting.

- Shear warp is an optimized version of the ray casting algorithm, developed by Cameron and Undrill. It simplifies the volume sampling to reduce the memory access costs, by transforming the viewing transformation such that the nearest face of the volume becomes axis aligned with an off-screen image buffer with a fixed scale of voxels to pixels. The volume is than rendered into this buffer using the far more favorable memory alignment, fixed scaling and blending factors. After the slices are rendered, the buffer is warped into the desired orientation and scaled in the displayed image.

- *Texture mapping* method is based on the texturemapping support of computer graphics hardware. The dataset is loaded into texture memory and is resampled by the texture-mapping functions of the graphics hardware and mapped to a rasterized polygon on the screen. The main disadvantage of this technique is that if the dataset does not fit into main memory, need to be swapped. There exist different solutions to this problem, which are based on considering the reorganization of the volume dataset.

The main technologies used for 3D rendering are: OpenGL, Direct3D and Java3D. There are software tools and packages developed to manipulate and visualize the image data, such as: VTK (Visualization Toolkit), H3D API, 3D-Doctor, 3DVIEWNIX, and ANALYZE.

V. 3D RECONSTRUCTION AND VOLUME COMPUTING

Using Dicom images we propose a method for 3D reconstruction of the investigated part of body and the representation of the pathological volume inside of it. A volume computing method is also proposed, in order to estimate the dimension of the pathological anatomic structure. We implemented some software modules for improved visualization of dicom images, ROI selection and 3d reconstruction.

3D visualization of medical images brings a plus of information in diagnosis process and could be useful when a pathological structure has to be extracted. For this purpose we propose a method for 3D reconstruction from Dicom images combined with a 3D reconstruction from the segmented images and the visualization of the both volumes in the same scene. For 3D reconstruction and visualization we implemented an application which uses vtk library (Visualization Toolkit).

The first step is the visualization of the 2D images. There exist different methods for displaying Dicom images. There are software applications that allow transforming these images in a common format. Different toolkits may also be used to create a Dicom viewer.

For the visualization of 2D images there are some parameters that can be established, such as: scale, window, level. In the left side of the image in Figure 1 we can visualize the parameters that can be adjusted in our implemented application for both 2D and 3D visualization of the dataset.



Figure 1. 2D visualization of a CT axial slice.

Scale parameter is used for zooming. A filter implemented in vtk is used to realize the magnification, based on linear interpolation.

The Window/Level values determine the brightness and contrast of the displayed slice. A high value for the Window parameter and a low one for Level parameter lead to a flat distribution of the grey values and even the boundary of the slice cannot be detected. In this case it is very hard to separate the bone from tissue or air.

In contrast, if a low value for Window and a high value for Level are used, we lose the information regarding the tissue and the bones are easy to be distinguished.

It is very important to set the Level and Window

values of a slice in the most appropriate way, depending on the region of interest. Otherwise, wrong interpretations may arise, this being critical in analyzing a medical image.

In the header of each Dicom file there exist information about the Window and the Level values and the range of these values. These parameters may be obtained using the *GetPointData()*, *GetScalars()* and *GetRange()* methods of the *vtkImageData* class.

In order to reconstruct the pathological zone, on every 2D images must be selected the region of interest. An interactive method is proposed, because that region has to be selected as accurate as possible. This method realizes the marking of some contour points. A line is traced between two adjacent points and after the last point was selected, the closed natural cubic spline that interpolates those points is calculated and displayed. Our module application allows to display every slice and to realize the selection with the mentioned method. Such a selection is shown in Figure 2, where we can see the bright outlined region in the mouth position of the human head.



Figure 2. Region of interest selection.

The 3D reconstruction is realized using surface-based and plane-based volume rendering. Surface rendering technique allows visualizing the obtained structure with a given opacity. To observe the internal structure represented inside, the opacity of the external volume has to have a low value. For surface rendering we used marching cubes mechanism, represented in vtk by some vtkContourFilter, vtkMarchingCubes, classes: vtkImageMarchingCubes. The instances of these classes represent contour filters which can lead to isosurfaces. We used the same filter for the structure reconstructed from selections as well as for the entire investigated part of the human body. In order to obtain a smoother structure from the selection, a surface smoothing may be applied before filtration. The vtkSrink3D class of the vtk toolkit allows smoothing by a subsampling on a uniform grid. Because the two surfaces are displayed with 2 actors, is very important to place them correctly in the scene.

A method for 3D visualization is Marching Cubes, which is based on isocontouring techniques. These techniques are used to extract the skin and bone surfaces and to display orthogonal cross-sections to put the

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isosurface in context. In [6] is defined that a density value of 500 will define the air/skin boundary, and a value of 1150 define the soft tissue/bone boundary.

- The main steps in representing the isocontour are:
- Read the input;
- For each anatomical feature of interest, create an isosurface;
- Transform the models from patient space to world space;
- Render the models.

For reading medical images, Dicom files or .vtk files may be used, as well as other image common formats. In order to transform Dicom files into other image format, different software application or tools may be used. For instance, we used *dicom2* application. This is a free command-line driven program which allows us to convert medical images and DICOM files to various other formats (*.bmp*, *.png*, *.raw*), while performing some rudimentary image processing tasks. The Figures 3 and 4 show the 3D reconstruction results obtained using Dicom files and *.raw* files.

As can be observe in Figure 3 and Figure 4, there exists a visible difference between the two methods, even if we choose the same value of the density and the same properties for the isosurface. This difference arises because if we read Dicom files using vtkDicomReader the slices are saved as JPEG 16 bit compressed, which cuts the higher frequencies in the images. The conversion from Dicom to .raw let the image uncompressed, which leads to better resolution. An improvement for using Dicom files can be achieved by performing histogram normalization. We observe that there is a great difference between these two types of visualization and it is crucial to be taken into account when we want to develop a strong reconstruction instrument tool, this problem being usually neglected by the software developers.



Figure 3. Skin isocontour extraction from a CT dataset saved as Dicom files.



Figure 4. Skin isocontour extraction from a CT dataset saved as .raw files.

Usually we can provide more context of the volume if we are able to see all the orthogonal planes (axial, coronal and sagittal), and to visualize the volume and the tumor in correlation with the slices used to obtain these volumes. In this case we can visualize just a part of the volume, the one generated between the selected slices.

We implemented this possibility by using plane-based rendering technique, available in vtk by using the *vtkImageActor* class that is able to combine a quadrilateral, polygon plane with a texture map. In the Figure 5 we can visualize the result of applying the planebased method.



Figure 5. Visualization of the orthogonal planes and the skin isosurface.

The pathological structure and the investigated anatomical part have to be displayed in the same 3D scene. The volume of the former offers important information for the physicians.

We propose a method for calculating the volume of a 3D structure. Different image's attributes may be read from Dicom file. The PixelSpacing attribute give us the distance between pixels. This attribute offers the distances on rows and columns between adjacent pixels' centers. For every 2D image the area of the selected region may be calculated based on the number of the pixels in that zone, using relation (1):

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$$A_{k} = x * y * \sum_{i=0}^{n-1} (nr _ pixels _ line_{i} - 1)$$
(1)

where:

 A_k – area of the selected zone on the k slice

- x, y distances between adjacent pixels' centers on rows and columns
- nr_pixels_line_i the number of pixels on line "i"
- n the number of pixels' rows on the selection

The thickness of a slice may be obtained from SliceThickness tag. For the distance between slices there exist an attribute named SpacingBetweenSlices, but it may be absent in Dicom file and appears only for MRI images. Moreover, some vendors do not establish in this tag the distance between slice's centers, but the distance between their margins. We propose to establish the distances d1 and d2 from two successive slices to the same origin, on the plane normal direction. The distance between slices is the difference between these two distances. Using this information the volume is calculated with relation (2):

$$V = h * \sum_{k=1}^{m-1} A_k + A_1 * \frac{g}{2} + A_m * \frac{g}{2}$$
(2)

where:

- V the structure volume
- h the distance between two successive slice's centers

m - the number of slices

 A_k - the area of slice "k"

A₁ – the first slice's area

 A_m - the last slice's area

g - the thickness of a slice

The proposed methods are integrated in our software module developed for ROI selection.

In the software component that we implemented for 3d reconstruction and visualization, the volume can be displayed with transparency, so the tumor can be observed. In Figure 6 the dark-grey structure located inside the rendered volume of the head represents the pathological volume. It is the volume reconstructed from selections. The entire volume can be rotated, to see the tissues and the tumor from different angles and perspectives.

Another important aspect in 3D medical image visualizing is the multiplanar reformatting, [10]. This technique allows visualizing the structure on the main planes used in medicine: axial, coronal and sagittal. To extract a slice in the desired orientation vtkImageReslice class may be used, from VTK toolkit.

In order to visualize the 2D projections of the volume on the three main planes, we have placed three cutter planes which intersect the volume in those directions. By moving a plane, in the correspondent right window is displayed the image reformed by intersection of that plane with the volume.



Figure 6. Visualization of the pathological structure and the investigated anatomical part in the same scene

For a more natural visualization mode of the two volumes (human part of the body and the tumor), direct volume visualization methods were implemented by using vtk classes such as *vtkVolumeRayCastCompositeFunction* and *vtkVolumeRayCastMapper*, together with some properties that were added to the volume and some cropping methods. An example of this kind of visualization is presented in Figure 7. The surgeon is able to explore into the volume and to extract some information that can be used in taking decisions regarding the treatment of the affected area.



Figure 7. Direct visualization of the volume

VI. CONCLUSION AND FUTURE WORK

Medical images are very important in assisted diagnosis and for the surgery domain. Useful information may be provided by visualization in 2D space, as well as in the tridimensional one.

We offer a method to represent in 3D space a pathological structure, related with the surrounding tissues. For this purpose a selection has to be made on every image slice. The proposed method for ROI selecting may be time consuming, but assures a good accuracy.

The volume of the structure being an important factor in medical evaluation, we offer a method for volume computing.

The multi-planar reformatting may be useful for observing how the tissue is affected in different directions.

Considering the proposed methods as a start, a neurosurgery navigation software tool can be developed for different medical techniques. Using the manual segmentation is well suited for such an application, to select the affected structure of the brain. This can be done in either Dicom files or on the specialized human brain atlases that already exist. Then, it is important to visualize both the entire brain volume and the pathological part, where the electrode must be placed. After the visualization of these two parts, a navigation system can be developed to move the electrode in the target position. Based on the LFP processing techniques, we can record the neural LFP signal and determine the best position of the electrode inside the brain.

As future work we will extend this application to make possible the integration of signal processing techniques needed for LFPs. This will be helpful in the evaluation of the neural activity in a certain region of the brain. Furthermore, we will develop a navigation system for DBS, able to move the electrode in the affected structure of the brain and to take some decisions regarding the exactly location of the electrode.

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