

Visualization of Segmented Structures in 3D Multimodal Medical Data Sets

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Abstract— The simultaneous inspection of images obtained using different medical scanning methods represents a common practice for accurate medical diagnosis. The term multimodality refers to multiple medical data sets obtained by scanning a patient with the same method at different time moments or with different scanning techniques. Recent research efforts in computer graphics have attempted to solve the problem of visualizing multimodal data in the same scene, for a better understanding of human anatomy or for pathology tracking. This paper proposes a method of integrating segmented structures from a contrast enhanced MRI sequence into the volume reconstructed from the slices of another MRI sequence obtained with different scanning parameters. A direct volume rendering (DVR) approach is used to represent focus and context information from the 3D data. The presented approach aims to help physicians in understanding pathologies and in the process of accurate diagnosis establishment.

Index Terms— computer graphics, visualization, medical diagnostic imaging

I. INTRODUCTION

In common medical practices, physicians usually have to inspect structures from multiple data sets acquired from different medical scanning techniques in order to establish an accurate diagnosis. This method is also used for the better understanding of the anatomy of the human body or for surgery planning. Most commonly used scanning methods are Computed Tomography (CT), Magnetic Resonance Imaging (MRI), Functional Magnetic Resonance Imaging (fMRI), Positron Emission Tomography (PET), Single Photon Emission Computed Tomography (SPECT) and 3D ultrasound [1]. The term *multimodality* describes the visualization of data from multiple data-sets in the same scene. It also refers to the inspection of data-sets acquired with the same medical scanning technique, but captured at different time moments. These types of scanning methods are usually performed to track the evolution of pathologies such as tumors or other medical conditions.

Scanning one patient with different modalities at the same time is very hard to achieve, if not impossible. Therefore, a patient has to move between the scanning processes. Even if the patient has the same relative position to the scanning machine, a perfect alignment cannot be reached. Prior to any visualization techniques, a registering algorithm that will align the coordinates of the used volume has to be implemented.

CT sequences are commonly used with MRI data in order to provide a broader perspective over the anatomy of a

structure. A large area of research in multimodality rendering techniques was developed in the fields of neurology and neurosurgery, because of the need to visualize multiple types of structures in the same scene.

In this paper we introduce a method of combining segmented data from one MRI sequence to another, along with a 3D visualization method. The reason for doing this is to embed best visible structures from both scanning procedures into one single visualization scene. Also, the presented method provides a better understanding of pathology and spatial location of a tumor.

The paper is organized as follows. Section II provides an overview of existing techniques in the field of registration, segmentation and visualization of multimodal data. Section III contains an introduction to MRI scanning techniques and also provides a medical background for the visualization problem of integrating structures from one scan to another. Section IV presents the technique used for registering multimodal data. Section V presents the algorithm used for segmenting MRI structures. In section VI the registered and segmented data is represented using a volume rendering approach. Section VII concludes this paper.

II. RELATED WORK

In order to solve the registration problem, a range of techniques have been developed, mostly divided into two main categories, namely rigid and non-rigid. Rigid techniques are most commonly used when scanning inner parts of the human body that usually don't exhibit any structural changes over a short period of time, such as brain, bones, etc [2]. Non-rigid techniques are used for registering structures that change their volume or position during a scan (lungs, elements of the digestive tract, etc) [3]. Both rigid and non-rigid algorithms are used for the alignment of medical images [4].

Image segmentation deals with the problem of partitioning the image into meaningful objects. It is commonly used for feature extraction and for a better understanding of a specific structure. As the segmented object presents a huge variety in size, properties, shapes, background noise, a large number of segmentation techniques have been developed [5].

The visualization of registered multimodality volumes presents specific challenges and numerous techniques were developed for each specific type of used data. A single scanning method comes with its own specific limitations. A combination of multiple scanning methods has a better potential of solving the problem of information visualization

This work was developed within the "BRAIN - An Investment in Intelligence" doctoral scholarship program, from the Technical University of Iasi, Romania.

within an anatomical context. MRI sequences can be combined with angiographic scans for the detection of hemorrhages or aneurysms. After combining these data, several anatomical features are used as input into a watershed algorithm for segmenting purposes [6]. For the detection of small tumors, a combination of MRI and PET or SPECT data has been introduced. Multimodality rendering can also be used for the purpose of segmenting some other anatomical structures of the human body, such as the brain or spinal cord [7]. Most visualization methods are based on Direct Volume Rendering (DVR), which creates output images directly from the volumetric data sets, without extracting any polygon-based geometry [8]. DVR and other volume rendering approaches are widely discussed in the related literature [9].

One straightforward approach that has been implemented for intermixing volume data from CT and MRI is based on a simple threshold operation. This method has the drawback that some data is lost from either volume. An extension of this method is inclusive opacity, where data from all volumes are sampled in order to compute the final color of the rendered pixel [10]. New multimodal rendering techniques commonly make use of the computational power of modern GPUs (Graphics Processing Unit), which present a high level of parallelism well suited for 3D visualization algorithms [11].

A method of combining data from MRI and fMRI, implemented on GPU, is introduced in [12]. The purpose of this combination is to provide a spatial context for the fMRI data that depicts the activated regions in the brain during cognitive tasks. Functional MRI data is usually obtained as multiple reconstructed volumes, as the patient has to perform a series of tasks that can involve movement, speaking etc. These volumes are usually registered by a medical framework.

Physicians usually have to employ pre-operative planning in order to better understand how surgery will take place or for determining an incision point. In the neurosurgical field, such techniques are widely spread. For better pre-operative support, various volume rendering applications offer methods for the multimodal visualization of data sets obtained from different medical scanning techniques such as CT, MRI, fMRI, PET, SPECT [7]. For a specific sampling location, a decision is made regarding how the corresponding point from each volume will contribute to the final color of the ray.

The visualization of inner structures usually plays a key role in understanding specific anatomies or pathologies. The most common method used is the implementation of clipping planes that separate the rendered volume into visible and hidden voxels. When dealing with multimodal data this approach is not suited for the visualization of structures that cannot be rendered visible by a simple clipping plane. Different strategies of implementing cutting surfaces have been implemented in [13].

Contextual cutaway views [14] have been introduced with the idea of presenting the object of interest in such a way that the surrounding materials are removed based on an importance factor. By applying this technique onto 3D ultrasound and registered CT or MRI data, the visualization of important volumetric features is greatly enhanced.

Most of the described methods do not present the possibility of selecting one structure of interest, like the tumor in our case. The visualization of the structure in a different pre-registered spatial context it is also not possible. Simple cutting planes fail to present a complete context while maintaining the focus on one specific structure. Also, the usage of transfer functions for selecting one structure of interest that will be integrated in another registered data set represent a laborious work and it is prone to high errors due to the noise presented by the MRI images.

Existing medical visualization frameworks such as 3DSlicer[15], ParaView [16], Voreen [17] present the features of registering various datasets or of segmenting specific structures of the human body, but lack the possibility of visualizing multiple data sets in the same visualization scene. The frameworks also lack the option of visualizing certain segmented structures from one data set in the spatial context offered by another data set.

III. MRI IMAGE ACQUISITION

The brain is one of the most commonly scanned parts of the human body. MRI is frequently used for scanning and separating substructures and tissues from within the brain. MRI is based on the property of nuclear magnetic resonance to produce images of human tissues based on their different response to an applied magnetic field. MRI scans are most commonly used for depicting soft tissues (brain, muscles, etc.). MRI is able to generate high contrast between soft tissue types, but fails to depict bone at the resolution of CT. The main advantage is that there is no radiation involved, but the image acquisition process usually takes longer compared to CT.

The most commonly used MRI sequences are: contrast enhanced T1 weighted (spin-lattice relaxation time) and T2 (spin-spin relaxation time) weighted. The use of contrast agent during a T1 weighted sequence is recommended when the blood flow has to be visualized. In case of existing brain tumors, this sequence is necessary for finding the proliferative parts, as a required pre-surgical step for a biopsy for example. The T2 weighted sequence is used mainly for visualizing different pathologies. In brain imaging, T2 weighted sequence provides various information concerning the cerebrospinal fluid (the location of large accumulation areas, the severity of a brain lesion, etc.) [18].

Recently, the comfort of the patient has become a key factor in most medical procedures. In a brain MRI scan, the patient is subjected to a lot of noise, while lying in a very narrow space. Because of this, physicians try to reduce the scanning time as much as possible. Time reduction involves taking as few slices as possible, without losing any important data. The slice thickness in brain T2 weighted scans is usually higher than in T1 contrast enhanced. In the data sets used in this paper, the slice thicknesses for T1 and T2 weighted sequences are 1.5 mm and 2.5 mm, respectively.

IV. REGISTRATION TECHNIQUE

There are three main types of image registration techniques: *Landmark based*, *Segmentation based* and *Voxel*

property based. Landmark based approaches imply the use of some external devices that are fixed to the patient, in order for a more accurate and fast registration process [4]. These techniques, however, tend to create a discomfort for the patient, especially in an MRI scan where the physical opening of the scanning device is quite narrow. Segmentation based techniques require the use of pre-segmented volumes. Although it can lead to some good results, the segmentation process can be very laborious and time consuming. Voxel property based techniques use the output images directly, and usually work with the intensity values. They require no pre-processing step and no user interaction, so they are most commonly used. The method we used in this paper is based on intensity values, due to the fact that segmenting the same structure in different MRI sequences can be a very hard thing to achieve. Since we want to register two brain MRI sequences with no significant time gap between scans, the most natural approach is to use rigid registration.

Image registration is mainly an optimization problem. Two data sets are used as input data. One is fixed, and the other is moved by the registration algorithm until a stopping criterion is reached. Different metrics can be used for providing a correspondence measurement between the two data sets.

There are several existing frameworks that deal with the registration problem: Insight Segmentation and Registration Toolkit (ITK) [19] or Automated Image Registration (AIR). In our approach, we have used ITK, as it contains different registration algorithms and multiple implemented metrics.

For similarity evaluation, we have used the Mean Squares Metric. This is a simple metric that computes the sum of mean squared difference in voxel intensity between the two input images:

$$MS(A, B) = \frac{1}{N} \sum_{i=1}^N (A_i - B_i)^2, \quad (1)$$

where A_i represents the i -th pixel of the first image, B_i represents the i -th pixel of the second image and N is the total number of pixels. This metric is commonly used with good results in intramodality registrations, but is not well suited for intermodality cases [20]. The pseudocode for the registering algorithm is provided as *Algorithm 1*:

```

Algorithm 1 RegisterMRISequences
RegisterMRISequences(volumeT1, volumeT2)
InitialTransf = Compute Initial Transformation
Apply computed transformation InitialTransf onto
the volumeT2
Do
{
V = Compute Value according to the Similarity
Metric
T = transformation that maximizes the images
similarity
Apply computed transformation T onto the
volumeT2
}while ( V < ε or maximum number of steps
reached)

```

The parameters values used in Algorithm 1 are $\varepsilon = 0.0001$ and the maximum number of steps is 200. The outputs of the registration algorithm are: a versor (in normalized form, so

w component is no longer necessary), translation coordinates and a rotation matrix that results from the versor and the translation coordinates. The output values after applying the registration algorithm to our data are:

$$\text{Versor} = (0.00205719 \quad -0.000825328 \quad 0.000155689)$$

$$\text{Translation} = (-0.351543 \quad -0.289986 \quad -0.792229)$$

$$R = \begin{pmatrix} 0.999999 & -0.000314772 & -0.00165001 \\ 0.000307981 & 0.999991 & -0.00411462 \\ 0.00165129 & 0.00411411 & 0.99999 \end{pmatrix}$$

When registering two volumes, translation and rotation operations are applied to one volume so that it is aligned with the other one. Fig. 1 presents two consecutive slices. On the upper row the slices have the same depth coordinate, and in the lower row a slight difference can be observed, due to different slice thicknesses.

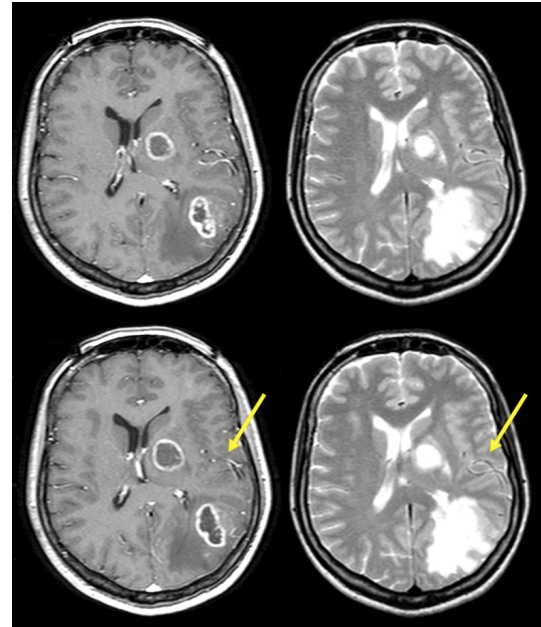


Figure 1. Two consecutive sets of slices: T1 contrast enhanced images on the left; T2 weighted images on the right. The arrows point to corresponding regions where the registration algorithm produces slightly misaligned results due to different slice thicknesses in MRI sequences.

V. TUMOR SEGMENTATION

In order to integrate data from one MRI sequence to another, we used a segmentation method to separate useful information. The segmentation algorithm classifies the voxels from the initial volume as belonging to either a region of interest, or to less important background data. We have segmented a brain tumor using the watershed algorithm [21]. The algorithm uses the variation of the gradient to classify voxels and provides good results in segmenting homogeneous regions that have well defined border areas (ridges). The brain tumors in the MRI T1 weighted sequence present such properties. The input image is treated as a height function, with the assumption that higher intensity values in the image indicate border areas. The watershed algorithm works by “flooding” the resulting output, and by assigning a value for every lower intensity area bounded by the local maxima that corresponds to

higher intensity values in the input image.

Two parameters control the output of the segmenting algorithm: threshold and level. Threshold sets the minimum height value as a percentage of the maximum height. A higher value will lead to a segmentation result with fewer regions. Level parameter controls the depth of the flooding process in the image. A value of 1.0 will provide the result of flooding the entire image, while a value of 0.0 will provide a basic segmentation, with a lot of oversegmented areas. Fig. 2 shows the result of applying the watershed algorithm on a MRI T1 contrast enhanced volume; the used threshold is 0.06 to and the level value is 0.5.

As the watershed algorithm outputs different regions for every area bounded by ridges, an additional threshold operation is used for selecting the tumor. This will discard all the points that are not in the region of interest, outputting only the tumor mask.

VI. VOLUME VISUALIZATION OF THE DATA

The data which has been processed so far is available in three dimensions, thereby easily lending itself to volume rendering techniques. Volume visualization is a branch of computer graphics which deals with the classification and representation of information from three-dimensional (3D) data sets. Such a means of data visualization is often more intuitive than traditional slice-based approaches, since it allows a better spatial separation of focus and context information. Volume visualization essentially simulates the propagation of light rays through a volume data set, based on an optical model. The model we employ in the paper is emission-absorption [9]. What this essentially means is that each point traversed by a light ray may attenuate the radiant intensity of this ray, or, conversely, emit its own light. Therefore, when reaching the viewer, light rays contain information resulting from the accumulated emission and absorption of all points along them. Analytically, this behavior is expressed by equation (2):

$$I(s_E) = I_0 T(s_0, s_E) + \int_{s_0}^{s_E} q(s) T(s, s_E) ds \quad (2)$$

where $I(s)$ is the intensity of a light ray at position s along its direction. $T(s_1, s_2)$ is the equivalent of absorption, and represents the transparency of the medium in between arbitrary positions s_1 and s_2 . $q(s)$ describes the emissive component at position s . s_0 and s_E are the initial and exit positions of the ray, i.e. the positions where the ray originates and where it reaches the viewer, respectively. The intensity $I(s_E)$ of the viewed light is the sum of an initial component I_0 modulated by its associated transparency, and the integrated effect of the emission-absorption components of all points traversed by the ray.

In computer aided visualization, equation (2) describes the mathematical model for volume rendering, and the generation of images from volume data involves the numerical computation of this formula. Our approach to reaching a numerical solution is based on a ray casting algorithm [22].

For every pixel in screen space, a ray is projected through the volume. Sample points are then taken along the directions of each ray, and opacity and color values are

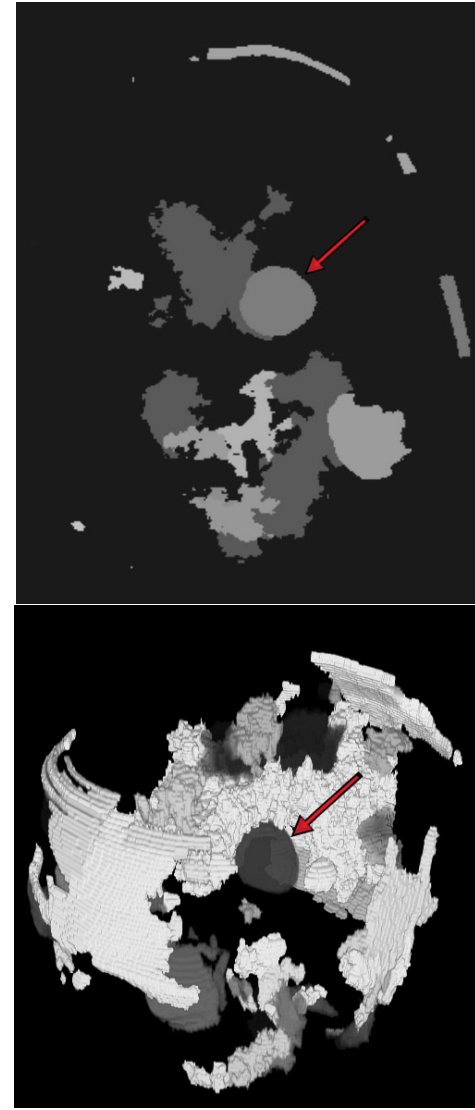


Figure 2 watershed segmentation algorithm applied for segmenting a brain tumor: 2D view (top), 3D view (bottom). Arrows are pointing to the tumor.

mapped to each sample point. The assigned colors and opacities are then combined along the direction of each ray, to form the color of the corresponding pixel. This approach mimics the behavior of light in the real world, where the colors perceived by a viewer are the result of light propagating through media with various optical properties. The combination of colors and opacities per ray is described by equation (3).

$$\begin{aligned} C_{acc} &= C'_{acc} + (1.0 - A'_{acc}) \cdot A_c \cdot C_c \\ A_{acc} &= A'_{acc} + (1.0 - A'_{acc}) \cdot A_c \end{aligned} \quad (3)$$

where C_{acc} and A_{acc} represent the color and transparency with the current point contributions accumulated to the values of the ray, respectively. C_c and A_c are the color and transparency of the currently sampled point. C'_{acc} and A'_{acc} represent the accumulated color and transparency until the current point of a ray is reached, respectively. Once each point has been accounted for, C_{acc} will have stored the color of the pixel associated with its respective ray.

One key aspect to be taken into consideration when performing visualization is to maintain focus while preserving context. This means that the information of interest should be highlighted, but other background information should also be present in order to provide a complete overview of the investigated data. This is illustrated in Fig. 3. The tumor has been separately classified through segmentation, which allows it to be isolated from the rest of the data. The image on the left in Fig. 3 shows a rendering of the MRI data set. Shading and illumination add a dose of realism to the image. However, the outer surface displayed in this image obscures the information of interest. This is solved in the image on the right from Fig. 3, where, though the manipulation of transparency, the segmented tumor is rendered visible and highlighted through an appropriate choice of color. The highlighted tumor is the information of focus, while the surrounding semi-transparent features provide the context.

One problem with MRI data is the high noise content, which makes it difficult to isolate proper semi-transparent surfaces. This can be seen in the image on the right from Fig. 3, where features easily distinguishable in the left image are a lot less clear. The ideal would be to preserve the sharp look of the left image, while showing focus information from the right one. We attempt this in Fig. 4, where a lens tool is used to look inside the data set. The lens is a circular region in image space, inside which the rendering parameters are altered. Specifically, our lens works by globally scaling the transparency of the voxels projected inside its area, thereby revealing previously occluded information. Voxels belonging to segmented areas can be discriminated based on their corresponding values in the segmentation mask, and are therefore unaffected by transparency scaling. Outside the lens, the unaltered rendering process preserves the sharpness of the skin. Aside from the segmented tumor, pre-segmented cerebral vasculature is also rendered in Fig. 4.

The external features of the data set are preserved, while the information of interest located inside the volume is better highlighted. The lens can easily be integrated into user-interfaces, allowing users to change its position and dynamically inspect the inside of the volume. The pseudocode for the described method is presented as *Algorithm 2*. It is executed in parallel for each pixel of the output image by the GPU fragment processors.

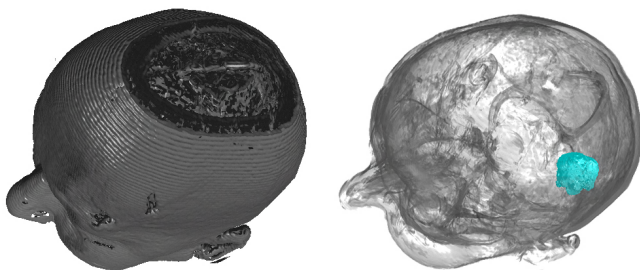


Figure 3. Volume rendering of the MRI data. The image on the left shows the shaded outer surface, which has been rendered semi-transparent in the image on the right to make the segmented tumor visible

Algorithm 2 RenderMultiVolumes

ComputeRayDirection(currentRay)

For each point P on the currentRay direction

```
{
    Sample all used volumes;
    If  $P \in \text{LensInterior}$ 
    Then
        lower opacity of the currentRay;
    If  $P \in \text{TumorMask}$ 
    Then
        currentRayColor = TumorColor;
    Get color attributes for point  $P$  from MRI
    volume
    Compose color attributes with the current ray
    color;
     $P$  = next point on the ray;
    Check exit condition for early ray
    termination (ray color alpha value > 0.95 or  $P$  is
    outside the ray)
}
```

The rendering was done on an NVidia GeForce GTX 260, in a viewport of size 1024 x 768. The data sets of the volumes reconstructed from T1 and T2 sequences have a resolution of 512 x 512 x 85 and 512 x 512 x 60, respectively. Table 1 presents data regarding performance. The results conclude that the volume rendering with the opaque outer surface is the fastest one, and the same volume with semi-transparent structures requires the most computational time. The circular lens allows some parts to be still opaque, while rendering only the region of interest, leading to an intermediate rendering time.

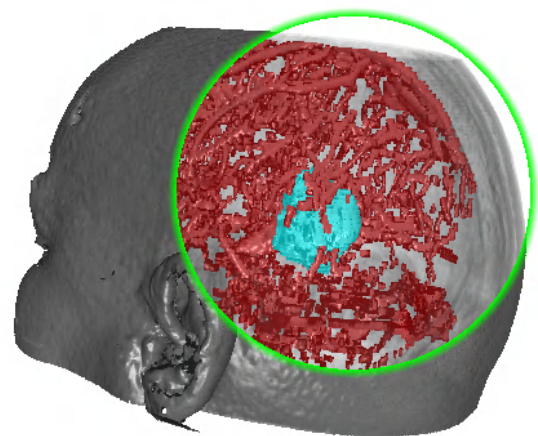


Figure 4. Circular lens used to visualize segmented information (tumor and blood vessels) inside the volume

TABLE I. FRAMES PER SECOND FOR THE RENDERED IMAGES

Volume	Frames Per Second
Volume in Fig. 3 left	9.52 fps
Volume in Fig. 3 right	3.64 fps
Volume in Fig. 4 (without the blood vessels)	7.83 fps
Volume in Fig. 4	6.84 fps

We further extend the concept of focus and context preservation with a more in-depth transfer function-driven classification approach.

Fig. 5 shows an image rendered using a complex multi-dimensional transfer function, which incorporates the gradient magnitude and local curvature into the classification process [23, 24]. Cerebrospinal fluid and other soft tissues are more easily identifiable in the T2 weighted sequence, while the tumor segmented from the T1 weighted sequence is rendered and highlighted alongside surrounding structures. We rendered now one single scene with data

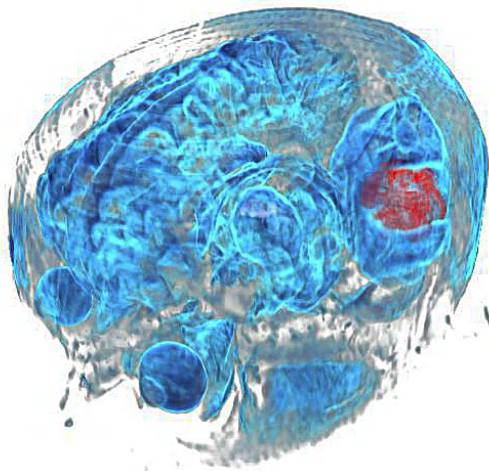


Figure 5. Classification using a multidimensional transfer function. The segmented tumor from one MRI data set is visible among other soft tissues rendered from a different MRI data set.

from both MRI sequences. The scene embeds best visible structures from both scanning procedures.

VII. CONCLUSION

Currently, many diagnosis and surgical planning processes require the inspection of multiple data sets acquired with different scanning techniques. Each existing scanning technique presents advantages and disadvantages and can provide physicians with information where the other methods fail. This is the reason why multiple scans are often required when trying to better understand the anatomy of a human organ or tissue. In some cases, such as tumor tracking, multiple scans with the same method but at different time moments are also needed.

In this paper, we have developed a method for visualizing a previously segmented structure from T1 contrast enhanced MRI sequence into the reconstructed volume from the slices obtained from T2 weighted MRI sequence. A DVR approach was used to represent focus and context information from within the data. Although the input data has a significant degree of complexity, the visualization methods run on modern-day GPUs, which means that the resulting images can be interactively manipulated and explored. We showed how a combined use of registration, segmentation and 3D visualization can make the data more easily, accurately and intuitively explorable. The techniques are meant to aid in the understanding of human anatomy, pathology, and in the diagnosis of related medical conditions.

ACKNOWLEDGMENT

The authors would like to thank the "Institute of Computer Graphics and Algorithms" from Vienna University of Technology for the help provided for this work to be implemented and the "Center of Excellence in Neurosurgery" at the Bagdasar-Arseni Hospital in Bucharest for their valuable inputs and comments.

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