Rapid and High-quality 3D Fusion of Human Brains CT-MRI Heterogeneous Data

Zexue He Minjie Li Jinyao Li Yiran Chen Yanlin Luo*

College of Information Science and Technology

Engineering Research Center of Virtual Reality and Applications, Ministry of Education(MOE)

Beijing Normal University

Beijing 100875, China

ABSTRACT

Using modern medical imaging techniques, brain data can be extracted through MRI and CT, which are two types of heterogeneous data information and have different focuses. Through fusion, more comprehensive information about the brain's anatomy can be obtained. This paper fuses heterogeneous data, separates heterologous data, integrates transfer function and renders GPU ray-casting volume to achieve rapid and high-quality 3D fusion of two types of data sources. In the data processing stage, the values of the volume data are fused, and at the CUDA-based ray-casting volume rendering stage we control and adjust the data integration and layered display through the hybrid transfer function. The experimental results prove the effectiveness of the proposed algorithm, which not only rapidly fuses two types of heterogeneous data, but also displays different kinds of tissues of brain after fusion, such as cerebrospinal fluid, gray matter, white matter, skin, muscle, and bone.

Index Terms: Human-centered computing—Visualization—Visualization techniques

1 INTRODUCTION

The worlds research cooperation project named Human Brain Project sets off a wave of deep understanding of the human brain. Because of the complexity of human brain, it's a major challenge for human to recognize themselves and overcome brain diseases. The Computed Tomography (CT) and Magnetic Resonance Imaging (MRI) data of the human brain are used in medical diagnoses and researches [11]. The above different approaches have different emphases on the expression of information. For instance, MRI can provide cross-sectional and longitudinal high-resolution images of soft tissues in brain, while CT focuses more on cross-section, which is perpendicular to the long axis of the human body. Therefore, fusing different data to reconstruct the entire brain is of great significance for more comprehensive information analysis. Through reconstructing 3D model from the medical slices (such as CT, MRI, etc.), we can display the complex features and spatial relationships of human organs or tissues and visualize the medical volume data.

Volume rendering technology is one of the main methods used in modern medicine and its applications. It presents two-dimensional image data to the user in a three-dimensional manner by displaying the internal structure of the data. H. Guo et al [3] proposed the transfer function design, which is the core issue of data visualization. The purpose of transfer function is to establish the correspondence between the voxel data and the optical properties, which determines the final three-dimensional imaging. Recently, scholars propose a variety of methods for transfer function design.

*e-mail: luoyl@bnu.edu.cn

Levoy [5] is the earliest person to propose transfer function limited in the two-dimensional space of grayscale and gradient. Since such function obviously couldnt effectively distinguish the different structures and complex boundary features, people then increase the dimension of transfer function. With the increase of the complexity of the organization structure in modern medical images, the difficulty of designing multidimensional transfer functions increases. The computers load also increases. Thus, designing a simple and effective transfer function becomes an ardent pursuit.

Currently, visualization of a single data source such as a medical slice has now achieved remarkable development. However, the data collected by different channels have different focuses. It will help a lot for the development of medical care and brain exploration if these data are accurately fused and integrated. For example, Q. Wang et al. [10] found that CT data is well presented for high-density features through experiments, whereas MRI data is superior to CT for soft tissue presentation and at a disadvantage when present high-density organizations, making it difficult to judge the relationship between lesion and other structures. Noticed the complementary function of CT and MRI, Seemann et al. [8] fused them to realistically depict the diagnostic, anatomical and pathological information of the auditory and vestibular system. And it 's important to utilize this complementary into other complex organ, like the brain. When doctors take brain tumor surgery, they may prefer to see high-density structures like the skull structure from CT and soft-tissue structures like the size and shape of tumors from MRI simultaneously to determine the best craniotomy position [10]. Therefore, the fusion of CT and MRI is of great significance to the reconstruction of the human brain.

Based on the above background, we propose a multi-source data fusion algorithm based on data fusion and integrated transfer function, which has both simplicity and scalability. Specifically, we complete the fusion of multi-source data at the data processing stage and separate out different organizations in the fusion data. Finally, in the image drawing stage, we realize the data integration and layered display by integrating the single-source data transfer function.

The paper is organized as follows. Sec.1 is an introduction of background. Sec.2 section introduces related work. Sec.3 describes the key technologies for the visualization in detail. Firstly, the CT data, MRI data transfer functions and the process design are introduced, then the data fusion and transfer function design are introduced. Sec.4 analyses the experiment, introduces the acquisition and processing of experimental data and gives the experimental results. The last section concludes the whole work.

2 RELATED WORK

In the volume rendering, the data passes through three different rendering stages including data preprocessing, lighting model construction, and image generation.

The fusion in the data preprocessing stage is more accurate and complicated than that in other stages. It is a direct fusion of multiple data from a single sampling point, including density values and computable gradients. Bramon et al. [1] used the mutual information

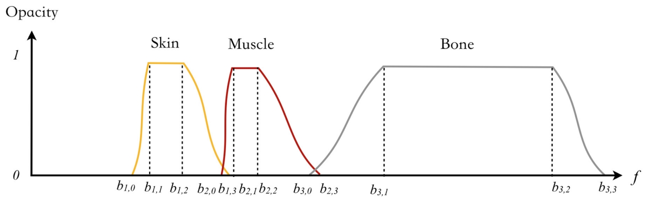


Figure 1: Trapezoidal transfer function of CT

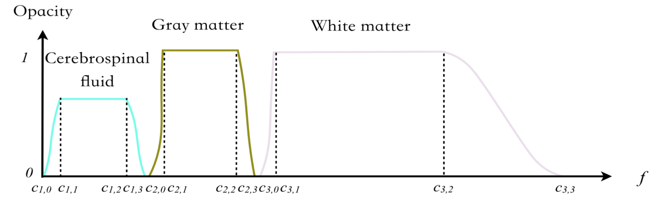


Figure 2: Trapezoidal transfer function of MRI

to obtain three-dimensional fusion information and integrated it into a common framework with a large amount of computation. Based on this method, then Bramon et al. [2] designed a fully automatic scheme for multimodal heterogeneous data visualization.

Fusion in the light accumulation phase has two methods: fuse the color and opacity of different heterogeneous data then accumulate; or accumulate them separately for each heterogeneous data then fuse. X. Liao et al. [6] proposed a three-dimensional fusion algorithm for PET and CT based on gray-scale difference, which the contribution to the result and the fusion weights were calculated.

Fusion in the image generation phase is the simplest and most intuitive step. Color blending is the most common method. Taylor [9] studied the limitations of traditional layered blending method and found that using a color blending with transparency can only display at most four levels. To ensure the correct visual perception, Kuhne et al. [4] proposed the color perception theory which solves the problem of blending two colors when the tone changes.

3 Methods

3.1 Visualization of CT volume data

For the visualization of brain CT volume data, tissues are usually divided into three layers: skin, muscle and bone [7]. To obtain more three-dimensional visualization results, the transfer function is designed to minimize the overlap between two adjacent substances. We described the transfer function as multiple trapezoid, and each one represents one classification such as boon, skin and muscle.

Assume that the j-th ($j = 1, 2, \cdots, K$) band is defined as $B_j = [b_{j,0}, b_{j,1}, b_{j,2}, b_{j,3}]$ with maximum opacity A_j and color T_j. In fact, there is an overlapping area between two neighboring tissues as illustrated in Figure 1 where we take $K = 3$ as example, the f in x-axis means scalar value of volume data like density.

Take a viewing ray V starting from viewpoint as an example, let f_i be the scalar value corresponding to sample point P_i on V, $f_i \in B_m (m = 1, 2, \cdots, K)$, the weight W_i is defined by

$$w_i = \begin{cases} \frac{f_i - b_{m,0}}{b_{m,1} - b_{m,0}} & f_i \in [b_{m,0}, b_{m,1}] \\ 1 & f_i \in [b_{m,1}, b_{m,2}] \\ 1 - \frac{f_i - b_{m,2}}{b_{m,3} - b_{m,2}} & f_i \in [b_{m,2}, b_{m,3}] \end{cases} \tag{1}$$

According to above w_i, the opacity value except the last band corresponding to the sample point P_i can be calculated as

$$\alpha_i = \begin{cases} g(\frac{f_i - b_{m,0}}{b_{m,1} - b_{m,0}}) A_m & f_i \in [b_{m,0}, b_{m,1}] \\ A_m & f_i \in [b_{m,1}, b_{m,2}] \\ \frac{[1 - g(\frac{f_i - b_{m,2}}{b_{m,3} - b_{m,2}})] A_m + g(\frac{f_i - b_{m+1,0}}{b_{m+1,1} - b_{m+1,0}}) A_{m+1}}{A_m + A_{m+1}} & f_i \in [b_{m,2}, b_{m,3}] \end{cases} \tag{2}$$

where $g(t)$ is the cubic function of the value in $[0, 1]$, $g(t) = t^2(3 - 3t)$.

For the last band its opacity is calculated as below

$$\alpha_i = \begin{cases} g(\frac{f_i - b_{m,0}}{b_{m,1} - b_{m,0}}) A_m & f_i \in [b_{m,0}, b_{m,1}] \\ A_m & f_i \in [b_{m,1}, b_{m,2}] \\ [1 - g(\frac{f_i - b_{m,0}}{b_{m,1} - b_{m,0}})] A_m & f_i \in [b_{m,2}, b_{m,3}] \end{cases} \tag{3}$$

The color $c_i = (r_i, g_i, b_i)$ of P_i can be got from its above α_i and the maximum color T_m of this m^{th} layer, so we can get accumulated value of its opacity and color according to conventional ray-casting algorithm by

$$\begin{cases} c_i^* = c_{i-1}^* + (1 - \alpha_{i-1}^*) \alpha_i c_i \\ \alpha_i^* = \alpha_{i-1}^* + (1 - \alpha_{i-1}^*) \alpha_i \end{cases} \tag{4}$$

where c_i^* and α_i^* are the accumulated opacity and color corresponding to one viewing ray through the pixels into the field volume implemented by one thread in CUDA.

3.2 Visualization of MRI Volume Data

Compared with the visualization of CT, the visualization of MRI is more complicated. Before the NITFI files are converted into RAW files, the brain tissue should be segmented from the whole dataset. Finally, human brain visualization of MRI data is performed.

Step 1: separating tissue

First, the human brain is extracted by using the BET (Brain Extraction Tool)[1] toolkit developed. And then the human brain is automatically extracted from the entire data set.The BET packet operates segmentation based on the active contour model and then removes the non-brain tissue from the head image.

Secondly, perform image segmentation and tissue separation. FAST method is used to spatially normalize the extracted brain, which divides the 3D image into different types of tissue. For example, MRI body data is divided into cerebrospinal fluid, gray matter and white matter, then the spatial intensity is corrected. Since some tissue will overlap in density intervals, we use linear transformation to map the three kinds of tissue to non-coinciding density intervals.

Finally, perform MRI image fusion. The center of gravity of the obtained three tissue is taken as the origin of the brain's center of gravity, and the r units are transposed to the three directions (x, y, z) respectively, then each tissue is filled with a deformable surface model. Ultimately, the three kinds of local brain tissue are combined to obtain the MRI volume data values of the entire brain. Each of the brain tissue has been separated. The final NIFTI data is input into the MIPAV for format conversion to get RAW data for display.

Step 2: MRI transfer function design

For MRI datasets, we illustrate it in Figure 2 in which one trapezoid expresses one band or layer for the segmented human brain MRI data. Each band has no overlapping region. There are three bands corresponding to CSF, the white matter and the grey matter.

Let $C_m (m = 1, 2, 3)$ as $C_m = [c_{m,0}, c_{m,1}, c_{m,2}, c_{m,3}]$. Because different bands are corresponding to different separated tissues, so C_m and C_{m+1} has no overlapping region. The opacity of P_i is defined by

$$\alpha_i = \begin{cases} g(\frac{f_i - c_{m,0}}{c_{m,1} - c_{m,0}}) A_m & f_i \in [c_{m,0}, c_{m,1}] \\ A_m & f_i \in [c_{m,1}, c_{m,2}] \\ [1 - g(\frac{f_i - c_{m,0}}{c_{m,1} - c_{m,0}})] A_m & f_i \in [c_{m,2}, c_{m,3}] \end{cases} \tag{5}$$

The color of P_i can be got from the color of C_m, $c_i = \alpha_i T_m$. We can get the accumulated opacity and color according to conventional ray-casting algorithm by the Eq. 4.

[1]http://poc.vl-e.nl/distribution/manual/fsl-3.2/bet/index.html

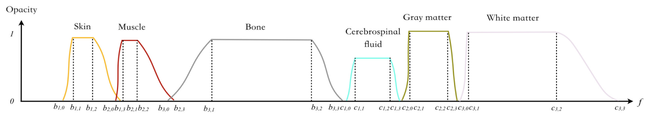


Figure 3: Hybrid transfer function

Table 1: Parameter presentation and its value of transfer function

Tissue	Parameter	MRI	CT	Hybrid
Skin	$[b_{1,0}, b_{1,3}]$	-	$[732, 1304]$	$[732, 1304]$
Muscle	$[b_{2,0}, b_{2,3}]$	-	$[1144, 1739]$	$[1144, 1739]$
Bone	$[b_{3,0}, b_{3,3}]$	-	$[1487, 3271]$	$[1487, 3271]$
Cerebrospinal fluid	$[c_{1,0}, c_{1,3}]$	$[1, 566]$	-	$[3267, 3837]$
Grey matter	$[c_{2,0}, c_{2,3}]$	$[570, 1108]$	-	$[3837, 4407]$
White matter	$[c_{3,0}, c_{3,3}]$	$[1117, 2835]$	-	$[4407, 6125]$

3.3 Three-Dimensional Fusion

After successful separation of MRI data, we start fusion of MRI and CT data. We select the same patient who performed CT and MRI scans at one visit. Through unifying data size, fusing data, separating heterogeneous data, mixing transfer functions, and CUDA-based GPU ray-casting volume rendering, we realize the three-dimensional fusion. The specific process is described as follows:

(1) Unify the volume data scale Usually the size of CT and MRI is inconsistent, so we can make them consistent by interpolation. In our method, a new pixel is inserted between its two neighboring pixels with their average value. Taking $512 \times 512 \times 23$ for CT and $256 \times 256 \times 23$ for MRI as an example, we doubled the data of the MRI in X and Y directions by inserting new pixels whose scalar values is obtained by averaging its two neighborhoods.

(2) Volume Data Fusion

Although the type and format of the two heterogeneous data are not the same, they store the same essential information, that is, the scalar values. For data fusion, the MRI tissue is filled in CT blank part where its value is 0 in the middle.

Suppose $\mathrm{vol}(i,j,k)$ is the value at position (x,y,z), and $h(\mathrm{vol}(i,j,k))$ is the fused value at the same position. $g(vol(i,j,k))$ is the value of CT and $h(\mathrm{vol}(i,j,k))$ is the value of MRI at (x,y,z). Then value of fused volume data is expressed as follows

$$f(\mathrm{vol}(i,j,k)) = \begin{cases} h(\mathrm{vol}(i,j,k)) & if\ g(\mathrm{vol}(i,j,k)) = 0 \\ g(\mathrm{vol}(i,j,k)) & else \end{cases} \tag{6}$$

(3) Separating CT and MRI data

The fused volume data contains two types of volume data. Because the voxel values have its own meanings at its coordinate systems for CT and MRI. If placed in the same coordinate system, they conflict. To solve this problem, a separation method based on volume data values translation for some tissue is proposed. The data values of MRI tissues are differentiated from CT by

$$f(\mathrm{vol}(i,j,k)) = h(\mathrm{vol}(i,j,k)) + max(g(\bullet)) \quad if\ \mathrm{vol}(i,j,k) \in MRI \tag{7}$$

where $max(g(\bullet))$ is the maximum value of the CT.

(4) Hybrid transfer function

After obtaining the transfer function of CT and MRI described as Figure 1 and Figure 2, we translate the MRI transfer function to right of the CT transfer function as a whole and get a hybrid one(shown in Figure 3). Determine the demarcation point between MRI and CT, ie. $max(g(\bullet))$ in Eq. 7. Before this point, the area corresponds to CT tissue; after it corresponds to MRI tissue. The corresponding values for different tissues are shown in Table 1.

(5) CUDA-based ray-casting volume rendering

The framework of CUDA-based ray-casting algorithm is shown in Figure 4. Firstly, after fusion volume data and hybrid transfer function are transferred to GPU texture buffer, it needs to determine the thread index in CUDA, and then tests the intersection between

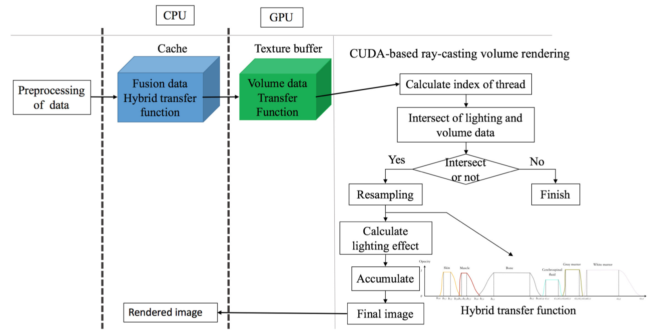


Figure 4: CUDA-based ray-casting volume rendering

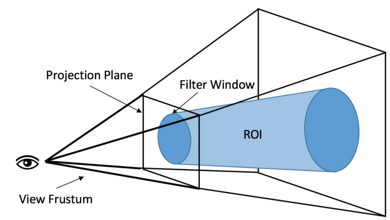


Figure 5: Diagram of layer filter

the viewing ray and the volume. If they intersect, resampling is done in the volume. Before accumulating each sample point, we need to decide which heterogeneous data the current sample belongs to and obtain its opacity as well as the color according to the hybrid transfer function. Then it accumulates the color and stops as soon as the accumulated opacity exceeds a certain threshold, then updates both the frame and depth buffer. Finally, it gets the color value of each pixel on the image and write the resulting value into the frame buffer to achieve the image display.

3.4 Layered Display

To facilitate the display of inner tissue of the brain, we define a layer filter and divide the volume data set into two parts: ROI and Non-interest areas. The three-dimensional region of interest is described by the shaded portion in Figure 5, The ROI is the intersection of the frustum based on projection plane and the entire volume dataset. The opacity is not 0 of the selected layer, while the opacity of the other layers is set to 0. Non-interest areas are then drawn by traditional GPU light transmission volume rendering.

4 Experiment And Discussion

4.1 Data Collection

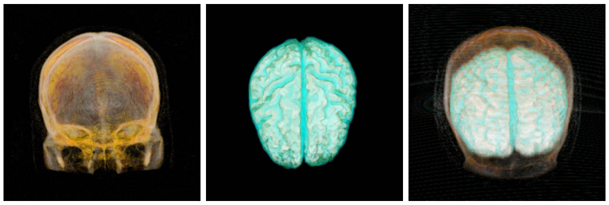
Our CT and MRI data is from Beijing Tiantan Hospital affiliated to Capital Medical University. The patients were examined CT and MRI at the same time. We obtain four patients CT and MRI data, 2 males and 2 females, aged 27 to 70 years, with 53.5 in average. CT and MRI scans were completed within 6 days by a Seimens. All data is 16-bit, DICOM (Digital Imaging and Communications in Medicine) format with a total size of 2.16GB, whose imaging content is the scanning result under different form positions.

4.2 Data Preprocessing

Preprocessing includes data formats conversion and data filtering. We use dcm2nii.exe[2] and mipav.bat[3] to converts DICOM format to RAW format. The criteria of files for visualization are following:

[2]https://www.nitrc.org/plugins/mwiki/index.php/dcm2nii:MainPage

[3]https://mipav.cit.nih.gov/



(a) CT (b) MRI (c) Fused image

Figure 6: The images of CT, MRI and the fused image

(1) Proper scanned position. The scan form must contain a complete skull without other redundant information (like the shoulder), otherwise it leads to information mismatch or adds extra burden to tissue.

(2) Complete scanned image. They must include the entire head or brain and have no large-scale information loss in any direction. Especially, they have the integrity of the top and bottom information.

(3) High scanned accuracy and enough layers. The accuracy and layer number together determine the clarity of the visualization.

Part of people A's CT data is used for single-source CT visualization with $512 \times 512 \times 28$ volume data scan layers and $0.4492mm \times 0.4492mm \times 0.5000mm$ accuracy. These of his MRI data used for MRI visualization is $256 \times 256 \times 23$ and $0.9375mm \times 0.9375mm \times 5.9998mm$. Then fuse these CT and MRI. Since the two scan volumes in the X and Y axes are similar in size, to unify the fusion volume data specifications, the MRI data is interpolated in the X-axis and Y-axis directions to expand it to 512×512 and retains small precision on the high Z-axis. The final fusion data is $512 \times 512 \times 23$ with $0.4492mm \times 0.4492mm \times 0.5000mm$ accuracy.

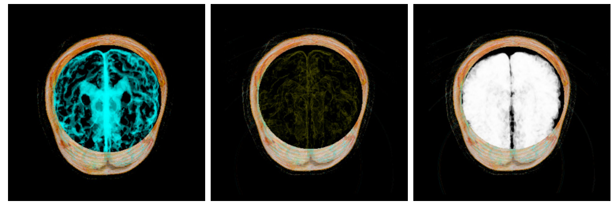
4.3 Experiments and Results

We have implemented our algorithm with Intel(R) Core(TM) i5-4570 CPU @ 3.20GHz equipped with 16GB of RAM on Windows 7 using OpenGL and CUDA 3.0. The graphics card is NVIDIA GeForce GTX 760 with 4GB of RAM memory. The system is written in C++ with SDK V3.0 provided by Leap Corporation and CUDA parallel architecture for accelerating calculation when real-time rendering with an interactive average frame rate of 150 fps.

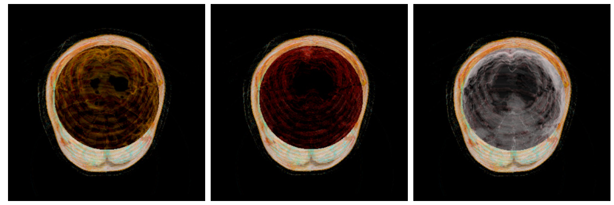
We achieve reconstruction of the human brain. Figure 6(a) and Figure 6(b) shows CT and MRI results separately, where the outline of skull such as eyes and the brain sulcus can be seen. In Figure 6(c), it can be clearly seen that the wrapped cerebrospinal fluid, gray matter, and white matter of MRI with a series of outer shell tissues such as skin, bone and cartilage and bone. From this specific people data, we conclude that there are no obvious intracranial lesions. Through our methods, both CT and MRI data can be successfully fused, and we can display the different layers of two heterogeneous data using the hybrid transfer function as shown in Figure 7.

5 Conclusion

Our work is to propose a 3D fusion method ,which is different from the traditional 2D fusion. We firstly realize CT and MRI volume visualization with our trapezoidal transfer function respectively. After interpolation for unified data scale and separating heterogeneous data, we fill MRI data into CT where its volume value is 0 and get fused volume data. Through the CUDA ray-casting volume rendering based on the hybrid transfer function, we display a high-quality brain anatomy quickly. These data are the hospital's real-world diagnosis data. The idea of separating heterogeneous data and integrating transfer functions can be applied on other data sources. Future works include extending our algorithm to two more types of heterogeneous sources.



(a) Cerebrospinal fluid (b) Gray matter (c) White matter



(d) Skin (e) Muscle (f) Bone

Figure 7: Six tissues of result fused-image

Due to the limited accuracy of the data obtained this time, the CT display has a ring fault, which can be circumvented by increasing the data accuracy. Our future works also include extending our algorithm to two more types of heterogeneous sources.

Acknowledgments

This work was supported by the Strategic Priority Research Program of the Chinese Academy of Sciences (Grant No.XD-B02030300), and National Social Science Foundation of China in 2015 (BCA150050).

References

[1] R. Bramon, I. Boada, A. Bardera, J. Rodriguez, M. Feixas, J. Puig, and M. Sbert. Multimodal data fusion based on mutual information. *IEEE Transactions on Visualization and Computer Graphics*, 18(9):1574–1587, 2012.

[2] R. Bramon, M. Ruiz, A. Bardera, I. Boada, M. Feixas, and M. Sbert. Information theory-based automatic multimodal transfer function design. *biomedical and health informatics*, 17(4):870–880, 2013.

[3] H. Guo and X. Yuan. Survey on transfer functions in volume visualization. *Journal of Computer-Aided Design and Computer Graphics*, (10):1249–1258, 11 2012.

[4] L. Kuhne, J. Giesen, Z. Zhang, S. Ha, and K. Mueller. A data-driven approach to hue-preserving color-blending. *IEEE Transactions on Visualization and Computer Graphics*, 18(12):2122–2129, 2012.

[5] M. Levoy. Display of surfaces from volume data. *IEEE Computer Graphics and Applications*, 8(3):29–37, 1988.

[6] X. Liao and W. Guo. Pet/ct three-dimensional fusion algorithm based on gray difference. *Science Technology and Engineering*, (14):4066–4069, 7 2013.

[7] Y. Luo. Distance-based focus + context models for exploring large volumetric medical datasets. *Computing in Science and Engineering*, 14(5):63–71, 2012.

[8] M. Seemann, J. Beltle, M. Heuschmid, H. Lwenheim, H. Graf, and C. Claussen. Image fusion of ct and mri for the visualization of the auditory and vestibular system. *European journal of medical research*, (9):47–55, 2 2005.

[9] R. M. Taylor. Visualizing multiple fields on the same surface. *IEEE Computer Graphics and Applications*, 22(3):6–10, 2002.

[10] Q. Wang, Y. Tao, Z. Zhou, Z. Ding, and H. Lin. Semantic lens: a visualization and inspection tool for multi-volume data. *Journal of Computer-Aided Design and Computer Graphics*, (9):1675–1685, 10 2015.

[11] C. Zhang. Research on the theory of data visualization in the age of large data. *Beauty and Times*, (1):76–77, 4 2017.