Hardware-accelerated 3D multimodal visualization techniques for tumor resection in neurosurgery

Abstract CARS
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Date: 08-01-2008

Purpose

Brain tumor resections, especially when the tumor is deeply embedded in the brain, are high-risk procedures. The difficulty lies not only in removal of the tumor itself but also in the process of gaining access to it without unnecessarily damaging surrounding tissues and brain structures. To highlight these tissues and structures different image modalities are needed such as CT for bone structures, MRI for brain matter, CT/MRI angiography for blood vessels, fMRI for cortical activation regions and diffusion tensor imaging (DTI) for fiber tracts. Furthermore, to correctly assess the spatial relation between these structures it is important to visualize and interact real-time with the image data in 3D. For this purpose, we propose a new rendering algorithm based on Graphics Processing Unit (GPU)-accelerated raycasting and depth peeling to visualize multiple volumetric datasets intersected with an arbitrary number of opaque or semi-transparent geometric models. Such models may represent foreign objects relevant for surgical applications such as virtual surgical tools, 3D pointers, measuring tools or grid lines for spatial orientation.

Methods

Image datasets acquired for a given patient commonly are spatially overlapping but not spatially aligned. To deal with this, most implementations for multi-volume visualization resample each dataset onto a larger high-resolution grid such that they share a common coordinate system, thereby simplifying simultaneous sampling. This approach however requires a time-consuming preprocessing step and introduces numerical inaccuracies due to double interpolation of the data, especially for low resolutions. Furthermore, resampling low-resolution data to a high-resolution significantly increases memory consumption.

Our rendering algorithm does not resample the data and renders each dataset in its own coordinate system and resolution. This preserves image quality, keeps memory usage to a minimum and allows interactive movement of volumes with respect to each other. This may be useful for visualization and interaction during the dataset registration process. The algorithm uses direct volume rendering (DVR) based on GPU-accelerated raycasting (see Figure 1A for a single volume) where samples are taken from the volume along virtual rays to produce the final output image.

<Insert Figure 1 here>
Figure1: (A) raycasting a singe volume. (B) multi-volume depth peeling: raycasting between each pair of depth layers (here 2nd and 3rd layer).

For multi-volume rendering each volume is positioned and oriented in space. To independently sample each volume, the sample position has to be known with respect to the volume's coordinate system. To prevent the need for checking volume positions at every sample step along the ray, we apply a method called <I>depth peeling</I> to subdivide the volume collection into regions bounded by so-called <I>depth layers</I>. For each region, the sample position with respect to each volume has to be checked <I>only once</I>. A scene of two volumes consists of four depth layers, two of which are highlighted in Figure 1B. Each region is rendered in a separate pass by performing raycasting between each pair of depth layers (see Figure 1B). By storing the raycasting result (the pixel colors) of each pass in a temporary buffer and passing this buffer to the next render pass, we can completely render the volume collection.

Results

We evaluated our visualization algorithm in two clinical cases, a healthy volunteer and a patient with a brain metastasis originating from a lung carcinoma. Table 1 lists the modality parameters and dataset properties of both cases.

<Insert Table 1 here>
Table 1: Modality parameters and dataset properties.

Figure 2 shows example visualizations of the two clinical cases we evaluated. Visible are the axial views of the brain (extracted by fitting an ellipsoid clipping object around the brain and cutting away everything on the outside). The healthy volunteer example shows anatomical context (T1-weighted MRI), cortical activations from finger tapping (fMRI) and the cortico-spinal tract (DTI) rendered as geometric tube structures. The tumor patient example shows anatomical context (T2-weighted MRI) and cortical activations from feet movements (fMRI). Even though perfectly visible on 2D contrast-enhanced MRI images, in the 3D visualization the tumor was difficult to distinguish from the surrounding brain tissue using DVR parameters only. For this reason we segmented the tumor using a third-party tool and imported it as a separate MRI volume.

<Insert Figure 2 here>
Figure 2: (A) Healthy volunteer T1-weighted MRI, fMRI, DTI (3 Tesla). (B) Tumor patient T2-weighted MRI, fMRI (1.5 Tesla).

Conclusions

We developed a new rendering algorithm based on GPU-accelerated raycasting and depth peeling to allow visualization of an arbitrary number of non-aligned volumetric datasets without the need for resampling them onto a common grid. The volumes can be interactively moved around and intersected with an arbitrary number of opaque or semi-transparent geometric models. A single such model, if convex, can serve as a clipping tool.The algorithm has been integrated into a flexible software framework and tested with two clinical cases, consisting of different combinations of T1/T2-weighted MRI, fMRI and a geometric tube representation of DTI fiber tracts.

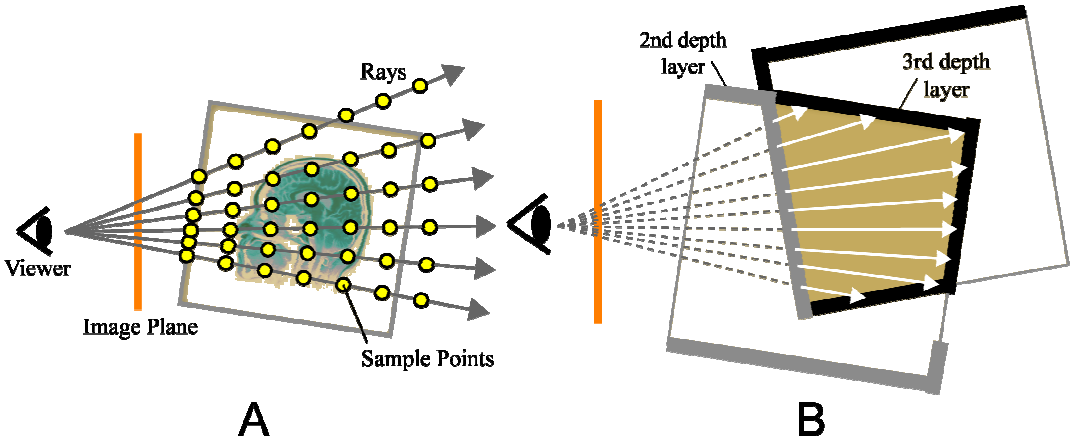

FIGURE 1

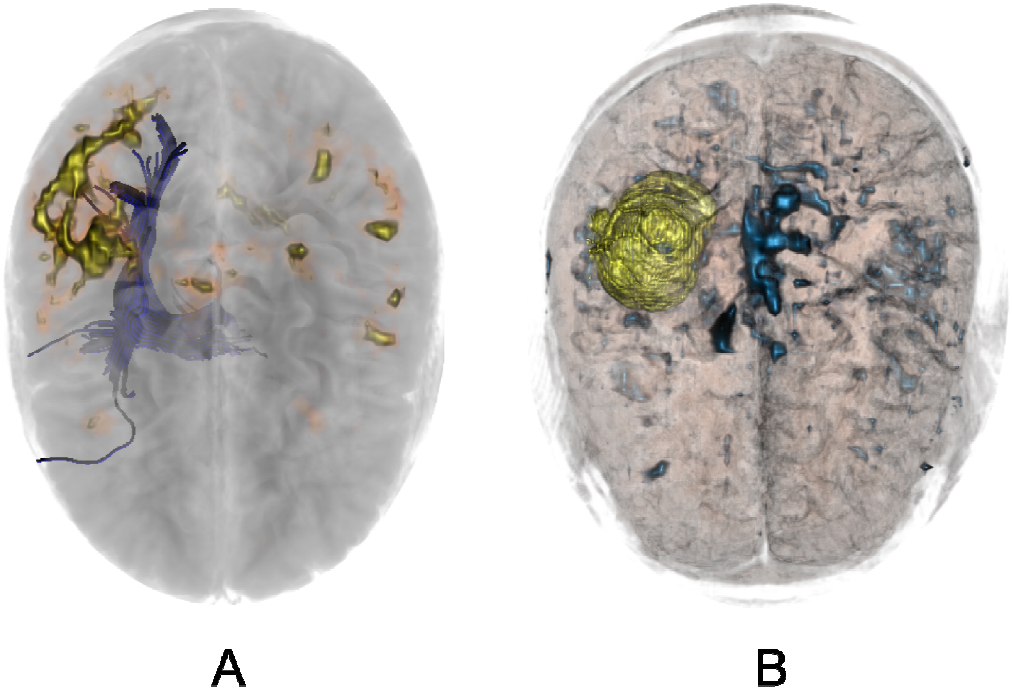

FIGURE 2

Case	Structure/region	Modality	Resolution
Healthy volunteer	Anatomical context Cortical activations Fiber tracts	T1-weighted MRI fMRI DTI	256x256x200 64x64x64 Geometry
Tumor patient	Anatomical context Tumor Cortical activations	T2-weighted MRI T1-weighted MRI fMRI	256x256x180 64x64x41 128x128x128

TABLE 1