4D Space-Time Techniques: A Medical Imaging Case Study

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Abstract

We present the problem of visualizing time-varying medical data. Two medical imaging modalities are considered - MRI and dynamic SPECT. For each modality, we examine several derived scalar and vector quantities such as the change in intensity over time, the spatial gradient, and the change of the gradient over time. We compare several methods for presenting the data, including iso-surfaces, direct volume rendering, and vector visualization using glyphs. These techniques may provide more information and context than methods currently used in practice; thus it is easier to discover temporal changes and abnormalities in a data set.

Keywords: J.3 *health, I.3.7 display algorithms, I.3.3 animations*

Other Keywords: *4D visualization, MRI, dynamic SPECT, direct volume rendering, isosurface, glyph*

1. Introduction

Time-varying data is commonly used in medicine. Physicians frequently follow progression of disease and make treatment decisions based on periodic scans of a patient. For example, multiple sclerosis (MS) is a degenerative disease characterized by scar tissue that appears as bright lesions in spin-spin (T2) and proton density (PD) Magnetic Resonance Imaging (MRI) brain scans. Thus, physicians use sequences of MRI images to diagnose MS and track disease progression over several months or years.

Similarly, in nuclear medicine, function of a particular organ may be analyzed by measuring the temporal change of the spatial distribution of radioactive tracer bound to molecules with known biological function. These tracers are designed to concentrate at the organ of interest; hence, they visualize organ function.

At present, nuclear medicine dynamic studies are generally limited to planar single photon imaging, which gives poor localization and cannot be accurately corrected for attenuation effects. To address these issues, we use the new dynamic SPECT (dSPECT) method [5][8] that allows us to obtain quantitative information about kinetic processes in the body, from the data acquired using a standard clinical acquisition protocol. The result of dSPECT reconstruction, which includes attenuation and resolution recovery corrections, is a 4D data set composed of a time-series of 3D SPECT images. There are currently no methods to display and analyze this type of data.

We specifically focus on kidney studies because the flow is easy to visualize, as illustrated in Fig. 1. The radioactive tracers in the bloodstream wash out in the kidneys and collect in the bladder. We expect the activity to come down the aorta abdominalis (1) and flow into the aorta renalis (2). Here the activity will be distributed over the kidney cortex (3) and then pass the medulla (4) to collect in the renalis pelvis (5). Then. approximately every 30 seconds, a small amount of urine containing the activity flows down the ureter (6) to collect in the bladder (7).

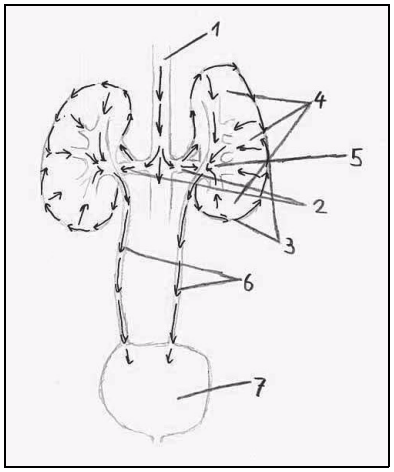

FIGURE 1. Hand-drawn diagram of flow through the kidneys

Currently, radiologists interested in temporal information from some imaging modality must manually compare 2D images of the same patient, acquired at different times, on a slice-by-slice basis. Such comparisons are difficult and time consuming; thus, not frequently done, particularly when the volumes are not aligned or the quantity of images is very large. Furthermore, 2D slices provide no information about 3D structure or rates of change.

We believe that visualizing time series data in 3D using flow visualization techniques could provide new insight into the information contained in the data and lead to improved diagnosis or treatment. For this reason, we are exploring techniques for visualizing time-varying medical data, and analyzing their effectiveness for MRI and dSPECT.

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2. Previous Work

Methods to visualize volume data, primarily isosurface extraction [3][13][17] and direct volume rendering [16][3][17] have been extensively studied. Recent developments have produced efficient data structures and algorithms for rendering time-series volume data [1][7]. However, we are unaware of other work extending volume visualization techniques to 4D medical data sets.

By contrast, several 4D visualization techniques have been developed for flow visualization. These include glyphs, streamlines/timelines, texture advection, and line integral convolution [4][6][17].

Initial investigation into the problems of visualizing dSPECT and MRI time series data can be found in [15] and [18]. In addition, a few recent attempts have been made to apply flow visualization ideas to tensor data from diffusion-weighted magnetic resonance imaging. Kindlmann and Weinstein use volume rendering with novel methods for assigning colour and opacity values [10]. Laidlaw et al. use oriented "brush strokes" to visualize tensors, in a manner similar to glyph visualization or texture advection [12]. Zhang et al. [20] visualize tensors with the aid of stream tubes and stream surfaces. These techniques are effective for tensor data in particular applications, but have not been applied generally to vector visualization in medical data sets.

3. Approach

Since methods to visualize 4D fluid flow have been extensively studied, we felt these techniques would be a good starting point for our investigation. Our approach is to look at techniques developed for other applications and evaluate how and when they work for 4D medical data. Results of this evaluation will be used to develop new techniques in places where existing methods are inadequate.

4. Data Preparation and Preprocessing

Our MRI data consisted of 11 time steps (each one month apart) with dimensions 256 x 256 x 22 slices. Brain tissue and MS lesions were segmented from each slice using methods given in [2] and [11]. Registration was necessary since a slight change in head position could produce misregistration artefacts as large as real lesion changes [9]. Registration was accomplished using Automated Image Registration [19]. Parameters for registration and additional preprocessing details can be found in [18].

Dynamic SPECT data was acquired with a Siemens e.cam camera with two heads, 90 degrees apart, and with single 180 degrees rotation. The data was reconstructed using the dSPECT reconstruction, which yields 4D dynamic SPECT data. The matrix size of the reconstructed spatial image was 35 x 50 x 80 (with voxel size 4.7 mm^3). Total acquisition time was 12 minutes and 64 temporal frames were recorded. Attenuation and resolution recovery correction were used in reconstruction [5][8].

4.1 Vector Extraction

Before visualizing the change over time in a data set, we needed to understand what changes we wanted to see.

For dynamic SPECT, we had clear expectations of how activity should flow, so we could use a flow simulation model to calculate flow vectors. First, a 3D region of interest mask was used to classify each voxel to a particular tissue. Using voxel classification and position, an average flow direction and velocity for the voxel were computed. These vectors were fit to the real data in a second iteration step. To compute the final flow direction and velocity we assumed a homogeneous flow field. For most tissues the vectors are nearly constant over time; only the ureter has a periodic flow with a maximum around every 30 seconds. The flow direction and speed were computed using the initial flow vector, the flow direction of neighbouring voxels, and the rate of change of the voxel time-activity-curve. The resulting vectors represented the flow of the radioactively labeled molecules.

For MRI, expectations of how intensities would change over time were less clear, and anatomical masks for every tissue type were unavailable. Hence, we defined the following quantities:

Quantity	Description
I(x,y,z,t)	Intensity in the volume, a function of 3 spatial dimensions and 1 time dimension (scalar value)
dI/dt	Change in I over time, calculated by forward differencing (positive or negative scalar value)
G(x,y,z,t)	Spatial gradient at each point, calculated by central differencing (vector)
dG/dt	Change in gradient over time, calculated by forward differencing (vector)

Note that dG/dt (the change in gradient over time) is equivalent to the spatial change of dI/dt; thus, this quantity may provide a good indication of spatial movement over time, while dI/dt should give us an idea of how intensities are changing temporally. However, these vectors are merely a starting point for exploration into the data set; their physiological meaning is unclear and it is not obvious that they will provide interesting or useful information.

4.2 Visualization

We explored several visualization methods: isosurfaces, volume rendering, and glyphs, to compare their effectiveness for two imaging modalities and applications. All of our methods were implemented with the aid of the Visualization Tool Kit [17]. In addition, we used IDL [14] for some dSPECT visualizations.

4.2.1 Isosurfaces

To illustrate spatial movement and volume changes over time, semi-transparent isosurfaces from different time frames were displayed together and coloured by time information. Isovalues were generally the same for all time frames, but this could be modified by the user interactively. Additional isosurfaces (of the brain for MRI and the kidneys for dSPECT) provided context and orientation cues. Furthermore, users could interactively rotate, zoom, and pan the display, change isovalues and opacities for each time frame, and step through time as an interactive animation.

For MRI, we had the advantage of segmented brain and lesion data. Thus, a very low isovalue could be selected to easily separate lesion or brain tissue from the background in the segmented data sets. For dSPECT, isovalues were found by trial and error, with the kidney having a lower isovalue than regions with high activity.

4.2.2 Direct Volume Rendering

We visualized intensity (I) and change in intensity over time (dI/dt) using direct volume rendering. For dSPECT intensity data (I), the transfer function was designed to highlight high intensity regions.

For dI/dt, it was designed to indicate magnitude and direction of the change at each voxel.User interaction and surface models of the brain or kidneys were incorporated similar to the isosurface program described above. In addition, animations showing cumulative changes over time could be generated.

In the segmented MRI data, non-lesion material had a value of zero; hence, size changes appeared as large intensity changes. This effect could easily be removed by using unsegmented data to calculate dI/dt; however, the effect is not necessarily undesirable since it highlights changes in shape, which may be important.

4.2.3 Glyphs

Glyphs were used to visualize flow vectors for dSPECT, and dI/dt, G, and dG/dt for MRI. In many cases, isosurfaces of the data were included for orientation purposes (i.e. brain and lesions for MRI and kidneys for dSPECT). Two types of glyphs were utilized: 3D glyphs with a cone geometry and hedgehogs with a line geometry.

Generally, glyph colour and length represented vector magnitude, while orientation illustrated flow direction. However, slight modifications were made for the 1D dI/dt vectors. In this case, colour represented whether the change was negative or positive, and length indicated the magnitude of the change. Two different approaches were taken regarding glyph orientation. In the first, glyphs were designed to point in exact opposite directions for negative and positive change. We believed that redundant mapping of colour and direction to change direction would emphasize this feature in the data. In the second approach, glyphs pointed in the direction of the surface normal, with the idea that lesion areas may be thought of as “growing outwards”or “shrinking inwards” in the direction of the surface normal.

5. Results and Discussion

5.1 Isosurfaces

Fig. 2 (see colour plate) illustrates results of isosurface extraction. A colour scale is used to encode time.

For MRI (Fig. 2 (a)), isosurface displays provide a 3D impression of how lesions are oriented within the brain, the amount of volume they occupy, and where large and small lesions are located. Since any number of data sets can be displayed at once, it is possible to see that some older lesions disappeared (blue areas) and some new lesions appeared (red areas).

In our dSPECT kidney study, we are interested in how fast the activity washes out and which areas contain the most activity. Fig. 2 (b) shows a shrinking iso-surface illustrating the washout process. The first iso-surface (shown in green), shows that most activity is contained in the cortex, while in the last one (blue), most activity is washed out and collected in the pelvis.

Note that because 3D objects are projected into two dimensions, colour combinations may be caused by isosurfaces lying behind one another rather than at exactly the same location. Interactive rotation of objects improves understanding of 3D orientation, contributing to the resolution of this problem. We also notice that increasing the number of isosurfaces causes complete occlusion of some objects. To address this, we developed tools to allow users to interactively change opacities and isovalues for individual contours.

Animations showing changes in isosurfaces allow all time steps to be viewed without occlusion. These animations can either be generated for a single viewpoint and viewed offline, or run interactively so the user can step back and forth through time frames and change parameters and viewing direction at any time.

5.2 Direct Volume Rendering

We use direct volume rendering to visualize scalar values I and dI/dt. For dSPECT, where there is a clear flow of activity, we found it more useful to visualize the intensity values and illustrate change over time using animation.The single focal point at the center of the activity makes it easy for viewers to follow the change in activity throughout the animation. Moreover, intensity values may be more natural to visualize than change in intensity.

Fig. 3 (b) and (c) show two frames from a direct volume rendered animation of dSPECT data. Areas with low activity appear green, while areas with high activity are coloured red. You can clearly see that in (b) most activity is contained in the kidney cortex and medulla. In (c), three time frames later, we can see that a lot of activity has washed out and collected in the pelvis.

By contrast, for MRI, we found that rendering intensities and displaying the time dimension using animation was not highly effective. For MS lesion data, animations showing intensity allow the user to see global changes (e.g. if many lesions in one area changed in a similar way). However, there is no clear focal point, and attentive search is required to identify the (more common) small, localized changes.

A direct volume rendered image of dI/dt changes in MS lesions is displayed in Fig. 3 (a). This figure illustrates that localized intensity changes occurred in the MS lesions. For example, the bluish spot in the middle represents an intensity drop, while several red and brown spots represent intensity increases.

5.3 Glyphs

For dSPECT, glyphs and hedgehogs are used to visualize flow of activity. Fig. 4 (c) shows the flow visualized using 3D glyphs. The cone geometry clearly shows flow direction; furthermore, glyph length and colour make it easy to see the speed of the washout.

In Fig. 4 (d), hedgehogs indicate flow towards the pelvis and down the ureter. Colour represents the concentration of activity; you can see that the concentration in the kidney cortex and medulla are higher than in the pelvis.

In an animation, we would see that most vectors remain the same in speed and direction. However, in the ureter, the flow direction would remain constant, but the velocity would change periodically, with a maximum approximately every 30 seconds.

Fig. 4 (a) and (b) show glyphs and hedgehogs for dG/dt vectors in MRI. As expected, no global pattern of flow can be seen. In (a), several glyphs point in a similar direction for a localized area near a lesion. This indicates a change in the lesion at that point. However, such patterns are much less frequent than we hoped, and require extensive searching by the user. In addition, context information is lost as the user zooms in to search for local patterns, so keeping track of the current position is difficult. A second, global view showing position may fix this problem.

In Fig. 5, glyphs are used to visualize dI/dt values from MRI. Here, global trends are easy to see, especially with glyph colouring. The user can then zoom into areas of interest to gain more detailed understanding of changes in that area.

A general problem with glyphs is that images tend to be cluttered. As a result, we are exploring other methods such as streamlines. Initial results are promising for dSPECT (see Fig. 6); however, we are encountering difficulties with the MRI data due to low image resolution and lack of a clear flow direction.

5.4 Challenges

We encountered several challenges worthy of mention. First, it is unclear which quantities are most informative. We experimented with some simple quantities, but have not validated these against any medical criteria. Further, we found the limited resolution in the slice dimension of our MRI data (22 slices) to be a problem. Rendering these data sets from a side viewpoint resulted in very blurry images. Interpolation to produce additional slices may reduce this problem, but would not remove the additional problem that some small lesions could be missed altogether due to partial volume effects. Increasing the number of slices during acquisition is not practical since this increases scan time such that patient motion becomes problematic.

6. Conclusions And Future Work

We have presented several methods for visualizing time varying medical image data. These techniques have the potential to compress large quantities of data into a single image, as well as provide new measures currently not used for diagnosis, such as rates of change. These techniques can provide more information and context than a slice by slice visualization could do; as a result, it is easier to discover temporal changes and abnormalities in a data set. Since gaining a short or long-term dynamic picture of a patient's physiology could help physicians understand disease progression, we believe tools such as ours could be of great use to physicians trying to formulate diagnoses or treatment plans.

Improved interaction and iterative development and evaluation of graphic interfaces will improve effectiveness of our visualizations. Particular attention should be paid to perceptual issues related to design. Correlation of new measures, such as velocity or rates of change, with existing disease measures will be essential for their validation. Other future work includes optimizing the programs for speed, exploring new visualization techniques, and considering other imaging modalities and applications.

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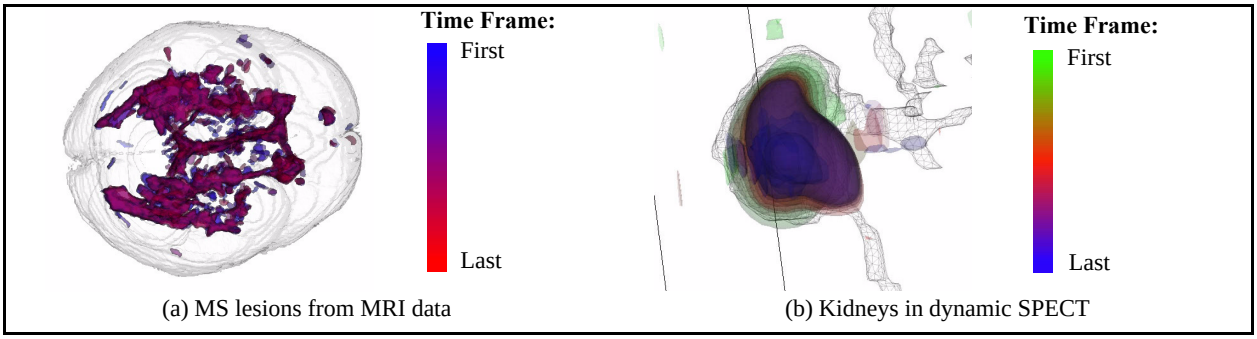
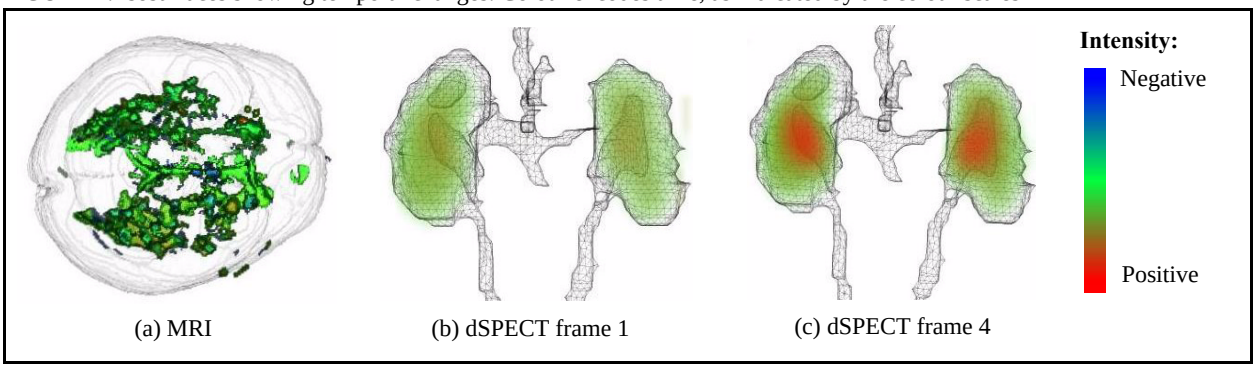


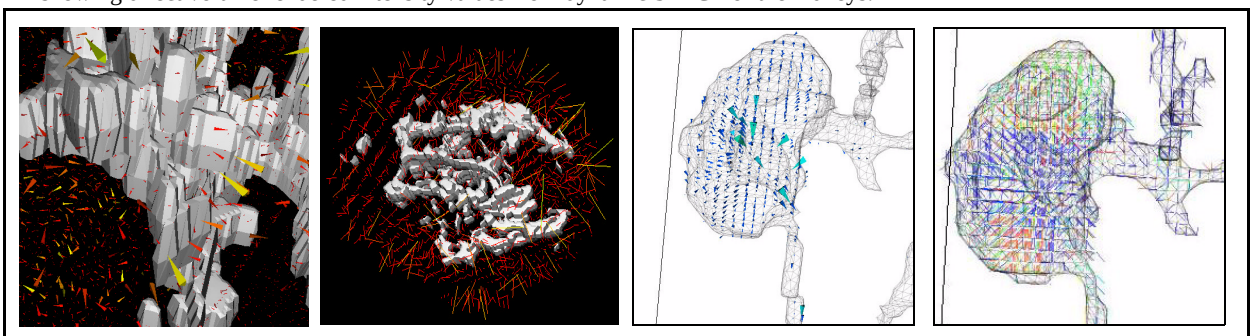
(a) MS lesions from MRI data (b) Kidneys in dynamic SPECT

FIGURE 2. Isosurfaces showing temporal changes. Colour encodes time, as indicated by the colour scales



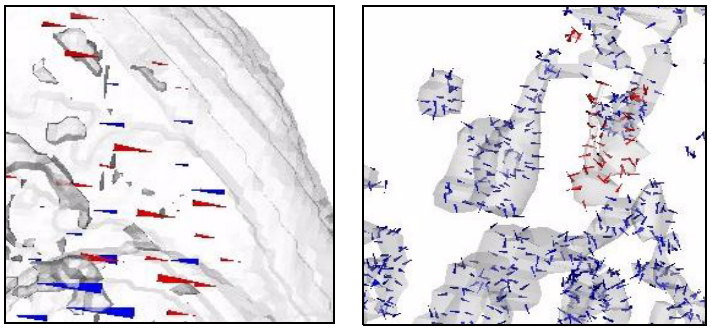
(a) MRI (b) dSPECT frame 1 (c) dSPECT frame 4

FIGURE 3. Direct volume rendering.(a) dI/dt values for MS lesions from MRI data. (b), (c) Two frames from an animation showing direct volume rendered intensity values from dynamic SPECT of the kidneys.



(a) dG/dt for MRI (b) dG/dt for MRI (c) Flow in dSPECT (d) Flow in dSPECT

FIGURE 4. Glyphs and hedgehogs. Glyph length indicates vector magnitude and orientation indicates vector direction. Color indicates vector magnitude (a, b, c) or amount of activity (d).



(a) (b)

FIGURE 5. Glyphs showing dI/dt values from MRI. Colour indicates vector direction (red = positive, blue = negative). (a) Glyphs point right for positive change and left for negative change (b) Glyphs point in the direction of the surface normal

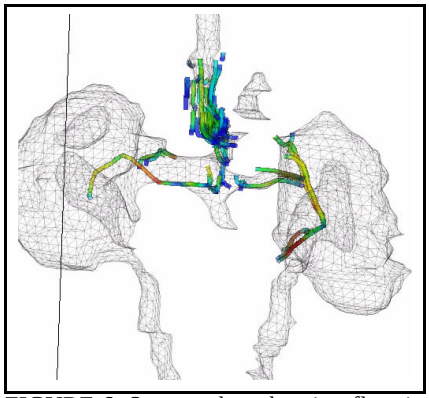


FIGURE 6. Streamtubes showing flow in dSPECT kidney data.