

Graphlets: A Method for Visualizing Dynamic Data

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1 Introduction

Dynamic contrast-enhanced MRI is often performed to characterize tissue by observing the passage of an agent injected into the bloodstream. MR images are acquired at regular intervals during a time period that begins prior to injection of the contrast agent, and extends through the agent's passage through the vasculature under study. The MRI signal observed during this time period can be transformed into a curve of contrast concentration over time [Ostergaard]. Parametric maps can be computed from the time-series and overlaid on an anatomical image for review by radiologists. Typical hemodynamic parameters include regional cerebral blood flow (rCBF), mean transit time (MTT), and regional Cerebral Blood Volume (rCBV). The shortcoming of this approach is that the parametric maps, although convenient, do not allow the clinician the opportunity to observe the full richness of the dynamic data.

2 Method

A new method for augmented visualization of dynamic data is presented in Figure 1. An acquired MRI slice is displayed side-by-side with a 2-D array of miniature graphs, referred to as graphlets. Each graphlet plots a curve that graphs signal intensity over time for a corresponding spatial location. The color of each graphlet's backdrop is determined from either the original MRI signal, or the computed parametric result. The user can conveniently navigate – selecting which region of the slice is rendered as graphlets – by using the mouse for real-time zooming and panning.

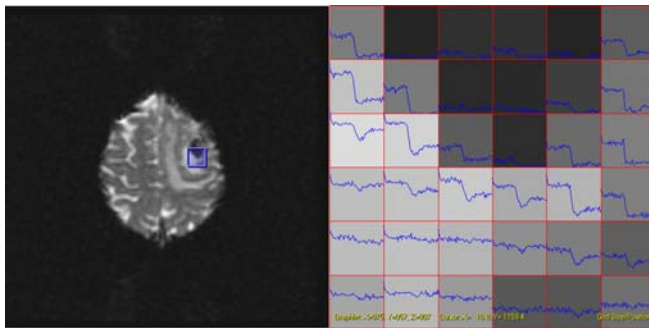


Figure 1: The portion of the image on the left that is contained within the blue box is rendered as graphlets in the image on the right. Each graphlet corresponds with a voxel in the image on the right.

Spatial locations can be defined as individual voxels or voxel groups computed based on the scaling theorem. Scale space is computed through a process of pyramiding that consists of smoothing the original MRI with a Gaussian kernel followed by downsampling, in order to avoid spurious artifacts. This allows the graphlets to be viewed at any of the 5 computed levels of scale space, as shown in Figure 2.

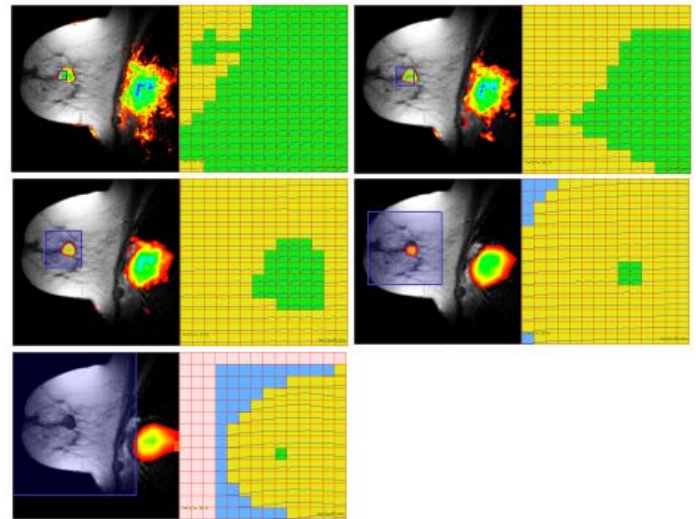


Figure 2: From left to right, and top to bottom, are graphlets from each of the 5 levels of scale space, ordered from fine to coarse. Each graphlet's backdrop is colored by tissue segmentations based on the parametric analysis (blue air, yellow breast, green tumor). Multi-scale graphlets allow the clinician to transition between “birds-eye” and detailed views of the data

The graphlets are augmented with cues, such as the lines and shading shown in Figure 3, that graphically display the intermediate results of quantitative analysis (statistics, slopes, areas). Now, these computed quantities can be visualized by clinicians to assist them with internalizing the full richness of the data. This empowers clinicians to combine the automatically quantified information with their own medical expertise.

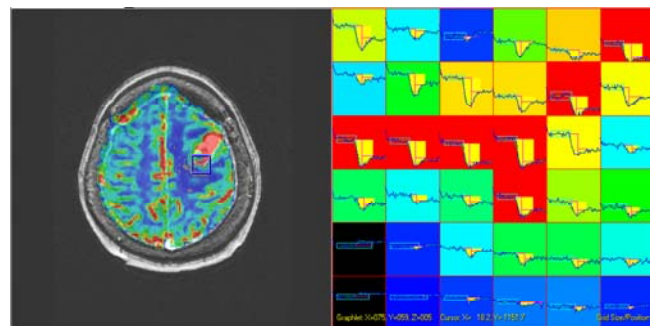


Figure 3: Left: A parametric map is overlaid with adjustable opacity on a gray, anatomical reference. Right: graphlets include visual cues that demonstrate the computed parametric quantities.

References

OSTERGAARD, L., WEISSKOFF, R.M., CHESLER, D.A., GYLDENSTED, C., ROSEN, B.R. HIGH RESOLUTION MEASUREMENT OF CEREBRAL BLOOD FLOW USING INTRAVASCULAR TRACER BOLUS PASSAGES, PART I: MATHEMATICAL APPROACH AND STATISTICAL ANALYSIS. *MAGN RESON MED* 1996; 36:715-725

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