Tissue Similarity Map of High Resolution Perfusion Weighted MR Imaging of the Brain

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Introduction: Dynamic susceptibility contrast (DSC) perfusion-weighted MRI (PWI) is a technique that allows assessment of brain physiology particularly for cerebrovascular disease, tumor imaging, aging, etc. However, the accurate quantification of hemodynamics is limited by the spatial resolution [1], arterial input function (AIF) determination [2], nonlinear ΔR_2* effects and enhanced noise in estimating the concentration of the contrast agent [3]. Our new approach is to investigate the differences in perfusion between tissues directly from their signal intensity time course characteristics s(t) rather than indirectly through the concentration time curve c(t). It avoids the need for defining AIF as well. The purpose of this study is to use high resolution PWI (1 x 1 x 4 mm^3) to create a tissue similarity map (TSM) to demonstrate the relatedness of one pixel's signal to the next, similar to the connectivity concept used in functional brain imaging.

Materials and Methods: All MR imaging was done on a 1.5 T scanner (Siemens, Sonata) with an 8-channel head coil. Parallel imaging was used with GRAPPA and an acceleration factor of 2. PWI was performed with a gradient echo EPI sequence (TR/TE: 2200/98 ms; FA: 60 degrees; FOV: 256mm x 256 mm; the acquisition matrix: 256 x 256 but interpolated to 512 x 512; 50 measurements were acquired over 110 seconds). The amount of contrast agent (Magnevist) injected was 0.1mmol/kg of body weight. Analysis of the PWI data was done using our home built SPIN (signal processing in NMR) software (Detroit, Michigan). Hemodynamics (MTT, CBF and CBV) were determined by deconvolving the tissue concentration–time curve with the arterial input function (AIF) using singular value decomposition (SVD) [4]. In order to create the TSM, a reference region-of-interest (ROI) was selected and used as a reference input function $s_{ref}(t)$. Then a mean squared error (MSE) of s(t) between the reference tissue and all other voxels over all measurements was obtained as follows:

$$MSE(\vec{r}) = \sum_{t=1}^{endpoint} (s(\vec{r},(t-\Delta ttp)) - s_{ref}(t))^2$$

where Δttp is the difference of time-to-peak (TTP) between the voxel and the reference ROI.

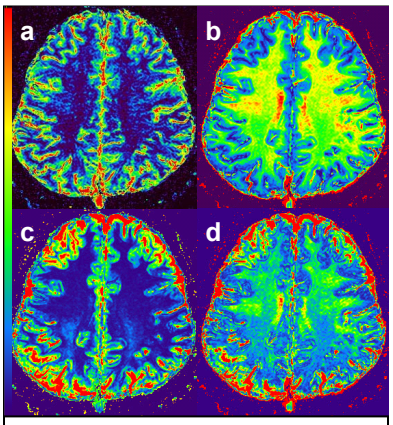

Figure 1. High resolution PWI CBV map and tissue similarity maps (TSM)
a) CBV map
b) TSM-nulling blood vessel
c) TSM-nulling white matter
d) TSM-nulling grey matter

Results and Discussions: TSMs are successfully obtained from high resolution PWI data. Figure 1 shows a high resolution CBV map and TSMs nulling different tissues from a normal healthy volunteer. White matter, grey matter and blood vessel ROIs are selected. In Figure 1c white matter is chosen as the reference ROI, so all the voxels from white matter with the same signal intensity time behavior are suppressed because of the lower value of MSE. This image also demonstrates that most WM pixels all behave the same way. Unlike conventional PWI parameter maps calculated from c(t), the TSM only deals with the original s(t), so it is less noisy and easily used to study variations within and between tissues. The summation of MSE over all time points endows the TSM with a high signal-to-noise ratio (SNR). The high resolution approach we take now makes it possible to clearly distinguish GM from WM. Figure 2 shows the clinical application of TSM in a multiple sclerosis case. We try to eliminate the appearance of CSF in the TSM analysis. The axial FLAIR image (2b) shows many hyperintense MS lesions in the deep white matter. In the post-contrast T1 image (2a) only two hypointense lesions and one gadolinium-enhancing lesion can be found. However the high-resolution TSMs are able to pick out the affected lesions and other white matter regions that are probably affected by MS (see Figure 2d) that are not visible even in the FLAIR images. This affected WM area that appears to connect the lesions can be seen in Figure (2e) as light green and again connecting the lesions. In summary, tissue similarity maps may be a very useful means to reveal information about tissues otherwise difficult to see with conventional PWI processing approaches.

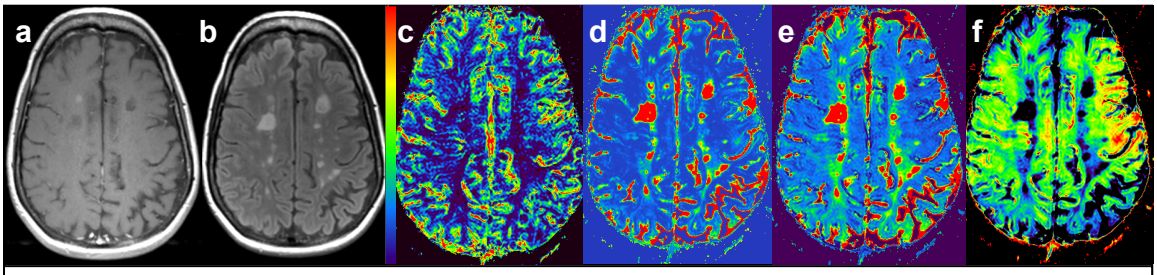

Figure 2. Clinical application of TSM in multiple sclerosis
a) T1-weighted imaging post-contrast; b) FLAIR; c) high resolution PWI-CBV map; d) TSM-nulling white matter;
e) TSM-nulling blood vessel; f) TSM-nulling MS lesion.

Conclusions: The combination of tissue similarity maps with high resolution PWI is a new means to more accurately reveal differences in perfusion characteristics between tissues and inter-tissue. It allows for much easier tissue segmentation. It may have immediate applications in stroke, tumor and multiple sclerosis studies where variations in the vasculature may be the key to fully diagnosing the hemodynamic status of the patient.

References:

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