Enhancing Image Contrast in Human Brain by Voxel Spread Function Method

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Purpose Gibbs ringing artifacts especially pronounced in the presence of magnetic field inhomogeneities [1] adversely affect different aspects of MRI images. In quantitative MRI when the goal is to quantify biological tissue parameters, they bias and often corrupt such measurements. The VSF (voxel spread function) method [1] provides a solid platform for correcting images and can be applied to a variety of quantitative gradient-echo-based MRI techniques. Elimination of Gibbs artifacts in VSF approach requires solution of high-rank matrix equation (VSF equation) and generally relies on certain approximations. Herein we propose a method for solution of VSF equation allowing for substantially improving visibility of sharp edges and apply it to demonstrate improved contrast of blood vessels in the human brain.

Methods VSF method relies on the solution of VSF equation $S_n(\mathrm{TE}) = \sum_m \Psi_{nm}(\mathrm{TE}) \cdot \sigma_m(\mathrm{TE})$, where $S_n(\mathrm{TE})$ is the measured MRI signal in voxel *n* at the gradient echo time TE, $\sigma_m(\mathrm{TE})$ is an ideal "non-contaminated" signal from the voxel *m* that would exist in the absence of Gibbs artifacts and magnetic field inhomogeneities, and the matrix $\Psi_{nm}(\mathrm{TE})$ defines signal leakage to voxel *n* from the neighboring voxels *m* (see definition in [1]). In [1] the VSF equation was solved using similarity approximation – an assumption that the ideal signal $\sigma_m(\mathrm{TE})$ from the voxel m can be approximated as $\sigma_m(\mathrm{TE}) = \sigma_n(\mathrm{TE}) \cdot |S_m(\mathrm{TE}_1)| / |S_n(\mathrm{TE}_1)|$ where TE_1 is the first gradient echo time. This approximation is justified if neighboring voxels belongs to "similar" tissues but it could lead to image artifacts at the boundaries between tissues with different MR properties where the MR signal can decay at neighboring voxels with different transverse relaxation rates *R*2*, To address this issue we propose to improve similarity approximation by a substitution

$$\sigma_m(\mathrm{TE}) = \sigma_n(\mathrm{TE}) \cdot [|S_m(\mathrm{TE}_1)| \cdot \exp(-R2_m^* \cdot (\mathrm{TE}-\mathrm{TE}_1))] / [|S_n(\mathrm{TE}_1)| \cdot \exp(-R2_n^* \cdot (\mathrm{TE}-\mathrm{TE}_1))] \quad (1)$$

Since information on R2* is not initially available, we use an iterative procedure - the original similarity approximation [1] is used to calculate initial values of R2* that are used subsequently in Eq. (1). This allows solution of VSF equation in the form similar to [1]

$$S_n(\mathrm{TE}) = \sigma_n(\mathrm{TE}) \cdot F_n(\mathrm{TE}) \quad (2)$$

with F-function calculated based on Eq. (1). Equation (2) permits calculation of the corrected R2* maps.

Experimental data were collected from 4 healthy volunteers (after local IRB approval) on a Siemens 3T Trio MRI Scanner, using 3D multi-gradient echo sequence with the resolution of 1×1×2 mm^3. We collected 10 gradient echoes and one phase-stabilization echo at the end of each excitation. FOV is 192mm×256mm, TR=50ms, TE_1=4ms, and ΔTE=4ms. The computing code was written in MATLAB.

Results Examples of the results are shown in Figures 1 and 2.

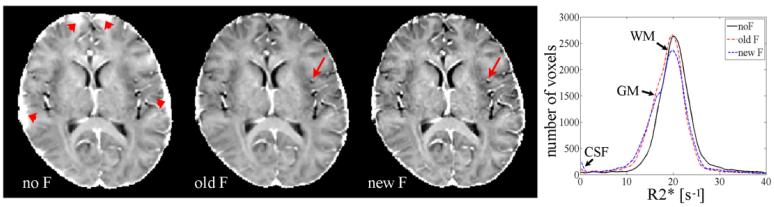

Figure 1. Example of R2* maps calculated using different F-function correction methods. First we note that both F-functions resolve field inhomogeneity artifacts on R2* maps (short arrows). Secondly, R2* map calculated with new F-function provides the sharpest contrast (example is pointed out by long arrows). Histograms of R2* values show increased number of smaller R2* by the new F-function. Importantly, the delineation between WM and GM is better resolved both in R2* maps and histograms (arrows point to peaks corresponding to different tissues). GM peak is only seen on the R2* map calculated with new F-function.

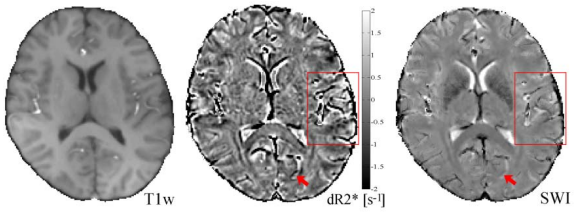

Figure 2. Example of T1-weighted image, the difference map of R2*(old F) minus R2*(new F) and susceptibility weighted image (SWI) from the same slice. dR2* map highlights the boundaries between compartments, such as WM, GM and CSF. The dR2* map also shows more blood vessels and substantially improved contrast between blood vessels and surrounding brain tissue as compared to SWI. Examples are outlined by a box and pointed out by an arrow.

Conclusion Herein we present an improved post-processing method for quantitative evaluation of tissue specific R2* relaxation maps. Compared to the original F-function approach [1], the new method is able to sharpened the R2* maps, especially in the areas of small objects, such as CSF/GM/WM boundaries and blood vessels. We also able to produce maps of blood vessel network with the contrast substantially improved compared to commonly used SWI.

Reference Yablonskiy, et al., *Voxel spread function method for correction of magnetic field inhomogeneity effects in quantitative gradient-echo-based MRI.* Magn Reson Med, 2013;70(5):1283-1292; PMC3604169.