Hybrid multi-baseline and referenceless PRF-shift thermometry

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Introduction Proton resonance frequency (PRF)-shift MR thermometry is a promising tool for guiding thermal therapies in the treatment of liver tumors and heart arrhythmias, but is complicated by organ motion and respiration. To address motion, multi-baseline subtraction techniques have been proposed [1,2] that use a library of pre-treatment baseline images covering the cardiac and respiratory cycle. However, main field shifts due to lung and diaphragm motion can cause large inaccuracies in multi-baseline subtraction. In contrast, referenceless thermometry methods [3-5] based on polynomial regression of background phase are immune to motion and main field shifts. While referenceless methods can be accurate in most regions of the heart and liver, the background phase in some parts of these organs can require large polynomial orders to fit, leading to increased risk that the hot spot itself will be fit by the polynomial. We present a hybrid method for thermometry of moving organs that combines referenceless and multi-baseline thermometry, and demonstrate that it estimates temperature with much lower error in volunteer heart and liver data than either method alone.

Theory The algorithm is an extension of regularized referenceless thermometry [5]. We assume that three sources contribute to image phase during thermal treatment: 1) background anatomical phase (i.e., baseline image phase), 2) spatially smooth phase deviations from baseline caused by main field shifts (i.e., polynomial phase), and 3) focal, heat-induced phase shifts. This leads to the following treatment image model at voxel j:

$$\left(\sum_{l=1}^{N_l} w_l x_{l,j}\right) e^{i(\{\boldsymbol{Ac}\}_j + t_j)},$$

where the w_l are the baseline image weights, the $\boldsymbol{x}_l$ are the (complex) baseline images, $\boldsymbol{A}$ and $\boldsymbol{c}$ are the polynomial basis matrix and coefficient vector, respectively, and $\boldsymbol{t}$ is the temperature-induced phase shift. The algorithm estimates $\boldsymbol{w}$, $\boldsymbol{c}$, and $\boldsymbol{t}$ while encouraging $\boldsymbol{t}$ to be sparse, reflecting knowledge that heat is applied focally. The w_l are real, positive, and sum to one.

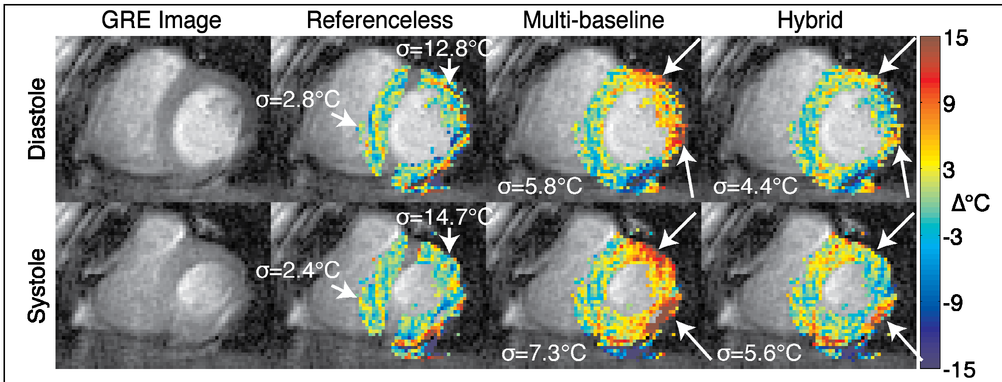

Figure 1: Free-Breathing Heart Results. *The new hybrid method yields significantly smaller temperature errors in the left ventricular myocardium than the other two methods when used alone.*

Methods We compared our algorithm with referenceless thermometry [5] and with multi-baseline subtraction performed using our method without polynomial phase regression. The algorithms were compared in terms of residual temperature error after model fitting. Sixth-order polynomials were used for the referenceless and hybrid methods. To compare algorithms in the heart, short-axis free-breathing images were acquired in a healthy volunteer (no heating) in real-time [6], using spiral acquisitions with four interleaves (TE = 5ms, 92ms/image) on a GE 3T Signa HDx scanner (GE Healthcare, Waukesha, WI, USA). The referenceless method was run independently in two separate regions; once in the septum and once in the left ventricular (LV) myocardium. The baseline library comprised 1.725s (75 images). We also compared the algorithms with real-time sagittal rFOV liver images of a healthy volunteer (TE = 16.2 ms, 365ms/image) [7]. The baseline library comprised 3.65s (10 images), and the referenceless method was run independently in central liver and rib regions.

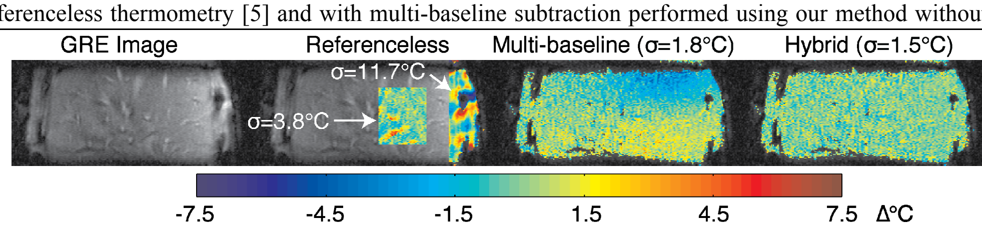

Figure 2: Free-Breathing Liver Results. *The new hybrid method yields significantly smaller residual temperature errors than the other two methods when used alone.*

Results Figure 1 shows temperature estimation results from heart images in diastolic and systolic phases (4.0s and 4.8s after library acquisition, respectively). Temperature is displayed within the septum and LV myocardium. Nominally, each method estimates zero temperature everywhere, however, Fig. 1 shows that while the referenceless method achieves small errors in the septum, it is unable to fully regress out the background phase in the LV myocardium, leaving large residual temperature errors there. The multi-baseline method achieves significantly lower errors in general, however, large errors remain near the lung and diaphragm. In contrast, the hybrid method achieves lower error throughout the myocardium. Figure 2 shows that for a liver image acquired 6.9s after the baseline library, the referenceless method achieves low errors within the liver but is unable to fit the rapidly-varying phase in the ribs. The multi-baseline method successfully removes temperature errors from fine spatial features, but spatially smooth errors remain. The hybrid method yields the smallest residual temperature errors throughout the liver.

Conclusion We have introduced a new hybrid method for PRF-shift thermometry in moving organs, and demonstrated its ability to estimate temperature with higher accuracy than conventional methods. The method requires no gating, navigator acquisitions, or susceptibility modeling. As in multi-baseline subtraction methods, the new method is capable of removing highly-structured background image phase in the presence of motion, but is also able to overcome main field shifts and requires a smaller baseline library. As in referenceless thermometry, the method is robust to susceptibility-induced main field shifts due to lung and diaphragm motion, but is also able to remove finer anatomical phase features.

Support NIH R21 EB 007715 and R01 CA 121163; GE Healthcare. **References** [1] KK Vigen et al. MRM, 50(5), 2003. [2] S Roujol et al. 17th ISMRM, p. 443, 2009. [3] V Rieke et al. MRM, 51(6):1223–1231, 2004. [4] WA Grissom et al. 17th ISMRM, p. 444, 2009. [5] WA Grissom et al. 6th ISBI, pp. 1235–1238, 2009. [6] K Nayak et al. MRM, 51(4):655–660, 2004. [7] AB Holbrook et al. In press, MRM 2009.