# STRATEGY FOR SIMULTANEOUS REGION-TRACKING AND TEMPERATURE-MONITORING IN THE LIVER DURING FREE-BREATHING

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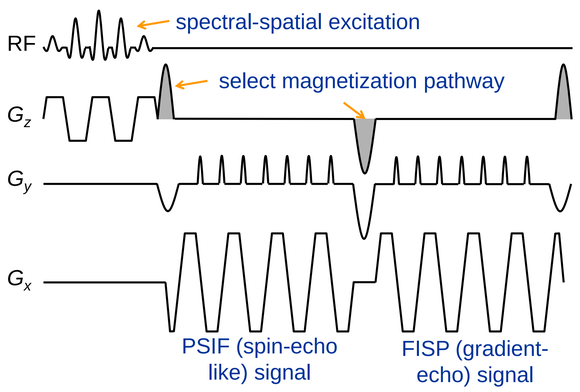
## ULTIMATE THERMOMETRY SEQUENCE (?)

- We may have stumbled upon the **'ultimate' MR thermometry sequence (?)**.
- Main characteristic: **an extra (spin-echo like) signal** is acquired in addition to the usual (gradient-echo) signal, at essentially **no cost in scan time**.
- This simple change may lead to a **surprising number of substantial benefits** for temperature-monitoring applications [1,2].
- We have implemented the sequence in 2D and 3D, with EPI readout as well as single-line readout. An example is shown below, for 2D multi-shot EPI:

EXAMPLE (2D multi-shot EPI version)

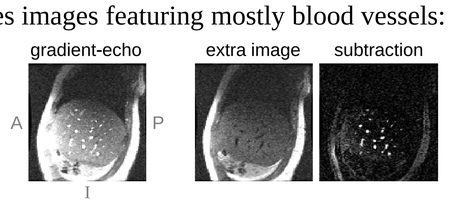



- Claimed benefits from acquiring the extra spin-echo like signal include: Improved **temperature-to-noise ratio** (TNR) [1], increased **temperature accuracy** in the presence of k-space offsets (when TE becomes more ill-defined) [2], and increased detectability of blood vessels for **motion tracking**.
- THE GOAL HERE WAS TO TEST **MOTION TRACKING**. MORE SPECIFICALLY, OUR SEQUENCE WAS USED ALONG WITH LANDMARK-BASED REGISTRATION FOR **SIMULTANEOUS REGION-TRACKING AND RELATIVE-TEMPERATURE (T) MAPPING**.

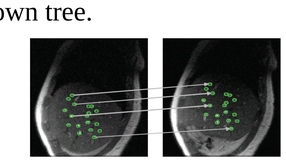
## MOTION TRACKING

- Blood vessels tend to be bright in gradient-echo images and dark in our extra images. A weighted subtraction gives images featuring mostly blood vessels:

Free-breathing *in vivo* images (2D non-EPI version, no heating, regular RF excitation)



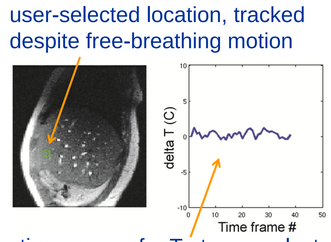

- Locations within a moving organ can be tracked based on the motion of all neighboring blood vessels [3]. As an analogy, this would be like tracking a nest by tracking all surrounding branches in a wind-blown tree.
- A very fast landmark-based registration algorithm establishes a match between blood vessels from different time frames:



- The matching process is based on a model that maximizes the *a posteriori* probability density conditioned on reference locations and images. Optimization is performed by estimating a coarse deformation field, and by then refining these estimates locally.
- This matching/deformation process could be performed very rapidly, at a rate of 215 frames per second with no special optimization on a 2.5 GHz Intel Core 2 Extreme processor.
- The result is a displacement map with known values wherever a sizeable blood vessel is present. Displacements at the target (or at any other desired location) are inferred/interpolated from the known displacements of neighboring vessels.

## METHODS

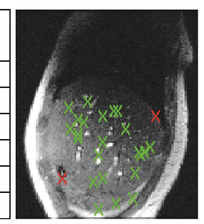
- **Test program:** Readers were presented with an image, and instructed to click anywhere in the liver. A green circle would appear where they clicked. The whole 50-frames dataset would then play as a movie, while our software tried to keep the overlaid green circle 'pinned' to the anatomy, in spite of breathing motion.




- **Scoring:** Five readers were asked to evaluate the registration results, and each reader ran the test program 5 times. The human eye is a great tool for detecting relative motion, and we used it here to detect whether the user-placed circle moves well with the underlying anatomy. Scores were given on a 1 to 5 scale, with 0 = un-related, 1 = large deviations, 2 = sizeable deviations, 3 = somewhat tracked, 4 = well tracked and 5 = pinned to anatomy.
- **Temperature measurements:** A referenceless method [4] with a 5x5 ROI centered at the pixel of interest was used. There was no heating in the *in vivo* experiment, i.e., $\Delta T(t) = 0$ C. (Not shown here, the method was also validated with heating in phantoms [1]). A 1.7 s averaging window was used for T results. T noise was calculated as the standard deviation of T.
- **Imaging parameters:** 3 T scanner, simplified version of sequence from Fig. 1 (echo-train length = 1, regular RF pulse instead of spectral-spatial), $TE_{PSIF}$ = 1.67 ms, $TE_{FISP}$ = 4.7 ms, TR = 6.4 ms, 128x96, 24x24 cm$^2$, 5 mm slice thickness, 62.5 kHz, 50 time frames, 8-channel coil.

## RESULTS

| READER | SCORE (0 is worst, 5 is best) | T noise at user-selected locations |
|---|---|---|
| # 1 | 4.0 ± 0.0 | 1.46 ± 0.95 C |
| # 2 | 4.0 ± 0.4 | 1.16 ± 0.69 C |
| # 3 | 4.4 ± 0.5 | 1.48 ± 0.80 C |
| # 4 | 4.6 ± 0.5 | 1.16 ± 0.45 C |
| # 5 | 3.4 ± 0.9 | 1.87 ± 1.65 C |
| **OVERALL** | **4.1 ± 0.7** | **1.43 ± 0.95 C** |



Scores from all 5 readers, and temperature noise at the user-selected locations. Each reader ran the test program 5 times, and results above are averaged over these 5 trials. Overall, the average score was above 4, meaning the readers judged that, visually, the locations they clicked on was well tracked by our software, despite free-breathing motion. All 5×5 = 25 user-selected locations are with an 'X' shown above, and the only two locations that received a score below 3.5 are shown in red.

## CONCLUSION

**In the present test, the readers judged that selected locations in the liver were well tracked, and T noise was at an arguably reasonable level (mean of 1.43 C). It would appear the proposed sequence shows promise in its ability to enable simultaneous region-tracking and temperature-monitoring.**

[1] Madore B, Panych LP, Mei C-S, Yuan J, Chu R. Multi-pathway sequences for MR thermometry. MRM 2011;66:658-668.

[2] Madore B, Chu R, Mei C-S, Yuan J, Chao T-C, Panych LP. Modified EPI dequence for improved MR thermometry. ISMRM 2011, Montréal, Canada:1767.