

# Automatic Cardiac Motion Estimation from Tagged MRI using Multiple Source Non-Rigid Registration Techniques

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**Introduction:** Most of the techniques that have been proposed to estimate motion from Tagged MR data using image postprocessing require a presegmentation step of the tags and endo-epicardial contours [1,2]. Our work presents a new approach to estimate motion from Tagged MR sequences using both horizontal and vertical tagged images and using a multi source non-rigid registration algorithm without requiring any segmentation and providing very good accuracy.

**Methods:** Tagged MR short axis images were acquired on five healthy dogs using a 3D fast gradient echo tagging sequence with respiratory and cardiac gating on a General Electric 1.5 T CV/i scanner (FOV 180mm x 180mm x 128-160 mm, acquisition matrix: 384 x 128 x 32, flip angle: 12°, TE/TR:3.4/8.0 ms, slice thickness: 4-5 mm, tagging separation; 2.8 mm). Human data was obtained from five normal healthy volunteers on a 1.5T Siemens Espree scanner. A gated, sequential, multi-phase 2D balanced-SSFP imaging sequence with a 1-1 SPAMM tagging preparation was employed [1] (FOV: 300mm X 300mm, acquisition matrix: 256x130, TE/TR= 5.0/2.5 ms, slice thickness: 5 mm, tag separation: 6mm, temporal resolution: 25 ms). Short axis horizontal and vertical tags were manually tracked by an expert to serve as a gold standard. Automatic estimation of the myocardial motion field was computed using a pair-wise non-rigid registration algorithm based on a semilocal B-spline parametric model. The registration algorithm inputs are both horizontal and vertical tagged sequences and as a result the bidimensional motion field is computed consistent with all the available information. A gradient descent optimization approach is used decoupling directionally the gradient of the criterion so that the horizontal estimation of the motion is driven by the horizontal tagged images and similarly for the vertical component of the motion. Laplacian regularization is clearly needed to guarantee the smoothness of the solution and to counter the intracavitary intensity variations. A multiresolution strategy was used to guarantee speed and robustness. The sequences were also represented in the B-spline space using this framework to construct the multiresolution. Manually traced points were compared with the estimated trajectories in terms of the Euclidean distance, and the mean squared error with respect to the manual tracings along the whole sequence was calculated. The variability of the expert manual tracing was also checked by performing six independent tracings in one slice from the experimental dataset and following the same measurement procedure (RMS point to point comparisons).

**Results:** Motion estimations using the proposed approach resulted in a mean squared error of  $0.51 \pm 0.15$  pixels (0.25 mm) for the animal data and  $0.46 \pm 0.11$  pixels (0.49 mm) for the human volunteer data. Figure 1 shows manual traces together with artificial tags results for end-systole in both the horizontal and vertical tagged images for an animal subject and a human subject. Variability of manual tracing resulted in a mean RMS value of  $0.26 \pm 0.06$  pixels.

**Conclusions and discussion:** This study suggests that fully automatic tagged MR image processing is feasible using multiple source non-rigid registration techniques. Subpixel accuracy is achieved thanks to the B-spline image representation. Furthermore, the analytical representation of the deformation is an optimal framework to obtain spatio-temporal derived parameters (such as strain) analytically from the computed displacement field.

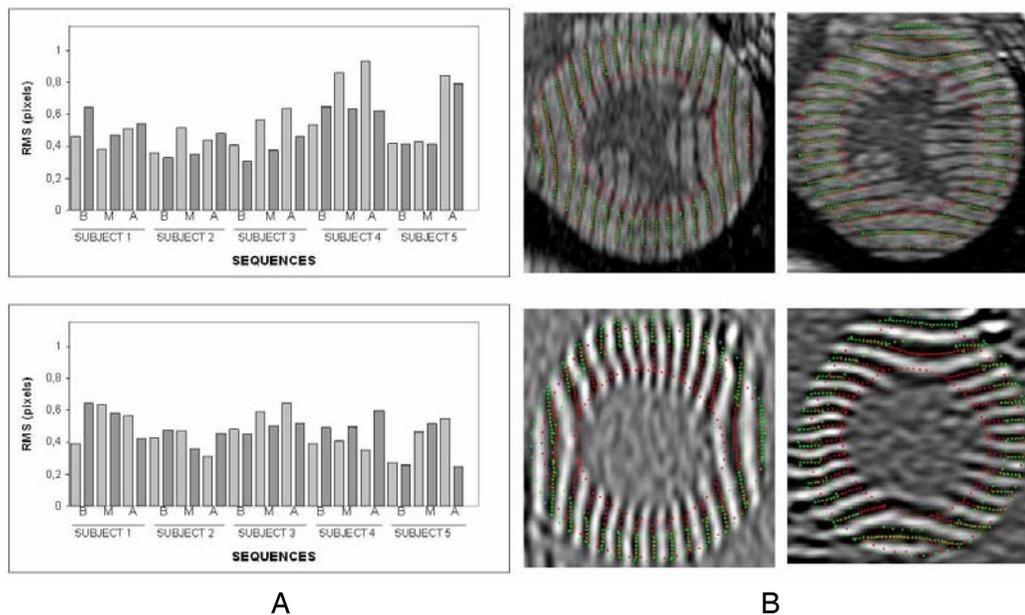


Figure 5. A) RMS error (pixels) from all the analyzed images (top: animal data; bottom: volunteer data). Light gray (horizontal error), dark gray (vertical error). Sequences grouped by subject and ordered by slices (B: basal, M: mid and A: apical). B) Manually traced points (green) are displayed together with automatically tracked points (red) at end-systole, showing the small error measured. RMS was calculated over all the tags present in the myocardium and along the frames analyzed within the sequence. The mean number of tags in the short axis images was 17 in the animal data, (~22000 point to point comparisons along the sequence), and 9 tags in the volunteer data (~3000 point to point comparisons).

## References:

- [1] Derbyshire et al., SCMR 2007, Feb 2007 in press.
- [2] Declerck J et al. , Phys Med Biol. 2000 Jun;45(6):1611-32.