Fully Automatic 3D Cardiac Tagged MRI Analysis using Multiple Source Non-Rigid Registration Techniques

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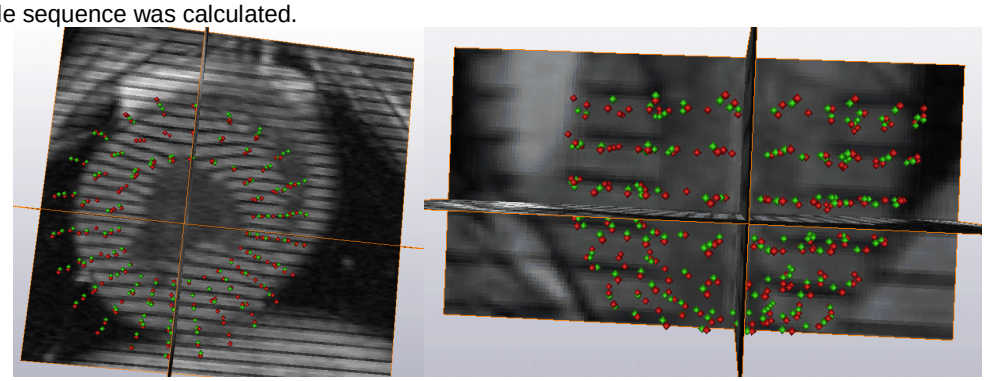
Introduction: Motion estimation from 3D Tagged MR commonly requires a presegmentation step of the tags and endo-epicardial contours [1]. This work presents a new approach to estimate motion from 3D Tagged MR sequences using all the short and long axis sets as inputs to a multi source non-rigid registration algorithm without requiring any segmentation. This new approach was compared with standard tag tracking methods and is shown to provide very good agreement.

Methods: The experimental animal data were acquired on five healthy dogs [2]. Tagged MR short axis cardiac images were acquired using a 3D fast gradient echo tagging sequence on a General Electric (Milwaukee, WI, USA) 1.5 T CV/i scanner. Imaging parameters were: FOV= 180mm x 180mm x 128-160 mm, acquisition matrix= 384 x 128 x 32, flip angle= 12º, TE/TR= 3.4/8.0 ms, 4-5 mm slice thickness, tagging separation 2.8 mm. Horizontally and vertically tagged short axis images were acquired independently. Long-axis stripe tag images were acquired using a 2D fast gradient echo pulse sequence using the following imaging parameters: FOV= 200 x 200 x 8 mm, acquisition matrix= 256 x 128, 12° flip angle, TE/TR= 3.2/8.0 ms, 4–5-mm slice thickness, tagging separation 6 mm, and 1 TR persegment for 8-ms temporal resolution. Respiratory and cardiac gatings were applied to have a good correspondence of all the datasets. The first 40 frames were used for the analysis as they were the ones that provided a good tag contrast. For conventional tag-tracking, short axis horizontal and vertical tags as well as long axis tags were manually tracked by an expert using FindTags software [3]. The three sets of tags were then used as inputs of Tag Tissue Tracker (TTT) [4] to perform the field fitting. As a result a mid myocardial mesh of the Findtags+TTT estimated motion was obtained for all the frames. On the other hand, our proposal for fully automatic estimation of the 3D myocardial motion was computed using a multiple source non-rigid registration algorithm based on a semilocal Bspline parametric model. The registration algorithm inputs are horizontal and vertical tagged short axis volume sequences and the long axis dataset. As a result the three dimensional 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 estimation of each component of the motion is driven by the tagged images of the corresponding direction. Laplacian regularization is used to guarantee the smoothness of the solution and to counter the cavity intensity variations. A multiresolution strategy was used to achieve speed and robustness. The corresponding mid-myocardial mesh comparable to the one obtained with FindTags+TTT was computed applying the estimated motion field. Both spatio-temporal meshes were compared in terms of the Euclidean distance (point to point comparisons), and the mean squared error along the whole sequence was calculated.

Results: Motion estimations using the proposed approach resulted in a mean squared error of and 0.90 ±0.07 pixels (0.45 mm). Figure 1 (top) shows the myocardia meshes corresponding to the Findtags+TTT (green) and the multi source non-rigid registration approach (red) at end-systole. Figure 1 (bottom) represents the RMS measurements for the five subjects.

Discussion and conclusions: This study suggests that fully automatic 3D tagged MR analysis is feasible using multiple source non-rigid registration techniques. Myocardial or tag segmentation is not required and therefore the method is completely unsupervised. Subpixel agreement is achieved thanks to the Bspline image representation. Furthermore, the analytical representation of the deformation is an optimal framework to compute analytically spatio-temporal derived parameters (such as strain) from the estimated displacement field.



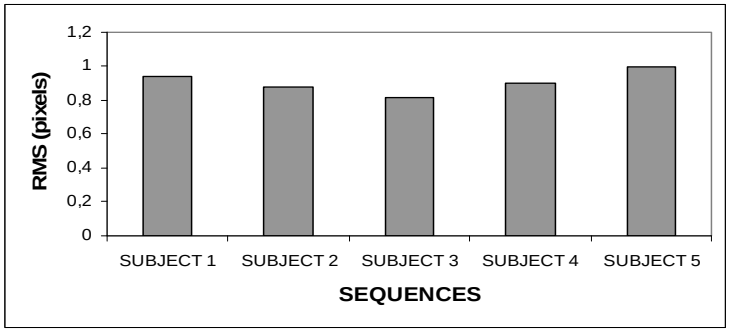


Figure 1. *Top*: 3D representation of the myocardial mesh for end-systole. FindTags+TTT mesh (green) is displayed together with automatically tracked mesh (red). *Botton*: RMS error (pixels) from all the analyzed subjects. The mean number of mesh points was 144 by time frame (~5500 point to point comparisons along the sequence).

References:

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