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Abstract:

Magnetic resonance tissue tagging has been proven a valuable tool in the quantification of myocardial motion. Cardiac tagged MRI technique enables non-invasive assessment of regional pathologies of the human heart. Myocardial motion may be reconstructed by detection and tracking of the tag points in a sequence of images. Our aim is to speed up and fully automate quantitative motion analysis of tagged cardiac MR images for routine clinical use. We extend here one of the previous approaches for automatic myocardial localization [5], which utilizes a HARP based tag extraction and myocardial segmentation using harmonic phase unwrapping consistency along expected semicircular paths. We also combined myocardial and tag localizations methods with a B-spline based motion field fitting technique and obtained a complete heart motion evaluation package.

Introduction:

Tagged MRI has been introduced to distinguish normal and abnormal myocardium [1,2]. Tag features are introduced into the image by intensity modulation of the object magnetization before the actual imaging using specific saturation pulses. When the volume is imaged after a certain time delay; the change of the intensity pattern in images reflects the motion of the underlaying myocardium. Tagging is particularly valuable in cardiac imaging, because the myocardial tissue provides few natural features for motion tracking. In addition, there is significant through-plane motion making it difficult to track a specific tissue over time, as imaging planes are kept constant in space. The tagged cardiac MR image analysis is composed of several stages: Segmenting the left ventricular (LV) myocardium is the first stage of the image analysis where inner and outer contours of LV cavity are drawn, usually manually. The second step is the estimating the tag locations within the LV wall. Once the relative position of the tags has been characterized by a string of detected tag points lying along tag lines, this information can be used to calculate a 3-D or 4-D parametric motion field [4]. At the end this field is utilized to calculate displacements or strains at any point in the myocardium. Harmonic phase tag analysis technique [3] provided a significant advance in the tag analysis process, but the need of user interaction at the evaluation stage remained, the analysis was restricted for 2D and development of a parametric myocardial motion model was not done. In this study, a motion analysis package, which is developed in MATLAB programming environment, is presented for left ventricular tagged MRI

Methods:

We used several human and animal tagged MR images, acquired by standard cardiac gated segmented k-space SPGR sequences with SPAMM tagging present in a 1,5 T Siemens Sonata clinical scanner using breath-hold techniques. In these images, tags appear as dark lines that move and bend as the object moves [Figure 1]. Phase images obtained by applying HARP technique [3,4]. Unwrapping the phase along semi-circular paths at a certain distance from LV cavity center and comparing the cumulative phase data at both end points forms the basis of our myocardial segmentation approach [5]. Once we identify a certain distance range with consistent phase matches, we can draw the limits of region of interest for the myocardium [Figure 2], and produce a mask image to be used in finding tags. We continue the analysis by detecting the tag locations. After the masked phase image is phase shifted by $\pi/2$, tag points are obtained by zero-crossing detection on the lines prependicular to tag lines [Figure 3]. The resulting tag points are classified into tag lines by fast sorting algorithms. Significant care is needed to make sure that these tag indexing is consistent over time and space.

A point on a tag line gives the displacement of that point in the direction perpendicular to the original tag plane. Therefore, after registering all of the image points that lie within the tag lines, We get a complete data set comprising a list of 1-D displacements [Figure 4]. Our data geometry consists of sets of horizontally tagged (tag stacks) and vertically tagged short-axis image planes. All perpendicular displacements of all tag points for each short-axis image plane, time frame and tag stack are used to formulate a 2-D B-spline tensor field to fit a smooth field of these displacements. If a 3-D tagging dataset is available, a modified technique is applied to identify tags in long axis images, in which myocardial locations already found in short axis images can guide the myocardial segmentation of long axis images. After that, displacement fields are combined to an inverse motion field and sampling of this field gives matching pairs of points between later time frames and the undeformed state. Finally, a forward motion field fitting is applied to track points and calculate specific displacements and strains [4].

Results and Discussion:

The final aim of this work is to completely automate the myocardial strain analysis of the heart. Although we have successfully evaluated myocardial 2D and 3D stain analysis automatically, we have still some key assumptions and limitations in our study. Some of these limitations are: Circular shape assumption of the epi- and endocardial boundaries of myocardium, lack of details of these contours, assumption of an approximate position of LV center. Since the automatically found myocardial contours are less accurate than actual contours of the myocardium, we can not use these contours for ejection fraction or myocardial calculations, but it is quite adequate for midwall strain calculations. We are still working on a region-growing extension of this approach to overcome first two limitations. The third limitation is really not an issue if a small care is given to roughly center LV during short axis imaging.

Conclusion:

This work demonstrates an approach for a fully automated regional cardiac function assessment technique for cine tagged MR images of the left ventricle.



Figure 1: An example of short axis cardiac MR image through mid myocardium with planar SPAMM tagging. Figure 2: The automatically generated region of interest is shown for this particular slice. Figure 3: Placement of tag points on masked phase image. Figure 4: Displacement vectors of tag points through space and time.

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