A mutual information approach to automatic detection of heart rejection in MRI

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Synopsis

This paper develops an automatic algorithm to detect early rejection of transplanted hearts imaged by tagged MRI. We consider a mutual information based approach that compares the similarities of the regional motions between a test heart and a healthy one. Low mutual information means that the test regional motions are quite different from the healthy template and are classified as abnormal. The experiment shows good results of our algorithm.

Introduction

The current gold standard for diagnosing and staging heart rejection after transplantation is biopsy, which is invasive and prone to sampling errors. Tagged cardiac MRI is a promising tool to *non-invasively* monitor *in vivo* heart rejection. In addition, MR tags provide motion features in images. Processing tagged images can provide dense motion maps of the heart [1], see Figure 1 for example. Classifying each motion vector helps cardiologists identify the rejection. However, the abnormal motions in the early rejection are only in regions and are not easily discernible from the normal ones. Human labeled abnormal motions are dependent on the operator and the task is labor-intensive. To reach consistent detection results, cardiologists need a tool to automatically detect regional rejection, which is the goal of this paper.

Assume that pixels x and y are at the same location in the heart, but are drawn from the test and the template hearts, respectively. The task of our algorithm is to determine whether the motion $\mathbf{u}(x)$ at x is similar to motion $\mathbf{u}(y)$ at y. If they are not similar, the pixel x is classified as abnormal.

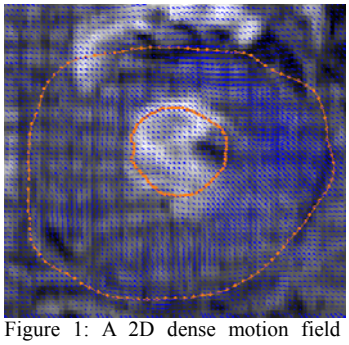


Figure 1: A 2D dense motion field derived from tag lines. The field reveals the 2D cardiac motion.

Methods

Data: We study rejection of heart transplants by using heterotopic working heart and lung model [2]. We use density-weighted spin-echo imaging to cover the 3-D volume of the heart with 8 slices at 10 time phases through the cardiac cycle. Cardiac tagging was achieved by a modified DANTE sequence. All MRI scans were performed on a Bruker AVANCE DRX 4.7-T system. The matrix size is 256×256 with resolution 156μm. All the algorithms are implemented with MATLAB®.

Curl and divergence: A motion field can be characterized by its curl and divergence that we adopt to compare pairs of pixels x and y. The curl and divergence are related to the myocardial motion. The ion currents in the cardiac cells trigger the contractions and elongations of the myocardial fibers that in turn generate the heart motion. Since ion currents are local, the myocardial motion has local motion in addition to the well-known global motion. The local curl and divergence capture this phenomenon. Monitoring the local curl and divergence patterns through the cardiac cycle provides another way to find out where local abnormal motions are. The curl $c(x)=\nabla\times\mathbf{u}(x)$ of the 2D motion $\mathbf{u}(x)$ can be obtained by a line integral using Stoke's theorem: $c(x)=\oint\mathbf{u}(x)\cdot d\mathbf{l}$, where $\mathbf{l}$ is the unit tangential vector of the closed integral path. Similarly, the divergence $d(x)=\nabla\cdot\mathbf{u}(x)$ can be computed using Gauss's law: $d(x)=\oint\mathbf{u}(x)\cdot d\mathbf{n}$, where $\mathbf{n}$ is the normal direction of the integral path. To compute the local curl and divergence at the pixel x, we let the integral path to be the one along the neighboring 8 pixels centered at x. We denote the two quantities $c(x)$ and $d(x)$ by a column vector: $\mathbf{c}(x)=[c(x), d(x)]^T$.

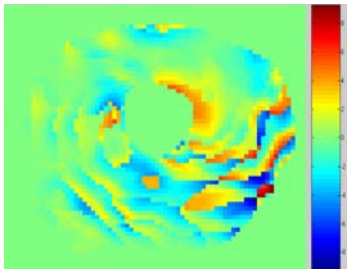


Figure 2: The curl map of the left ventricle.

Classification by mutual information: Due to the presence of noise during MR imaging and errors during preprocessing, we treat $\mathbf{c}(x)$ as a random vector which has probability distribution $p_x(\mathbf{c})$. Assuming Gaussian distribution, we pick a window of size 5×5 centered at the pixel x to estimate the mean and the variance. Now, the motions $\mathbf{u}(x)$ and $\mathbf{u}(y)$ have representations in terms of probabilities. The problem of comparing the similarity between $\mathbf{u}(x)$ and $\mathbf{u}(y)$ becomes that of studying the mutual information $I(x;y)$ between $p_x(\mathbf{c})$ and $p_y(\mathbf{c})$. Mutual information $I(A;B)$ between two probability distributions $p(a)$ and $p(b)$ is defined as $I(A;B)=\sum_{a,b}p(a,b)\left[\log p(a,b)-\log p(a)p(b)\right]$. $I(A;B)$ is 0 when $p(a)$ and $p(b)$ are independent. When the motion $\mathbf{u}(x)$ is very different from $\mathbf{u}(y)$, we expect that $p_x(\mathbf{c})$ and $p_y(\mathbf{c})$ are almost independent and then $I(x;y)$ is close to 0. This is how we utilize mutual information to classify the abnormal motions. We introduce a function $f(x)$ to indicate the class of the motion $\mathbf{u}(x)$; $f(x)$=1 means that the motion $\mathbf{u}(x)$ is normal and −1 abnormal. To classify the motion $\mathbf{u}(x)$, we design the following decision rule: $f(x)=\begin{cases}1\ , \text{ if } I(x,y)>\tau\\ -1, \text{ if } I(x,y)\le\tau\end{cases}$, where τ is the threshold determined by the user.

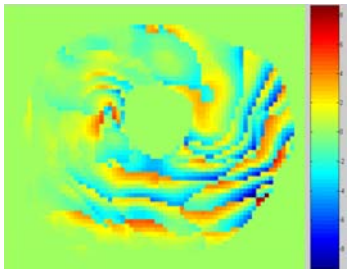


Figure 3: The divergence map of the left ventricle.

Results

Figure 1 shows a rat heart imaged on post-transplantation day 3. We first manually segment the left ventricle. The dense motion field obtained by the algorithm in [1] is superimposed on this image. We use the motion field to compute the maps of curl and divergence, shown in Figures 2 and 3 respectively. A sequence of tagged MR images of a native, healthy heart was processed to obtain the templates of the curl and divergence. We use a software to register the test and the template hearts. To run our algorithm, the parameter needs specified is τ, which is set to be 0.001. We apply our proposed classification method to the maps of the curl and divergence, leading to the result shown in Figure 4. In this figure, the dots represent the portion with detected abnormal motions that correspond to the rejection regions.

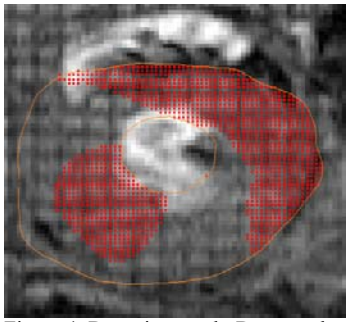


Figure 4: Detection result. Dots are the pixels classified as abnormal.

Conclusion

We developed an automatic method to detect the abnormalities of cardiac motions. This is used to determine heart rejection. The method first estimates the probability distributions of the curl and divergence and then classifies each pixel by the mutual information between the test and the healthy hearts. Our result shows that our algorithm is good. Tagged MRI and the algorithm will provide a non-invasive diagnosis tool to detect heart rejection.

Acknowledgements

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References

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[2] Y. L. Wu, K. Sato, H.-H. Chang, J. B. Williams, T. K. Hitchens, J. M. F. Moura, and C. Ho, *ISMRM*, 2004.