MR functional cardiac imaging: Segmentation, measurement and WWW based visualisation of 4D data

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Abstract

This paper considers the problem of ventricular segmentation and visualisation from dynamic (4D) MR cardiac data covering an entire patient cardiac cycle, in a format that is compatible with the web. Four different methods are evaluated for the process of segmentation of the objects of interest: The K-means clustering algorithm, the fuzzy K-means (FKM) algorithm, self-organizing maps (SOMs) and seeded region growing algorithm. The technique of active surface is then subsequently applied to refine the segmentation results, employing a deformable generalised cylinder as geometric primitive. The final ventricular models are presented in VRML 2.0 format. The same process is repeated for all the 3D volumes of the cardiac cycle. The radial displacement between end systole and end diastole is calculated for each point of the active surface and is encoded in colour on the VRML vertex, using the RGB colour model. Using the VRML 2.0 specifications, morphing is performed showing all cardiac phases in real time. The expert has the ability to view the objects and interact with them using a simple internet browser. Preliminary results of normal and abnormal cases indicate that very important pathological situations (such as infarction) can be visualised and thus easily diagnosed and localised with the assistance of the proposed technique. ©1999 Elsevier Science B.V. All rights reserved.

Keywords: 4D MR cardiac images; K-means clustering algorithm; Fuzzy K-means (FKM) algorithm; Self-organizing maps (SOMs); Seeded region growing algorithm; Active surface; Surface triangulation; VRML 2.0 format

1. Introduction

Heart wall motion measurement is one of the most sensitive and early indicators of coronary stenosis. Echocardiography monitors the motion of the ventricular wall, but is limited by a small field of view and a lack of three-dimensional (3D) tissue tracking [1]. Four-dimensional (4D) imaging provides the capability of quantification of ventricular structure and function. Depending on the imaging modality, ventricular volume, myocardial mass, segmental wall motion, segmental wall thickening and regional myocardial perfusion can be measured. Precise measurements of these variables should allow improved diagnosis of ventricular disease and better evaluations of the efficiency of interventional cardiology.

Advanced algorithms and software tools are required to efficiently handle and visualise the spatio-temporal information present in 4D models of the heart muscle and its chambers and to allow the experts to reach an early, confident and sensitive diagnosis. A general model-based surface detector for modelling for tracing the 4D endocardiac and epicardiac left ventricular boundaries was developed in [2]. Gradient based left ventricular boundary detection was reported for MR and SPECT images on a slice by slice
basis, prior to surface reconstruction [3]. A unified approach for only temporal analysis of non-rigid motion from 4D heart data was reported by recovering the temporal evolution of the main modal amplitudes by a Fourier analysis [4]. MRI tagging studies have been performed where the left ventricular (LV) function is analysed by calculating the eigenvectors and eigenvalues of the strain tensor [5].

The process implemented in this study includes 3D segmentation of the chambers of interest, surface modelling employing a set of radial curves, measurement of functional quantities and visualisation of their values in colour and real time animation of the modelled coloured surfaces, using a WWW compatible format.

2. The physics of 4D cardiac MR imaging

A number of techniques have been employed for the acquisition of 4D images of the heart, some of them introduced recently to the clinical practice.

(i) Multislice spin echo MR imaging with acquisition triggered by the R wave of the ECG provides static information about the heart. It has long acquisition times, produces static images and often suffers from motion artefacts [6].

(ii) Gradient echo MR imaging provides information about both the anatomy and function of the cardiac muscle, producing strong contrast between the myocardial wall and the blood pool [7]. A large number of phases (up to 24) are captured in each cardiac cycle. However, gradient echo acquisition requires ECG gating and therefore is not real time. The resolution of the images has a typical value of 2 mm along the short axes plane and up to 8 mm along the third dimension. The myocardium is often less easily distinguishable from soft tissue along the inferior wall of the left ventricle (LV). In the case of spin echo, the blood pool appears dark with the myocardium having intermediate values whereas in gradient echo the blood pool appears bright.

(iii) Ultrafast MR imaging and real time echo planar techniques allow image acquisition times of 50 ms or less, achieving real time imaging. Thus these images do not suffer from motion artefacts and are excellent data sources for assessing myocardial function and perfusion [8]. MR cardiac imaging clearly outperforms echocardiographic studies in delineating the endocardium from blood [9]. Real time imaging allows for image acquisition under stress conditions, either physically or pharmacologically induced [10].

(iv) Myocardial tagging is an MRI technique for placing fiducial markers for non-invasive heart wall motion tracking [5]. A sequence of radio frequency and magnetic field gradient pulses is triggered by the rising edge of the R wave of the patient’s ECG. The pulses saturate parallel planes of magnetisation perpendicular to the image plane, which appear as dark lines at the imaging plane. At end diastole these lines become parallel. As the heart contracts, their deformation reveals the underlying deformation of the myocardium.

Cardiac MR imaging, in conjunction with Gadolinium (Gd) marked DTPA tracer, as a contrast medium, can collect functional information concerning wall motion and myocardial perfusion. The presence of Gd accelerates spin–lattice interactions, thus increasing the T1 signal. Comparative studies have shown excellent correlation between radionuclide studies (SPECT or PET) and 4D cine gradient echo MR images [11].

3. Cardiac chamber segmentation techniques and their evaluation

Gradient echo untagged MR images have been made available for this study. Therefore, the blood pool was imaged at higher values than the surrounding myocardial tissue. It was decided to segment the blood pool, which offers the ability to calculate the chamber volume, as well as model the endocardiac surface. The chambers of interest are the two ventricles (LV and RV) which were segmented up to the level of the mitral and the tricuspid valves.

Four different segmentation techniques were employed and evaluated.

3.1. Clustering algorithms for unsupervised MR image segmentation

The goal of clustering is to reduce the amount of data by categorising similar data items together [12]. Such grouping is pervasive in the way humans process
information. Clustering is hoped to provide an automatic tool for constricting categories in data feature space. Clustering algorithms can be divided into two basic types: hierarchical and partitional. Hierarchical algorithms are initialised by random definition of clusters and evolve by splitting large inhomogeneous clusters or merging small similar clusters. Partitional algorithms attempt to directly decompose the data into a set of disjoint clusters by minimising a measure of dissimilarity between data points in the same clusters while maximising dissimilarity between data points in different clusters.

3.1.1. The K-means algorithm
The K-means algorithm is a partitional clustering algorithm, which is used to distribute points in feature space among a predefined number of classes [12]. An implementation of the algorithm applied, in pseudocode, can be summarised as follows:

Initialise the centroids of the classes, \( i = 1, \ldots, k \) at

random \( \mathbf{m}_i(0) \)

\( t = 0 \)

REPEAT

FOR the centroids \( \mathbf{m}_i(t) \) of all classes

locate the data points whose Euclidean distance from \( \mathbf{m}_i \) is minimal

set \( \mathbf{m}_i(t + 1) \) equal to the new centre of mass of \( x_i \), \( \mathbf{m}_i(t + 1) = x_i/n_i \)

\( t = t + 1 \)

UNTIL \(|\mathbf{m}_i(t - 1) - \mathbf{m}_i(t)| \leq \text{error, for all classes } i\)

The K-means algorithm evolves by minimising the following quantity:

\[
E = \sum_j (\mathbf{x}_j - \mathbf{m}_c(x_j))^2,
\]  

where \( j \) is the number of data points index and \( \mathbf{m}_c(x_j) \) is the class centroid closest to data point \( \mathbf{x}_j \). The above algorithm was employed to segment spatio-temporal (4D) MR cardiac images. The grey level value of the image voxels is the feature considered by the algorithm. The number of different classes was selected to be four, corresponding to voxels containing blood, myocardial tissue, other tissue and air. The last class corresponds mainly to the subject’s exterior and to the lung space. The class “blood” at this cross section of the human body usually corresponds to the contents of the heart chambers and the descending aorta; the aortic arch is not usually imaged at this type of the examination. Experimentation showed that increasing the number of classes does not affect the accuracy of the blood segmentation.

3.1.2. The fuzzy K-means algorithm
The fuzzy K-means algorithm (FKM) is a variation of the K-means algorithm, with the introduction of fuzziness in the form of a membership function [13]. The membership function defines the probability with which each image voxel belongs to a specific class. The FKM and its variations have been employed in several types of pattern recognition problems [14].

If we assume a number of \( n \) unlabelled data points which have to be distributed over \( k \) clusters, a membership function \( u \) can be defined, such that

\[
u : (j, \mathbf{x}) \rightarrow [0, 1],
\]

where \( 1 \leq j \leq k \) is an integer corresponding to a cluster. The membership function assigns to a data point \( \mathbf{x} \), a positive, less than or equal to 1, probability \( u_j(x) \) which indicates that the point \( \mathbf{x} \) belongs to class \( j \). To meet computational requirements, the membership function is implemented as a 2D matrix whose first index indicates the cluster whereas the second indicates the value of the data point. If the membership function is to express mathematical probability, the following constraint applies:

\[
\sum_{i=1}^{n} u_{ij} = 1, \quad \forall \text{ clusters } j.
\]  

The FKM algorithm evolves by minimising the following quantity:

\[
E = \sum_{j=1}^{k} \sum_{i=1}^{n} u_{ij}^p (\mathbf{x}_i - \mathbf{m}_j)^2,
\]

where the exponential \( p \) is a real number greater than 1 and controls the fuzziness of the clustering process. The FKM algorithm can be described in pseudocode as follows:

\[
t = 0
\]

 initialise the matrix \( u \) randomly

 REPEAT

 calculate the cluster centroid
using the formula:

$$m_j(t) = \frac{\sum_{i=1}^{n} u_{ij}^p x_i}{\sum_{i=1}^{n} u_{ij}} , \quad j = 1, \ldots, k$$

(5)

calculate the new values for u:

$$u_{ij}(t) = \left( \frac{\sum_{i=1}^{n} (|x_i - m_j|)^{2(p-1)}}{|x_i - m_j|} \right)^{-1}$$

$$t = t + 1$$

UNTIL ($|u_{ij}(t - 1) - u_{ij}(t)| \leq \text{error}$ or

3.1.3. Self-organizing maps (SOMs)

The self-organizing map (SOM) is a neural network algorithm, which uses a competitive learning technique to train itself in an unsupervised manner. Kohonen first established the relevant theory and explored possible applications [15,16]. The Kohonen model comprises of a layer of neurons $m$, usually 1D or 2D, each neuron of which is connected to each input vector (data point) $x \in \mathbb{R}^n$ with a weight vector $w \in \mathbb{R}^n$. Each time a data point is input to the network, only one neuron $j$ is selected to fire, according to the following rule:

$$j = \arg \min_{i=1}^{m} \|x - w_i\|^2.$$  

The firing neuron $j$ and its neighbouring neurons $i$ have their weight vectors $w$ modified according to the following rule:

$$w_i(t+1) = w_i(t) + h_{ij}(t)(x(t) - w_i(t)), $$

(7)

where $h_{ij}(t) = h(||r_i - r_j||, t)$ is a kernel defined on the neural network space as a function of the distance ($||r_i - r_j||$) between the firing neuron $j$ and its neighbouring neurons $i$, as well as the time (defined as the number of iterations $t$). This kernel has the shape of the “Mexican hat” function, which in its discrete form has maximum value at inter-neuron distance in the case of $i = j$ whereas its value drops in a Gaussian manner as the distance increases. The width of this function decreases monotonically with time $t$. In this way convergence to the global optimum is attempted during the early phases of the self-training process, whereas gradually the convergence becomes more local as the size of the kernel decreases. Each time a new signal is fed into the network, the neurons compete and the one with the weight vector closest to the signal, according to Eq. (6) is selected to fire. The firing neuron adjusts its weight vector so that it matches even better the incoming signal. Its neighbouring neurons modify their weight vectors so they also resemble the input signal, but less strongly, depending on their distance from the winner. This learning mechanism is completely defined by the $h_{ij}(t)$ kernel, as it has been described above.

The above process achieves spatial coherence within the network of neurons as long as the input signal is concerned. This property is equivalent to clustering since after self-training, the neurons form clusters which reflect to the input signal (data points).

3.2. Seeded region growing algorithm

A 3D adaptive region growing procedure was applied in order to segment MR cardiac images. The user selects a voxel inside the chamber, which serves as the seeding point for a three-dimensional (3D) region-growing algorithm. The modification from the classic algorithm lays to the criterion of accepting new voxels as belonging to the object of interest: a new voxel is accepted if its value is close to the current average value of the selected voxels. After its acceptance, the new voxel contributes to the calculation of the new average value of the selected voxels. This approach proved to be sufficient to segment the blood pool from the myocardial tissue because of the high contrast between them. The 3D seeded region growing algorithm can be described in pseudocode as following:

push the seed voxel into the stack

**REPEAT**

pop the last voxel from stack

IF (the voxel complies with the selection criterion) AND (it is not marked) THEN

mark it as “object voxel”

push its six neighbours

(3D) in the stack

UNTIL the stack is empty

3.3. Assessing the results of the LV segmentation

Six phases of spin echo cine MR images, equally distributed along the heart cycle, including end sys-
Table 1
MR cardiac image segmentation: comparison between manual and automatic techniques as a function of cardiac averaged for all patients

<table>
<thead>
<tr>
<th>Cardiac phase</th>
<th>Region growing</th>
<th>K-Means</th>
<th>Kochonen</th>
<th>Fuzzy K-means</th>
<th>Manual</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Normal</td>
<td>Pathologic</td>
<td>Normal</td>
<td>Pathologic</td>
<td>Normal</td>
</tr>
<tr>
<td>1</td>
<td>3394</td>
<td>4934</td>
<td>3388</td>
<td>4703</td>
<td>3655</td>
</tr>
<tr>
<td>2</td>
<td>2888</td>
<td>3801</td>
<td>2739</td>
<td>2967</td>
<td>2608</td>
</tr>
<tr>
<td>3</td>
<td>1397</td>
<td>2207</td>
<td>1529</td>
<td>1727</td>
<td>1524</td>
</tr>
<tr>
<td>4</td>
<td>2037</td>
<td>2383</td>
<td>1764</td>
<td>2004</td>
<td>1798</td>
</tr>
<tr>
<td>5</td>
<td>2803</td>
<td>3582</td>
<td>3098</td>
<td>3754</td>
<td>3094</td>
</tr>
<tr>
<td>6</td>
<td>3115</td>
<td>3894</td>
<td>3411</td>
<td>3743</td>
<td>3648</td>
</tr>
</tbody>
</table>

Table 2
Percentage of error in volume estimation of each of the four different automatic techniques for all 3D phases, relative to the manual segmentation results

<table>
<thead>
<tr>
<th>Cardiac phase</th>
<th>Region growing</th>
<th>K-Means</th>
<th>Kochonen</th>
<th>Fuzzy K-Means</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Normal</td>
<td>Pathologic</td>
<td>Normal</td>
<td>Pathologic</td>
</tr>
<tr>
<td>1</td>
<td>−0.21</td>
<td>−3.37</td>
<td>−0.03</td>
<td>1.47</td>
</tr>
<tr>
<td>2</td>
<td>−11.38</td>
<td>−11.53</td>
<td>−5.63</td>
<td>12.94</td>
</tr>
<tr>
<td>3</td>
<td>−10.61</td>
<td>−6.52</td>
<td>−21.06</td>
<td>16.65</td>
</tr>
<tr>
<td>4</td>
<td>−16.33</td>
<td>−2.36</td>
<td>−0.74</td>
<td>13.92</td>
</tr>
<tr>
<td>5</td>
<td>8.34</td>
<td>9.29</td>
<td>−1.31</td>
<td>4.94</td>
</tr>
<tr>
<td>6</td>
<td>5.43</td>
<td>2.70</td>
<td>−3.55</td>
<td>6.47</td>
</tr>
</tbody>
</table>

Table 3
The coefficient of determination for linear regression between the automatic and manual segmentation for both normal and abnormal cases

<table>
<thead>
<tr>
<th>Automatic techniques</th>
<th>Normal</th>
<th>Abnormal</th>
</tr>
</thead>
<tbody>
<tr>
<td>Region growing</td>
<td>0.9425</td>
<td>0.9286</td>
</tr>
<tr>
<td>K-Means</td>
<td>0.9895</td>
<td>0.9936</td>
</tr>
<tr>
<td>Kochonen</td>
<td>0.9749</td>
<td>0.8933</td>
</tr>
<tr>
<td>Fuzzy K-Means</td>
<td>0.9688</td>
<td>0.9935</td>
</tr>
</tbody>
</table>

The following conclusions can be drawn from the above results, concerning the accuracy of automatic segmentation techniques:

– In normal LV segmentation, K-Means achieves an average error of 5.39% in volume measurement, with region growing being the worst with a 8.72% error.
In abnormal LV segmentation, region growing and K-Means achieve an error between 6% and 9%, with Fuzzy K-M and Kohonen being substantially worse (over 15–20%).

The abnormal LV volume tends to be overestimated by most methods.

Similar results are reflected in Table 3, where the K-Means algorithm achieves better correlation with the manual segmentation technique against the other tested techniques. Thus, in the present study, the K-Means algorithm was finally selected to segment cardiac ventricles for both normal and abnormal cases.

4. Endocardiac active surface modelling and definition of the measured parameter

The sequence of 3D images resulting from the segmentation step is binary with the pixels belonging to the chamber of interest having non-zero values. A surface modelled as a generalised cylinder is firstly initiated so that it surrounds the segmented object [17]. The cylinder starts to deflate until it reaches the non-zero voxels. The movement of the nodes of the modelled surface is presumed radial only. The connection between the nodes is supposed to be stiff enough to preserve the smoothness of the modelled surface after its final convergence. The surface is a stack of radial curves $R = R(\theta, z)$ and therefore can model only radial surfaces. The resulting surface can be mathematically formulated as follows:

$$R = R(\theta, z).$$

The organs of interest are usually convex (as the left ventricle – LV) and slightly concave (as the right ventricle – RV). In almost all cases the radial surface is capable of modelling the ventricular heart chambers. The active surface deflates at a constant rate, until each node encounters the object’s boundary. The rule that requires at least two neighbouring pixels to be locked before a node is permanently locked implements the initial energy term that is often mathematically described in active snakes implementations. This term enhances the system’s immunity to spurious noisy pixels as well as the smoothness of the resulting modelled surface.

Since the data are untagged MR images, the only measurable quantity was the radial displacement be-
between the end diastolic and end systolic phase (tagged MR images provide data with circumferential and radial displacement, allowing for the definition of a strain tensor). The radial displacement between the end diastolic and end systolic phase was measured for each node of the modelled epicardiac surface, encoded in shades of grey and normalised for the maximum and minimum displacements of all the 4D models of the study.

Fig. 5 shows the results of the K-Means LV segmentation, after the surface modelling, by superimposing the boundary on the relevant image slices for a normal study at end diastolic and end systolic phases.

5. Surface triangulation, creation of cardiac spatio-temporal (4D) models and WWW compatible file production

Having modelled the endocardiac surface of the ventricular chambers, the triangulation step follows in a straightforward manner. The elementary triangle $t_{ij}$ consists of nodes $p_{ij}, p_{i+1,j}, p_{i+j+1}$. where $p_{ij}$ denotes the $i$th node of contour $j$. The coordinates of each node are converted from cylindrical to Cartesian and stored into a text file along with the elementary triangles. The requirement was that the output file should be in WWW compatible format to allow WWW storing, transmission and retrieval, so VRML 2.0 was selected. Using the VRML’s scripting language, the series of the modelled surfaces covering the entire cardiac cycle, was animated in real time. Furthermore, the measured radial displacement was applied to the triangulated surfaces as texture. In this manner, myocardial wall motion abnormalities are visualised both as shade of grey information and as real time motion, allowing the expert to assess accurately and quantitatively infarcts or ischemic tissue.

Figs. 6 and 7 show the end diastolic and systolic phases captured from the animated VRML files of a normal LV and an abnormal LV, respectively. The radial displacement of each node between diastole and systole is encoded in shades of grey on the modelled endocardiac surfaces (light corresponds to small displacement and dark to large displacement). The asymmetric contraction of the abnormal LV, whose light region seems to remain almost still during the heart cycle, indicates an infarct.
6. Conclusions and future work

A technique has been presented for the visualisation of the anatomy and function of the left and right ventricular myocardium from gradient echo 4D untagged MR cardiac data. The principle steps of the method are: automatic 3D segmentation of the chambers of interest, surface modelling using a set of radial curves, definition and measurement of functional quantities and visualisation of their values and real time animation of the modelled textured surfaces, using the VRML 2.0 format.

The automatic segmentation techniques have shown to correlate well (5%) with manual segmentation results in normal cases. Automatic segmentation is less robust in abnormal cases, but with an average volume error below 10%. K-Means classification proved the most robust when both normal and abnormal cases are considered. Automatic cardiac segmentation is still a subject for research.

A fast and efficient WWW based technique has been developed for spatio-temporal model production of human cardiac chambers. WWW software tools have proven appropriate for visualisation and measurement of cardiac functional parameters. Preliminary results indicate diagnostic value of the proposed technique in recording perfusion abnormalities.

In the near future, we intend to extend our experimental tests to a wide range of pathologic situations to assess the system’s diagnostic usefulness.

References


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