

A Novel Technique to Classify Intra Cardiac Tumor and Thrombus in Echocardiography

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Abstract— This paper describes an automatic method for classification and segmentation of different intra cardiac masses in tumor echocardiograms. Correct diagnosis of the character of intra cardiac mass in a living patient is a true challenge for a cardiologist. To improve diagnosis accuracy, a novel fully automatic classification method based on Kernel Collaborative Representation is proposed to distinguish intra cardiac tumor and thrombi in echocardiography. First, a region of interest is cropped to define the mass area. Then, a unique globally denoising method is employed which yields better noise attenuation and edge enhancement, without destroying the important cardiac structures. For segmentation, SLIC method, based on a local version of K-means is used. Finally, the motion, the boundary as well as the texture features are processed by a Kernel Collaborative Representation Classifier to distinguish two masses. The proposed detected contours closely approximate the manually traced ones. The better accuracy and simple implementation make the proposed method beneficial to help the cardiologists make a diagnosis before the surgery.

Keywords— Automatic classification, echocardiography, Intra cardiac tumor and thrombi, Simple Linear Iterative Clustering, Collaborative Representation

I. INTRODUCTION

Intra cardiac masses are abnormal structures found within or adjacent to the heart. These structures lead to severe cardiovascular disorders and require careful diagnosis for prompt resection and treatment. There are two main types of intra cardiac masses namely: tumor and thrombi. Tumor is the swelling of a part of body caused by abnormal growth of tissues which exhibits mobility and thrombi is a blood clot (solid mass of platelets).

Tumor is again divided into two: primary tumor and secondary tumor. Primary cardiac tumors are rare entities. They originate from the heart and can occur in any tissues of it. They can be cancerous or non-cancerous. Approximately 75% of them in adults are benign, with the majority composed of myxomas. It has an irregular shape and a gelatinous consistency. Secondary tumors are more common than primary. They do not originate in the heart. They move to the heart after developing in another area of the body. Cardiac tumors may not cause symptoms or may produce a severe cardiac dysfunction like sudden heart failure or sudden drop in blood pressure due to bleeding in pericardium. They cause obstruction to the left ventricular filling. Patients are present with the embolization, intra cardiac obstruction and constitutional signs. Because of the high risk of embolization and sudden death, the tumors need prompt resection.

Intra cardiac thrombi are common findings in patients with ischemic stroke. This may lead to atrial fibrillation, enlarged atrial chamber and low cardiac outputs. Most patients with thrombi are treated with heparin and thrombolysis.

For the non invasive and low cost nature, echocardiography is widely used in diagnosis of intra cardiac masses. Echocardiography uses standard two-dimensional, three-dimensional, and Doppler ultrasound to create images of the heart. Echocardiography, also called an echo test or heart ultrasound, is a test that takes “moving pictures” of the heart with sound waves. You don’t have to stay in the hospital. It’s not surgery and doesn’t hurt.

The patient’s heart movements can be seen on a video screen. The echocardiographic identifications of intra cardiac masses have great impacts on the medical doctors’ decision, since different diseases are related with diverse therapy options. In general, the echocardiogram sequence shows that most intra cardiac tumors have a narrow stalk and a broad base. The surface may be friable or villous. The internal echoes are heterogeneous. The tumors show continuity with the atrial wall, with a high degree of mobility. The echocardiographic appearances of the thrombi are motionless, dense, ovoid, and echo reflecting.

Although intra cardiac tumors and thrombi are different in pathology, they behave similarly in echocardiography. Often, they are misinterpreted. In most hospitals, echocardiographic identifications are carried out by cardiologists manually. The diagnosis is time-consuming. Recognition depends on the image quality and techniques, as well as the cardiologist’s experience. Hence, the demand for an automatic classification is increasing, which is potential to improve the diagnostic accuracy and to guide which case should be recommended for a surgery. The ultrasound image analysis has been successfully employed in the computer-aided diagnosis for cardiovascular disease, such as revealing valuable ultrasound features in early stroke prediction, designing fuzzy rule-based decision support system in the diagnosis of coronary artery, and applying adaptive block matching methodologies in carotid artery wall and plaque dynamics. Nevertheless, it is still challenging in intra cardiac masses identification due to the similar echocardiographic appearance of two masses and the suboptimal image quality including large amount of speckle noise, signal drop-out, artifacts, and missing contours. So a novel method is required to classify the intra cardiac tumor and thrombi in echocardiograms

II. LITERATURE REVIEW

In recent years many works have been done in this area. The ultrasound image analysis has been successfully employed in the computer-aided diagnosis for cardiovascular disease, such as revealing valuable ultrasound features in early stroke prediction [7]. Stroke prevention includes treatment of carotid atherosclerosis, the most common underlying cause of stroke, according to a specific diagnostic algorithm. However, this diagnostic algorithm has proved insufficient for a large number of mostly asymptomatic subjects, which poses a significant research challenge of identifying novel personalized risk markers for the disease. This article illustrates the potential of carotid ultrasound image analysis towards this direction, with ultrasound imaging being a low-cost and non invasive imaging modality and ultrasound-image-based features revealing valuable information on plaque composition and stability.

In [2], fuzzy rule-based decision support system (DSS) is presented for the diagnosis of coronary artery disease (CAD). The system is automatically generated from an initial annotated dataset, using a four stage methodology: 1) induction of a decision tree from the data; 2) extraction of a set of rules from the decision tree, in disjunctive normal form and formulation of a crisp model; 3) transformation of the crisp set of rules into a fuzzy model; and 4) optimization of the parameters of the fuzzy model. The proposed methodology presents some limitations. The studied population was of high risk for CAD, and thus, the results are not representative for the general population.

In [10], an automatic method for classification and segmentation of different intracardiac masses in tumor echocardiograms is described. An objective image analysis method may be useful in heart diseases diagnosis. Image texture analysis is used to distinguish various types of masses. The presented methods assume that image texture encodes important histological features of masses and, therefore, texture numerical parameters enable the discrimination and segmentation of a mass. This technique is based on the network of synchronized oscillators is proposed for the image segmentation. This technique is based on a 'temporary correlation' theory, which attempts to explain scene recognition as it would be performed by a human brain. This theory assumes that different groups of neural cells encode different properties of homogeneous image regions (e.g. shape, color, texture). Monitoring of temporal activity of cell groups leads to scene segmentation. A network of synchronized oscillators was successfully used for segmentation of Brodatz textures and medical textured images.

In recent years there has been a growing interest in the study of sparse representation of signals. In [26] the authors concentrated mainly on the study of pursuit algorithms that decompose signals with respect to a given dictionary. Using an over complete dictionary that contains prototype signal-atoms, signals are described by sparse linear combinations of these atoms. Applications that use sparse representation are many and include compression, regularization in inverse problems, feature extraction, and more. K-SVD is an iterative method that alternates between sparse coding of the examples

based on the current dictionary and a process of updating the dictionary atoms to better fit the data. The update of the dictionary columns is combined with an update of the sparse representations, thereby accelerating convergence. The K-SVD algorithm is flexible and can work with any pursuit method (e.g., basis pursuit, FOCUSS, or matching pursuit).

In [18], the authors proposed a novel image denoising strategy based on an enhanced sparse representation in transform domain. The enhancement of the sparsity is achieved by grouping similar 2D image fragments (e.g. blocks) into 3D data arrays which they call "groups". Collaborative filtering is a special procedure developed to deal with these 3D groups. They realize it using the three successive steps: 3D transformation of a group, shrinkage of the transform spectrum, and inverse 3D transformation. The result is a 3D estimate that consists of the jointly filtered grouped image blocks. By attenuating the noise, the collaborative filtering reveals even the nest details shared by grouped blocks and at the same time it preserves the essential unique features of each individual block. The filtered blocks are then returned to their original positions.

In [17], the authors empirically compare five state-of-the-art superpixel algorithms for their ability to adhere to image boundaries, speed, memory efficiency, and their impact on segmentation performance. They then introduce a new super pixel algorithm, simple linear iterative clustering (SLIC), which adapts a k-means clustering approach to efficiently generate superpixels. Despite its simplicity, SLIC adheres to boundaries as well as or better than previous methods. At the same time, it is faster and more memory efficient, improves segmentation performance, and is straightforward to extend to superpixel generation.

It is still challenging in intra cardiac masses identification due to the similar echocardiographic appearances of two masses and the suboptimal image quality including large amount of speckle noise, signal drop-out, artifacts, and missing contours. While these methods may be effective for specific types of images, they are unsatisfactory in the intracardiac mass segmentation owing to the movement of cardiac chamber during the cardiac cycle. In the systolic stage, the chamber shrinks so small that it is filled with an intracardiac mass, with the atrial wall and the mass boundary overlapped. Considerable efforts have been made on the application of the computer aided classification, like the multilayer feedforward artificial neural network (ANN) the back propagation neural network (BPNN), the support vector machine (SVM), and the ensemble learning. Most of these classifiers require training stages and supervision from experienced cardiologists. Therefore, it is meaningful to find a stable classifier with a great capacity of generalization without any training process.

Here we aim at extending the idea of KCRC by further improving formulation details of KCRC and presenting specific methods to perform dimensionality reduction in kernel space.

III. PROPOSED SYSTEM

In this method, a novel method is proposed to classify the intra cardiac tumor and thrombi in echocardiograms. Different from other approaches, the contribution of this method is

incorporating the kernel collaborative region based classification into the algorithm.

The workflow diagram of this method is illustrated in Fig. 1. It involves the frame decomposition, automatic region of interests (ROIs) selection, globally despeckling, intracardiac mass segmentation, feature extraction, and classification.

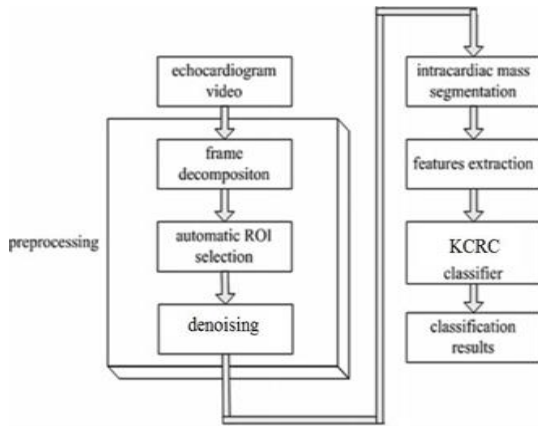


Fig.1. Workflow diagram for the proposed classification method

METHODOLOGY:

A. Frame Decomposition

The video means multiple frames. The captured video is converted into frames using matlab codes. The cardiologists acquire echocardiogram sequences when diagnosing the disease. To segment the intracardiac mass and evaluate its movement, the echocardiographic sequences are divided into consecutive frames beforehand. The typical duration of an echocardiogram sequence is about 3–4 s. The frame rate is 39 frames per second. Each decomposed frame is 480 × 640 pixels. Besides the scanned region, an echocardiogram depicts texts and labels, containing information about the patient and scanning transducer, as shown in Fig. 1. Compared with moving heart in two successive frames, these texts and labels are static. After subtraction of two successive frames, the static information are all removed, while the sector scanned region containing moving heart is remained. Then, the profile of the sector scanned region is detected and a rectangle covering the sector is identified. Finally, the original image is cropped to keep the scanned region for further analysis.

B. Automatic ROI Selection

In order to focus on the mass area, a ROI containing the mass and its surrounding tissues are defined. A coarse-to-fine iteration strategy for subwindows clustering is applied to automatically select the ROI. Fig. 1 depicts that compared with the mass and the myocardium, the cardiac chamber owns unique texture features, with lower intensities and uniformed distributions. Such intensity differences help to assort the images into two classes: the uniform areas (chamber) and the texture areas (the mass or the myocardium).

The classification is implemented with a coarse-to-fine strategy. The size of the initial subwindows is 40 × 40. Each

time, several texture features of subwindows, including the mean, the variance, and the gray level co-occurrence matrix (GLCM) [9] are calculated and input into a fuzzy K-means algorithm to cluster the similar subwindows. The uniform subwindows in a coarse position, which, in turn, are searched to get a fine position with half size of subwindows. The iteration ends when all remaining subwindows share the same intensity distribution. In a short axis view echocardiogram, the chamber usually lies near the cardiac center. So in the fine position, the Euclidian distance between each subwindow and the cardiac center is computed to trim off far-away windows and obtain final chamber location.



C. Denoising

Image denoising is the process of removing unwanted noise from an image. The noise can take a variety of forms and is introduced in differing amounts at each step during the acquisition of the image.

Speckle in ultrasound image is seen as a granular structure. This is caused by the constructive and destructive coherent interferences of backscattered echoes from the scatterers that are typically much smaller than the spatial resolution of medical ultrasound system. The speckle accompanies all coherent imaging techniques, namely LASER, SONAR, and synthetic aperture radar imagery (SAR). They are produced by interfering echoes of a transmitted wave form, which emanate from heterogeneities of the objects being interrogated. In this case, there is a possibility that a dark spot could be interpreted by a medical doctor as corresponding to a blood vessel or a cyst with relatively low reflectivity, while in fact, it might be merely caused by echoes compensating each other at opposite phases. Denoising operation removes the Gaussian noise.

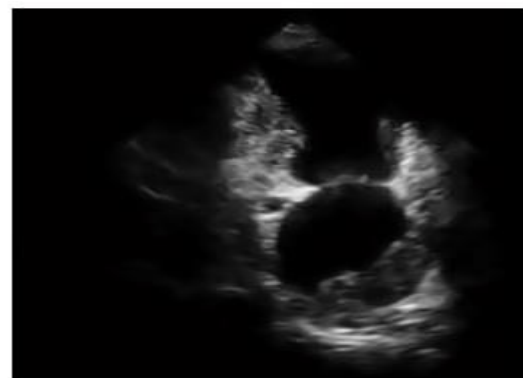


Fig. Denoised image

D. Intracardiac Mass Segmentation

As the basis for the further features extraction, extracting the boundary of the mass is of great importance. Since the intra cardiac mass has a base connected with the atrial wall, the mass and the atrial wall should be segmented together.

1) Initial Contour

Edge detection is a fundamental tool used in most image processing application. It is the process of detecting boundaries between objects and the background in the image, at which the image brightness changes sharply. There are many algorithms to perform edge detection. All of them are classified into two categories Gradient and Laplacian. Edge detection based on Gradient method initially calculates first derivative of image, and then find its corresponding local maxima and minima values to detect the edges. While, in the Laplacian method after obtaining the second derivative of the image it looks for zero crossing. The Canny edge operator is utilized to get a rough initial contour. In the Canny operator, the sigma of a Gaussian filter and the gradient threshold are both set as 1 edge operators perform Gradient method. These operators include a small kernel rolled up together with the image, which helps in estimating first order directional derivative of the image brightness distribution. This kernel finds edge strength in the direction, which are orthogonal to each other, usually vertically and horizontally. The total value of the edge strength is then obtained by the combination of both the components. Here by creating a matrix centered on each pixel it calculates the edge value. Moreover, if the calculated value is larger than provided threshold, then that pixel is classified as an edge. Canny edge detection is used as it has low error rate (good detection of only existent edges), good localisation and minimal response (only on detector response per edge).

2) SLIC Segmentation

Image processing is the process of reducing processing complexity by examining only those regions in the image that are of interest. It implies a higher level description of the image. Segmentation can be carried out using Simple Linear Iterative Clustering (SLIC) method.

SLIC is a simple and efficient method to decompose an image in visually homogeneous regions. It is based on a spatially localized version of k-means clustering. Each pixel is associated to a feature vector $\psi(x,y)$ and then k-means clustering is run on those. SLIC takes two parameters: the nominal size of the regions (superpixels) *regionSize* and the strength of the spatial regularization *regularizer*. The image is first divided into a grid with step *regionSize*. The center of each grid tile is then used to initialize a corresponding k-means (up to a small shift to avoid image edges). Finally, the k-means centers and clusters are refined by using the Lloyd algorithm, yielding segmenting the image. The parameter *regularizer* sets the trade-off between clustering appearance and spatial regularization.

SLIC adapts k means clustering but it is somewhat different from k means. Proposed method generate superpixels which is faster than the existing methods, more memory efficient, exhibits state-of-the-art boundary adherence and improves the efficiency of segmentation algorithms. The result of grouping pixels exhibiting similar features within local or global neighbourhood is termed as superpixel. Computer vision research experts have conceptualised Super pixel for many decades and contributed number of super pixel based approaches to improve accuracy and reduce complexities in image processing techniques.

Super pixel map depicts many desired properties:

- Representational efficiency: Pixel wise representation of image exhibits pair wise constraints between units, which needs to parse through in-between pixels to interact with target pixels. Connectivity and neighbourhood constraints plays important role. The seed-point in super pixel representation models much longer-range interactions between super pixels.
- Computational efficiency: The complexity of images from hundreds of thousands of pixels to only a few hundred super pixels reduces the computational cost and increases the image processing speed.
- Visual Meaning: The perceptual view of super pixel gives uniform and meaningful representation of image based on texture and color.
- It is near-complete: The structure of the image is mostly conserved, because super pixels are results of an over-segmentation. The loss due from pixel-grid to superpixel map is very little.

Simple linear iterative clustering is an adaptation of k means for super pixel generation, with two important distinctions:

- The number of distance calculations in the optimisation is dramatically reduced by limiting the search space to a region proportional to the super pixel size. This reduces the complexity to be linear in the number of pixels *N* and independent of the number of super pixels *k*.
- A weighted distance measure combines color and spatial proximity while simultaneously providing control over the size and compactness of the super pixels.

SLIC is simple to use. The fact of good pixel packing, and uniformity in size of pixels determine the performance of the proposed algorithm. The efficiency of the algorithm is measured by boundary recall and under-segmentation error measures. The k-means clustering generates superpixels by clustering pixels based on the color similarity and pixel proximity in the image plane. The clustering is done on the five-dimensional [labxy] space, where [lab] is the pixel color vector in CIELAB color space and xy is the pixel co-ordinates. The maximum possible color distance between two nearing colors in the CIELAB space (assuming RGB input images) is limited and the spatial distance is determined by the image size. The spatial distance is to be normalised in order to apply the Euclidean distance in this 5D space. Hence, new distance measure that considers superpixel size is applied, which enforces color similarity as well as pixel proximity in this 5D space, so that the expected cluster sizes and their spatial extent are mostly equal. By default, the only parameter of the

algorithm is k , the desired number of approximately equally sized super pixels.

SLIC algorithm consists of five steps.

Step 1: Initialize cluster centers $C_k = [l_k, a_k, b_k, x_k, y_k]^T$ by sampling pixels at regular grid steps S .

Step 2: Assign each pixel i associated with the nearest cluster center then introduce a distance measure D , which determines the nearest cluster center for each pixel.

Step 3: Compute new cluster centers by averaging all of the clusters in the cluster.

Step 4: Compute residual error E between new cluster center locations and previous cluster center locations

Step 5: Repeat assignment and update steps iteratively until the error converges.

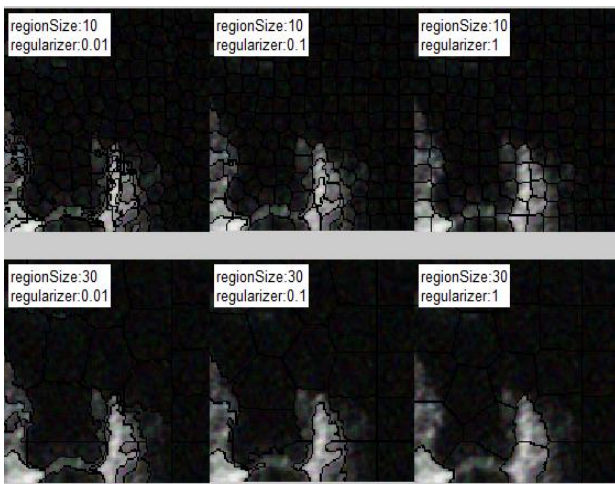


Fig. SLIC Segmentations

E. Feature Extraction

When identifying intra cardiac mass in an echocardiogram sequence, usually the cardiologists make the judgment based on two rules: the motion feature (the mass movement) and the boundary feature (the base length). Although two masses show differences in echo reflections, texture characteristics are visually indistinguishable due to the poor image quality. They are always omitted clinically. However, texture features, especially the mass internal echo is quite important in the classification. Here, for each segmented mass, three types of features are computed: the motion feature, the boundary feature, and the proposed texture features. The motion feature is a primary factor in mass recognition. During a cardiac cycle, intra cardiac tumors show high degree of mobility, while the thrombi stay motionless.

Another essential boundary feature is the base length. An Intra cardiac tumor has a narrow stalk connected to the atrial wall, whereas a thrombus lies entirely on the wall. The overlap length of these two masses with the atrial wall is different. Here, the base length is the Euclidian distance between two mass-atrial separation points. The base length of a thrombus is much longer than that of a tumor. In addition, texture characteristics derived within the mass are also considered. Three kinds of texture features are extracted. The GLCM is a common method for the texture feature analysis.

Five features derived from the GLCM (contrast, entropy, autocorrelation, energy and homogeneity) are computed.

E. KCRC Classifier

Image classification analyzes the numerical properties of various image features and organizes data into categories. To overcome the shortcoming of CRC in handling data with certain distributions (e.g. the same direction distribution), kernel technique is smoothly combined with CRC. Sparse representation classification (SRC) plays an important role in pattern recognition. Recently, a more generic method named as collaborative representation classification (CRC) has greatly improved the efficiency of SRC. By taking advantage of recent development of CRC, this paper explores to smoothly apply the kernel technique to further improve its performance and proposes the kernel CRC (KCRC) approach.

In CRC, the dictionary D is constructed by all training samples and a test sample y is coded collaboratively over the whole dictionary, which is the essence of CRC. Kernel function, also described as kernel technique, has become a simple yet useful tool in pattern recognition.

It is well-known that data nonlinearly transformed to high dimensional space is more separable. It could also avoid the same direction distribution of data. Obviously, the new features in kernel space also can be applied to CRC. However, mapping to high dimensional space makes optimization problem in CRC more complicated so that the dimensionality in the kernel feature space has to be reduced. The nonlinear mapping mechanism is formulated as

$$y \in R^m \rightarrow \phi(y) = [\phi_1(y), \phi_2(y), \dots, \phi_s(y)] \in R^s.$$

where $\phi(y)$ is the high dimensional feature associated to the sample y and $s \gg m$. Define that $d^{[j]}_i$ denotes the i th atom in D with the j th class label, in which $1 \leq i \leq n = \sum_{j=1}^k n_j$, but the class label $[j]$ will be removed for the convenience of description. According to the nonlinear mapping mechanism, the original dictionary D becomes a much higher dimensional one: $\Phi = \{\phi(d_1), \phi(d_2), \dots, \phi(d_n)\} \in R^{s \times n}$, and the test sample becomes $\phi(y) = \Phi x$. The model of KCRC can be formulated as

$$\hat{x} = \arg \min_x \|x\|_p \text{ subj. to } \|\phi(y) - \Phi x\|_q \leq \epsilon.$$

However, Eq. (10) is even harder to solve than the previous problem Eq. (5) because the high dimensionality leads to high complexity.

A dimensionality reduction matrix R , namely a projection matrix, can be defined or constructed by utilizing the methodology of KPCA [12] and KFDA [13]. With the matrix $R \in R^{s \times c}$, we could obtain

$$R^T \phi(y) = R^T \Phi x.$$

where R is related to the samples in the kernel space. In fact, each atom in R is a linear combination of samples in kernel feature space. Namely

$$\mathbf{R} = \Phi\Psi = \{\varphi(d_1), \dots, \varphi(d_n)\} \cdot \{\psi_1, \dots, \psi_c\}$$

where $\mathbf{R} = \{\mathbf{R}_1, \dots, \mathbf{R}_c\}$ and ψ_i is the n -dimensional linear projection coefficients vector corresponding to the $\mathbf{R}_i =$

$\sum_{j=1}^n \psi_{i,j} \varphi(d_j) = \Phi\psi_i$. $\Psi \in \mathbb{R}^{n \times c}$ is called pseudo-transformation matrix. Then we put Eq. (12) into Eq. (11):

$$(\Phi\Psi)^T \varphi(y) = (\Phi\Psi)^T \Phi x$$

from which we can get $\Psi^T K(D, y) = \Psi^T Gx$, where $K(D, y) = [K(d_1, y), \dots, K(d_n, y)]^T$. $G(G_{ij} = K(d_i, d_j))$ is defined as the kernel Gram matrix that is symmetric and positive semi-definite according to Mercer's theorem. Since G and $K(D, y)$ are given a priori, the last step is to find Ψ instead of finding \mathbf{R} . Several methods are introduced in [9, 12, 13] to determine the pseudo transformation matrix Ψ . Particularly, when Ψ is an identity matrix, no dimensionality reduction is applied. Moreover, Ψ can also be a random projection matrix to achieve dimensionality reduction.

After substituting the constraint in CRC model with equivalent kernel function constraint, we have

$$\hat{x} = \arg \min_x \|x\|_p \text{ subj. to } \|\Psi^T K(D, y) - \Psi^T Gx\|_q < \varepsilon$$

which is the model of KCRC approach. Additionally, a small perturbation would be added to $\Psi^T G$ if the norm of a column is close to 0. Namely, add a small number to every element of matrix $\Psi^T G$. The model of KCRC can be formulated to another form shown as follows:

$$\hat{x} = \arg \min_x \|\Psi^T K(D, y) - \Psi^T Gx\|_q + \mu \|x\|_p$$

from which we could derive two specific algorithms. With $p=2, q=2$, the l_2 minimization model can efficiently solve x with low computational complexity. The regularized least square algorithm is applied to solve this optimization problem.

IV. EXPERIMENTS AND RESULTS

The whole classification method was applied on the sequences after they were recorded and stored by the cardiologists. All sequences were processed from frame decomposition, automatic ROI selection, globally denoising, intra cardiac mass segmentation, and nine feature extraction. The KCRC was applied to the whole dataset to identify the masses.

V. CONCLUSION

In this paper, a new method is proposed for the classification of intracardiac tumor and thrombi in the echocardiograms. The mass area in ROI is automatic defined by a coarse-to-fine strategy. The denoising process yields better noise attenuation and edge enhancement, without destroying the important cardiac structures. The SLIC method is applied to segment the mass. Our detected contours closely approximate the manually traced ones. Nine features including the cardiologist's original selected features and new

texture characteristics are then extracted. They are capable of distinguishing two masses, whose values are identical with the clinical observations. Finally, all features are implemented to the KCRC. The simple classifier is able to identify the intra cardiac mass with an overall accuracy of 98% and a sensitivity of 100%. It can detect all intracardiac tumors. The better accuracy and simple implementation make the proposed method beneficial to help the cardiologists make a diagnosis before the surgery, providing a realistic performance benchmark for further research efforts.

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