Automatic left ventricle mitral valve detection and motion characterization

P. Brigger, S. Lundby and M. Kunt

Signal Processing Laboratory, Swiss Federal Institute of Technology
EPFL-Ecublens, CH-1015 Lausanne, Switzerland
email: brigger@lts.de.epfl.ch

RÉSUMÉ

L'objectif de ce travail est le développement d'un système automatique pour une analyse objective et quantitative de la valve mitrale du ventricule gauche dans une séquence d'images échographiques. Le ventricule gauche est le plus affecté par différentes maladies (infarctus post-myocardial, myocardite, etc.). La planification d'interventions médicales, l'analyse des conséquences d'un traitement (médical ou chirurgical) et la comparaison de séquences d'images nécessitent une description quantitative des différentes pathologies. Nous aimerions présenter une méthode d'analyse pour étudier le mouvement de la valve mitrale. La méthode s'avère stable dans le temps et robuste dans différents milieux bruités.

ABSTRACT

The work in this paper is directed towards the development of an automatic system for an objective and quantitative analysis of the left ventricle mitral valve in a sequence of ultrasound images. The left ventricle is the one most affected by different diseases (post-myocardial infarction, myocarditis, etc.). The planning of medical interventions, the analysis of the consequences of treatment (medical or surgical), and comparisons of different image sequences imply a quantitative description of the different pathologies. Here, we would like to present a possible analysis method for the movement of the mitral valve. The method is stable over time and robust in noisy image environments.

1 Introduction

For twenty years, medical radiology has developed imaging techniques to observe the interior of the human body. Some of these techniques include magnetic resonance (MRI), computed tomography (CTI, also called scanner imagery), nuclear medicine imagery (NMI) or ultrasound imagery (USI). Technical developments include systems which produce gray-scale cross-sectional images in real time allowing a spatio-temporal heart description. The left ventricle is the one most affected by different diseases. Pathologies might present themselves in different forms: regional disfunctioning (e.g. post-myocardial infarction, myocarditis), global disfunctioning with enlarged ventricle (congestive cardiomyopathy) or hyperkinesia with thickened myocardial walls muscle (hypertrophic obstructive cardiomyopathy (HCM)). The planning of medical interventions, the analysis of the consequences of treatment (medical or surgical), and comparisons of different image sequences imply a quantitative description of the different pathologies. These requirements make necessary automatic object detection by image analysis (segmentation), shape description, temporal characterization, the introduction of objective measuring criteria and algorithms which are stable over time and robust in noisy image environments.

In this paper, we deal exclusively with 2-D ultrasound images that have been obtained in collaboration with the Intensive Care Unit of the Centre Hospitalier Universitaire de Lausanne (CHUV). Ultrasound images have become popular for non-intrusive analysis of inner organs [1]. Furthermore, among the different pathologies, we are dealing with the one concerning the mitral valve (MV) of the left ventricle. In reference [2], the authors analyse the structural abnormalities of the papillary muscles by constructing an in-vitro model of the left ventricle. In reference [3], the different factors favoring the initiation of systolic anterior motion of the mitral valve (SAM) are studied in a model of the left ventricle in a pulsatile flow system simulating the left heart. A model left ventricle was developed in [4] for the study of mechanical dynamics. In reference [5], a finite element model was developed to examine deformation and stress patterns in the pathologic mitral valve under systolic loading conditions.
Surprisingly, only little work exists providing a quantitative analysis of heart pathologies, which is perhaps due to the lack of objective measuring systems to quantify the degree of sickness. In this work, we would like to address the problem of objective and quantitative description of the mitral valve.

2 Problem description

In a healthy heart, the heart opens and closes following the cardiac rhythm. The heart activity can be decomposed into four cycles (Fig. 1):

1. Phase diastole: the valve is open and the blood can enter the heart cavity.
2. End of the diastole phase: the valve closes.
3. Phase systole: the valve is closed and the blood is expulsed through the aorta.
4. End of the systole phase: the valve opens again.

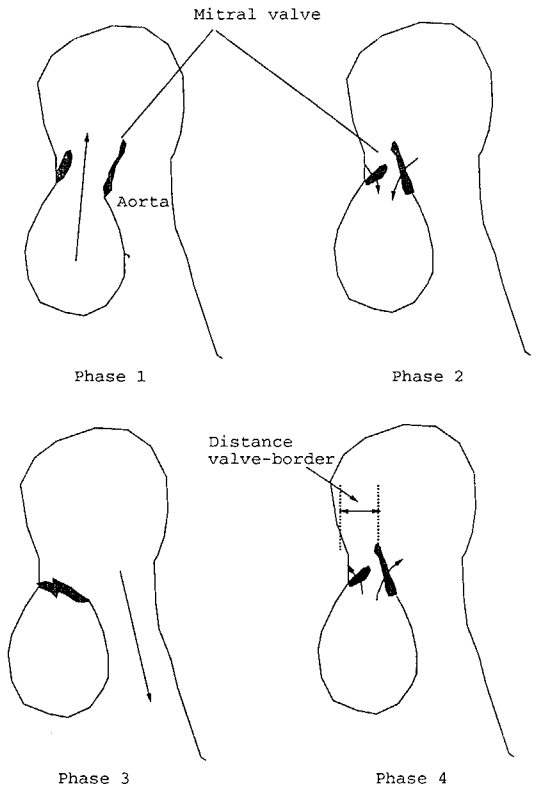

Figure 1: Illustration of the four phases of the valve activity.

The doctors from the CHUV have proposed a criterion which consists in measuring the distance between the valve and the endocardial left wall of the hearth throughout time. A healthy valve is characterized by a fast and permanent closure of the valve before blood expulsion through the aorta. In a sick heart, the valve is usually bigger in size and the left heart muscle is larger, resulting in a smaller exit channel for the blood, which implies systolic anterior motion of the mitral valve (SAM) that has a tendency to pull the MV towards the aorta with the blood flow. This movement hinders the blood to leave the heart cavity properly and may even imply improper closure of the valve. Patients with a defective MV often feel tired or even depressive because of a bad blood circulation and a lack of oxygen.

For medical analysis, it is important to quantify the valve motion. Consider the illustration in Fig. 2 for a healthy valve, where the distance between the top of the valve and the left heart wall remains constant when the valve is closed (Phase 1), then increases very rapidly (Phase 2) and only for a short moment when the valve is opened (Phase 3) and closes again firmly (Phase 4). For a malfunctioning valve (Fig. 3), the distance is more or less constant when the valve is closed (Phase 1), increases rapidly when the valve is opened (Phase 2), and then takes a certain time to return to the normal state (Phase 3). The distance may even increase again (Phase 4) when SAM takes place and the valve opens again. In this paper, an automated system for the detection of the MV and the LV endocardial border is given as well as an analysis method of the MV motion.

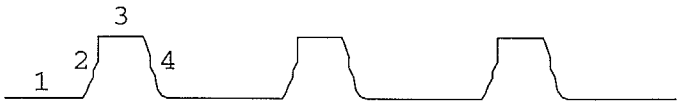

Figure 2: Illustration of the distance evolution for a healthy heart.

Figure 3: Illustration of the distance evolution for a diseased heart.

Image analysis is carried out using mathematical morphology [6]. It is appropriate, because it efficiently deals with size and contrast features. The language of MM is that of set theory. Sets represent binary and gray-level images. The image is compared to a probe of known shape, which allows to detect image features resembling the probe. This probe is called the *structuring element* and it is of simpler shape and size than the original object. Information about size, shape, and orientation can be obtained by transforming the image object using different structuring elements.

3 Technical approach

Three frames of an original sequence are displayed in Fig. 4. Image analysis is based on several steps:

1. Filtering of the sequence to remove granular noise.
2. Detection of the MV, marking of the top extremity of the valve.
3. Locating the left endocardial border.
4. Measuring the horizontal distance between the marker of the MV and the border. It permits to draw a graph which can be used by the doctors for subsequent analysis.

The different steps will be detailed in the next subsections.

Figure 4: Example of the first three frames of an echo-cardiographic image sequences.

3.1 Filtering

USI is a particular noisy image acquiring method. Removal or partial removal of this noise may not affect the visual image quality and may not suppress useful information, while at the same time it can facilitate the further image analysis such as segmentation and feature extraction. Techniques such as alternate sequential morphological filtering, which consist of alternate erosion-dilation operations which are sequentially iterated with increasing size, have shown good results in various applications [7, Chpt. 10], but they are not suited here because the image modifications are too important. We have obtained excellent results using a medium filter, which preserves the image features. Visually, the filtered image is quasi indistinguishable from the original, but subsequent analysis is much simplified and more accurate.

3.2 Marker extraction for the MV and endocardial border

There are two different markers to be extracted: the top of the mitral valve as well as the left ventricular border. In order to automate the detection process, a number of hypothesis are necessary which reflect the detection strategy used by a human observer. First of all, the valve is usually a thin, elongated object. Moreover, it is in many of the frames in a rather vertical position (Fig. 4). An excellent transformation to extract such kind of data is the *top-hat transformation* [8, 6]. It is defined as the difference of the original image with its opened version. Using a thin, horizontal structuring element allows us to obtain fine and mainly vertical objects, including the valve. Unfortunately, it also extracts small and wide objects, which have to be removed by an additional closing operation with a vertical structuring element. An opening of small size allows us to eliminate the holes in the valve. We now have a simplified sequence that contains only objects with a shape similar to that of the valve. However, a lot of parasite objects persist which are difficult to distinguish. At this point, looking for image areas which do not contain the valve is easier, and it will then allow to remove parasites inside this mask.

As a matter of fact, many parasite objects are situated inside the muscle tissue surrounding the heart cavity. Luminance intensity in echographic imaging is proportional to the thickness of the tissue, and thus the muscle tissue can be easily detected with a threshold operation. A closure followed by an opening operation eliminates small pieces of the valve which might have been detected by the threshold operation. The mask is shown in Fig. 5.

All objects which do not fall inside this mask are retained. The valve is presented in most of the frames, while other (parasite) objects appear and disappear in a sporadic manner. They are removed by introducing the time axis: an opening operation by a 3D structuring element will only retain those objects that are correlated in time, i.e. the mitral valve. It is now present in most of the frames, and can be interpolated for frames where it is missing.

It is straightforward to detect the top most point of the valve by a raster scan in direct video order.

The left-ventricular border is easily found from the mask image (Fig. 5). It is sufficient to extend a line from the point found on top of the valve to the left side until the mask image is hit. Three frames of the sequence with the markers for the top of the valve and the left border are indicated in Fig. 6.

Figure 5: Marker for the heart walls (excluding the MV)

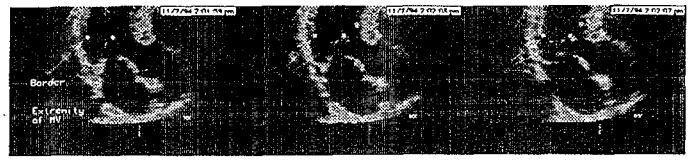

Figure 6: Tracked MV and left endocardial border (white points)

3.3 Temporal evolution characterization

The distance between the mitral valve and the left ventricle border is plotted in Fig. 7 for an image sequence of 26 frames. It nicely confirms the theoretical expectations. We can see that in the early systolic phase, the distance remains constant and then increases as the valve opens. It then decreases very rapidly as the valve closes and the heart expulses the blood through the aorta. Due to the SAM, the valve reopens again as can be observed by the slowly increasing distance and then gradually closes again.

4 Conclusions

In this paper, an automatic system was presented that allows a quantitative description of the movement of the mitral valve. A quantification measure is proposed by measuring the distance between the top of the mitral valve and the left ventricle endocardial border. It allows an accurate temporal description of the movement of the mitral valve. In the future, it will be interesting and necessary to apply the system to different image sequences of diseased as well as healthy hearts and to compare the different results obtained. It will have to be confirmed by doctors that this description method does provide a useful measure in clinical practice.

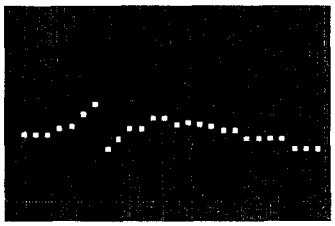

Figure 7: Temporal distance evolution

5 Acknowledgments

The authors would like to thank Dr. X. Jeanrenauld from the Intensive Care Unit of the Centre Hospitalier Universitaire de Lausanne (CHUV) for his precious advises.

References

[1] R.C. Waag. Medical ultrasound. *IEEE Transactions on Biomedical Engineering*, BME-30(8):429–449, 1989.

[2] X.P. Lefebvre, A. P. Yoganathan, and R. A. Levine. Insights from in-vitro vlow visualization into the mechanism of systolic anterior motion of the mitral valve in hypertrophic cardiomyopathy under steady flow conditions. *Journal of Biomechanical Engineering*, 114(3):406–413, August 1992.

[3] X. P. Lefebvre, S. He, R. A. Levine, and A. P. Yoganathan. Relationship between papillary muscle position, diastolic ventricular flow patterns and initiation of systolic anterior motion of the mitral valve in hypertrophic cardiomyopathy. In *Winter Annual Meeting of the American Society of Mechanical Engineers*, volume 20, pages 579–582, Atlanta, December 1991.

[4] C. M. Purut, M. C. Mauney, and P. K. Smith. An improved apparatus for in vitro study of mitral valve dynamics. In *Proc. of the 13th Annual Int. Conf. of the IEEE Engineering in Medicine and Biology Society*, volume 13, pages 2129–2130, Orlando, October 1991.

[5] K. S. Kunzelmann, R. P. Cochran, E. D. Verrier, Ch. J. Chuong, W. S. Ring, and R. C. Eberhart. Finite element analysis of mitral valve pathology. *Journal of Long-Term Effects of Medical Implants*, 3(3):161–179, 1993.

[6] J. Serra. *Image analysis and Mathematical Morphology*, volume 1. Academic Press, 1982.

[7] J. Serra. *Image analysis and Mathematical Morphology*, volume 2. Academic Press, 1988.

[8] F. Meyer. *Cytologie quantitative et morphologie mathématique*. PhD thesis, Ecole Nationale Supérieure des Mines de Paris, Fontainebleau, 1979.