

Review and Analytical Discussion of Cardiac Segmentation

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Purpose: Segmentation of the myocardium provides valuable information for diagnosis and treatment in cardiac pathologies. From the segmentation, we can measure the ventricular volume, ejection fraction, wall thickening, wall motion and myocardium mass whose information can help in the diagnosis of myocardial hypertrophy, myocardial infarction and ventricular arrhythmias among others [1,2]. But the detection of the myocardium is very challenging because of the signal loss, the presence of papillary muscles and that the borders are in contact with other organs that have similar intensities. Therefore, a lot of algorithms have been implemented to solve these issues but the problem still remains open. We will review the state-of-the art of the myocardium segmentation by describing the pros and cons of every method and complementing with new techniques the previous review of segmentation methods in short axis cardiac MR images [3].

Methods: Manual segmentation is very time consuming and it can be altered by inter- and intra-operator viability. Therefore, some semi-automated and automated methods are required and the main techniques are as follows: **1) Image-based:** Traditional methods of segmentation such as thresholding, region-growing, edge-detection and watershed. These methods have difficulty dealing with noise, grey scale variations and low gradients [4]. **2) Snakes:** it is a deformable contour that evolves under the direction of internal and external forces. External forces attract the curve to certain features of the image, such as the gradient or the region homogeneity whereas internal forces control the smoothness of the curve. An interesting work with snakes can be found in [5] which use two active contours one for the endocardium and another for the epicardium, a region-based term, an inter-contour force to regulate the separation of the two contours and a DDGVF (Dynamic Directional Gradient Vector Flow) an edge-based force which incorporates directional gradient information to push the contour passing the papillary muscles. In [6] they also incorporate a circular shape constraint to address the weak boundaries and poor contrast with the surrounding structures. The limitations of snakes are high sensitivity to initialization, local minima and the difficulty to work on images with noise or low contrast images. **3) Level Set:** It is a segmentation method based on an evolving surface in a higher dimensional space represented as a signed distance function. The evolution of the surface is based on energy function minimization. It is widely used in medical segmentation due to its numerous advantages which include the ability to deal with changes in topology, break and merge throughout the deformation and form sharp corners, allowing segmenting multiple objects or tracking objects that change a long time. In myocardium detection, these merits can be useful to separate the papillary muscles from the blood pool as described in [7]. There are a wide variety of works with the level set method whose main difference is the prior. Some examples of incorporation of priors are statistical shape models representing segmented training sequences by embedding functions and approximating these by a principal component analysis (PCA) [8] or elliptical shape constraints which approximates the myocardium by two ellipses and minimize the distance to the prior [9]. The level set segmentation performs well in noisy data but it can still be dependent to initialization or fall into a local minima. **4) Active Shape Models and Active Appearance Models:** It is a statistical shape model built up from a hand segmented training data. The model is compressed, commonly using PCA on the aligned data to capture the variability present in the training set. The representation of a new shape can be given by the linear combination of the principal axes obtained by PCA around the average shape. To search the model of an unseen image is required to find new target points for example edges, around the model points and given the shape model to estimate the rotation, scaling, and translation parameters which best fit these new target points followed by an update of the shape model [10]. Constraints are placed on the shape parameters to guarantee that the evolution of the shape has a similar shape to the training set. Active Appearance models (AAM) are an extension of active shape models whose main difference is that in addition to the shape variability, the texture variation is also incorporated to the model. In [11], the authors show how this approach can be applied for the segmentation of cardiac perfusion MRI. A novel multistage hybrid appearance model methodology is presented in [12] which combine the strengths of ASM that find local structures fairly well to the strengths of AAM because of AAM is less sensitive to local structures and boundary information. A time factor was also added in [13] to model the motion and consider the whole image sequence as a single shape/intensity sample. The main issues of these two methods are that the creation of a training set is a tedious and time-consuming task and that the accuracy of the segmentation relies in the variability of the training data set. **4) Graph Cuts:** It is a graph based image segmentation that finds a globally optimal segmentation solution by representing the image with a graph and obtaining the partition of the graph with the minimum cut [14]. Graph Cut has recently become very popular due to its efficient global optimization despite the sensitivity to the noise, the difficulty to include high level information in the formulation of the graph cut and the limitation to a set of energy functions. An interesting work can be found in [15] where the authors calculate a 2D spatial prior from every image by intersecting a model-based a priori information with each image plane and combine it with pixel intensity and edge information in the graph cut optimization. In [16], a parametric shape prior is incorporated and the authors minimize the energy function through an EM-style approach. **5) Atlas-based segmentation:** An atlas describes the relationships between several different structures and it can be obtained from a single segmented image or by integrating information from multiple segmented images [17]. An image can be segmented by mapping its coordinate space to that of the atlas. This process is known as registration [17]. As there are typically substantial shape differences among individuals non-rigid transformation may be desirable. To relate the image with the atlas a measure of alignment is required. One of the most used is normalized mutual information because it only measures the statistical dependencies between the intensity distributions but not the dependencies between the intensities directly. The main issue is that there is no anatomical constraint incorporated, making the atlas have little influence in the segmentation [3,18].

Discussion: A lot of methods and variants have been proposed to solve the heterogeneous and discontinuous epicardium wall and the separation of the papillary muscles from the endocardium wall. Although, the results shown are very promising the problem is still open. According to [3] based on the participant to MICCAI'09 the methods gave a higher error in the apical slice than in basal or mid-ventricular slices and the best results were obtained by image-based techniques. But these techniques require user interaction and cannot assess the ventricular shape whereas other methods like [19] and [20] whose methods use ASM and atlas registration, respectively offer a good compromise between performance and ambiguity. In conclusion, it is difficult to decide what method performs better.

References: [1] Y. Wu et al. *BMEI* 2009, 1-5. [2] H. Sun et al. *MICCAI* 2010. [3] C. Petitjean et al. *MedIA* 2011, 15(2): 169-184. [4] M.Lynch et al. *COMPUT BIOL MED* 2006, 36(4): 389-407. [5] S. Phumeechanya et al. *EMBS* 2008, 214 – 217. [6] L. Liu et al. *Inform Tech J* 2009, 8(4):486-494. [7] M.Lynch et al. *COMPUT MED IMAG GRAP* 2006, 30(4):255–262. [8] T Kohlberger et al. *MICCAI* 2006. 9(pt1):92-100. [9] M Alessandrini et al. *CinC* 2010, 409 - 412. [10] T.F.Cootes and C.J.Taylor. *BMVC* 1992. 266-275 [11] M. Stegmann et al. *Intl. Soc. Mag. Reson* 2001, 9:827. [12] S. Mitchell et al. *IEEE Trans. Med. Imag* 2001, 20(5):415-423. [13] B. Lelievredt et al. *IPMI* 2001, 446. [14] Z. Wu and R. Leahy. *IEEE Trans. Pattern Analysis and Machine Intelligence* 1993, 15(11): 1.101-1.113. [15] X. Lin et al. *EMBS* 2005, 3: 3059-3062. [16] J. Zhu-Jacquot. *ICASSP* 2008, 521-524. [17] T. Rohlfing et al. *The Handbook of Medical Image Analysis* 2005, 3:435-486. [18] X. Zhuang et al. *SPIE* 2008, 6914(2008): 691408. [19] S. O'Brien et al. *MIDAS* 2009. [20] M. Jolly et al. *MIDAS* 2009.