Analysis of 4D Cardiac Magnetic Resonance Images

Mikkel B. Stegmann
Informatics and Mathematical Modelling, IMM, Technical University of Denmark, DTU
Richard Petersens Plads, Building 321, DK-2800 Kgs. Lyngby, Denmark
Tel. +45 4525 3422, Fax 4588 1397, e-mail: mbs@imm.dtu.dk

Introduction

Magnetic resonance imaging (MRI) has been shown to be an accurate and precise technique to assess cardiac volumes and function in a non-invasive manner and is generally considered to be the current gold standard for cardiac imaging[1]. Measurement of ventricular volumes, muscle mass and function is based on determination of the left-ventricular endocardial and epicardial contours as shown in Fig. 1. Since manual contour delineation is both laborious and subjective, automated segmentation is highly desirable as a fast, objective and reproducible alternative. Automated segmentation thus enhances comparability between and within cardiac studies and increases accuracy by allowing acquisition of thinner MRI-slices otherwise prohibited by the vast amounts of data produced.

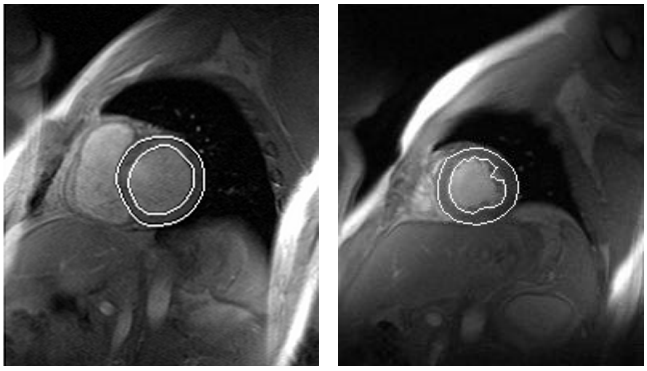

Fig. 1. Examples of automated delineation of the endo- and epicardial contours of the left ventricle in a single slice of short-axis cardiac MRI. Each image shows the right ventricle to the left of the contours and the dark region to the right is the lung.

To address the above issues we are currently investigating and developing methods for automated segmentation of the left ventricle. The research falls into two main segmentation applications, i) estimation of ejection fraction, related to the amount of blood pumped out at each heart beat and ii) estimation of regional myocardial perfusion. This presentation is limited to the former.

Data

MRI data for an ejection fraction study is typically a multi-slice multi-phase short-axis cine-sequence, i.e. true four-dimensional data. Temporal registration to the heart cycle is obtained by ECG-triggered MR-acquisition. This ensures that frame 1 of the sequence corresponds to maximal expansion of the ventricle, i.e. the end-diastole. Temporal sampling frequency is 55 ms and the duration is one cycle, i.e. the number of frames depends on the heart rate. The spatial sampling frequency is highly anisotropic – due to the trade-off between dynamic and spatial resolution – in this case volumes of *N*x256x256 voxels are acquired, where the number of slices, *N*, is approx. 25 (see Fig. 2). Refer to the web address[5] for a movie showing a full 4D data set.

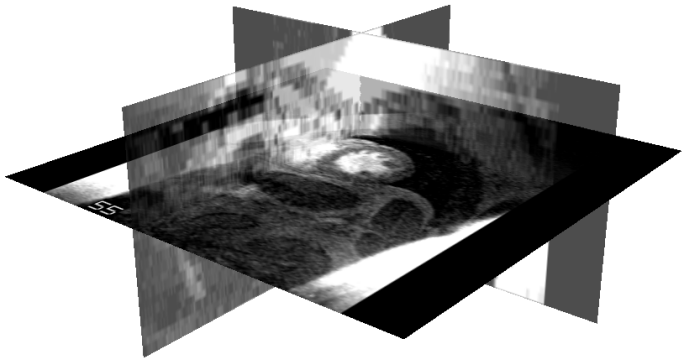

Fig. 2. Cardiac MRI volume visualized using three orthogonal cutting planes (secondary planes are semi-transparent).

The above specifications may vary dependent on hospital practice and scanner manufacturer. The data presented here is produced using a Siemens 1.0 Tesla Impact MR scanner.

Method

To perform single-slice segmentation we use statistical models of shape and appearance, namely the deformable model: Active Appearance Model[2] (AAM). In this section the outline of the method is presented. For details refer to[2,3].
AAMs elegantly encompass learning shape and texture (appearance) variability from examples simultaneously. The major steps in the analysis are as follows:

Training

1) A set of representative images is chosen and annotated by experts. 2) The training set is spatially aligned using a Generalized Procrustes Analysis. 3) A prototype shape is chosen, i.e. a mean shape is estimated. 4) Appearance variation is collected in a consistent manner by establishing a piece-wise affine warp between the prototype and each training example. 5) To derive a specific and compact representation of the biological shape (landmarks) and appearance (pixels) variation a principal component analysis (PCA) is performed on the aligned training set (w.r.t. shapes and pixels). 6) The compact parameterisation from the PCA is then used to generate synthetic images of the object in question (e.g. left ventricle).

Segmentation

1) The model is automatically placed in an initial configuration over the (unseen) image. 2) Using a principal component multivariate linear regression model, new images are generated to fit the unseen image in the best possible way. If the process converges with a satisfactory result, a match (of the ventricle) is declared.

Step 1 of the segmentation process is accomplished using a developed initialisation method[4]. After a match has been declared, a further refinement is carried out using simulated annealing-based optimisation[3].

Case study

In a single-slice study, 14 spatially corresponding short axis end-diastolic MRIs were selected from 14 individuals. The chosen slice position represented low morphologic complexity and high contrast. The images were acquired using an ECG-triggered breath-hold fast low angle shot (FLASH) cinematographic pulse MR sequence. The image matrix size was 256x256 pixels. The endocardial and epicardial contours of the left ventricle were annotated manually by placing 33 landmarks – i.e. corresponding points between the 14 hearts – along both the endocardial and epicardial contours.

AAMs were built on the set of slices using a leave-one-out scheme, thus leading to 14 evaluations. Consequently, each model consisted of 13 examples leaving one annotation (ground truth) to compare against. Each model consisted of approx. 2200 pixels in the texture model and 66 points in the shape model. More than 95% of the combined variation (texture and shape) was explained using 10 model parameters. The mean landmark accuracy of all 14 leave-one-out evaluations was 1.06 (±0.56) pixels, calculated as mean distance to the associated border[3]. Example results are given in figure 1. Using a multi-scale image representation the segmentation time per slice is below one second on a normal PC.

Summary and a look to the future

Automated cardiac image analysis is expected to replace resource demanding, error prone and subjective routine post processing.

Future work will include multi-slice multi-phase models striving towards a full-volume, full-cyclic statistical model of the human heart. Challenges herein are i) higher morphologic complexity (presence of so-called papillary muscles inside the ventricular blood pool), ii) lower contrast and iii) a substantial increase in memory requirements and computational complexity. In addition, one major challenge remains, i.e. to obtain the landmarks, which is very cumbersome due to the vast amount of data produced in true 4D models.

In summary, the results up till now have been promising and future developments of the methods into true 4D models are expected to yield an accurate, objective and fast alternative allowing for implementation in clinical practice and for large-scale research studies.

Acknowledgements

DMSc Henrik B. W. Larsson, M.D. Jens C. Nilsson, M.D. Bjørn A. Grønning and M.D. Dorthe Pedersen, H:S Hvidovre Hospital are gratefully acknowledged for providing data and revealing the details of cardiac MR acquisition.

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About the author

Mikkel B. Stegmann received his M.Sc. in Engineering from The Technical University of Denmark, DTU, in 2000 and is currently enrolled in the mathematics Ph.D. programme at Informatics and Mathematical Modelling, IMM, DTU with the project title *"Automated Segmentation and Analysis of Cardiac MRI using Statistical Image Analysis"*. The Ph.D. project is a collaboration between IMM and The Danish Research Centre for Magnetic Resonance, H:S Hvidovre Hospital and is funded by The Danish Medical Research Council.