Automated Segmentation of Cardiac Magnetic Resonance Images

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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 borders. Since manual border detection is laborious, automated segmentation is highly desirable as a fast, objective and reproducible alternative. Automated segmentation will thus enhance comparability between and within cardiac studies and increase accuracy by allowing acquisition of thinner MRI-slices.

This abstract demonstrates that statistical models of shape and appearance, namely the deformable models: Active Appearance Models [2], can successfully segment cardiac MRIs.

Methods

In this section, the outline of the AAM method is presented. For details, refer to [3, 4]. 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 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 thin-plate or 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 (e.g. of the ventricle) is declared.

Step 1 of the segmentation process is accomplished using an initialisation method described in [4, 5]. After a match has been declared, a further refinement [4] is accomplished based on the random-sampled optimisation scheme, Simulated Annealing.

In the current 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 over 15 heart cycles using an ECG-triggered breath-hold fast low angle shot (FLASH) cinematographic pulse sequence. Slice thickness=10 mm; field of view=263x350 mm; matrix 256x256. The endocardial and epicardial contours of the left ventricle were annotated manually by placing 33 landmarks - i.e. corresponding points between and within populations - along both the endocardial and epicardial contours. The annotation was performed by two experts.

Results

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 pixels, calculated as mean distance to the associated border [4]. Example results are given in figure 1. A typical segmentation was performed within a few seconds. Preliminary work using a multi-scale image representation has shown that this could be reduced to below one second.

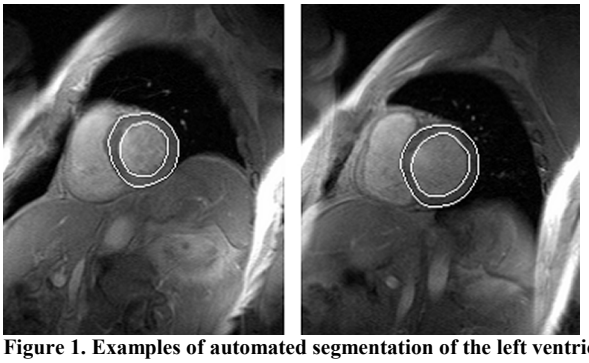

Figure 1. Examples of automated segmentation of the left ventricle in short-axis cardiac MRI.

Discussion

It has been shown that statistical image analysis can be applied successfully on 2D cardiac MRI with low morphologic complexity and high contrast. An initialisation technique has been designed which yielded a fully automated localisation of the left ventricle. Refinement of the model fit using simulated annealing was utilized for increased landmark accuracy yielding a mean landmark accuracy of 1.06 pixels.

Segmentation of 2D cardiac MRIs using AAMs has previously been done by Mitchell et al. [6]. A total of 102 images were used for the training set reaching a mean point accuracy of approx. 1 pixel on the endocardial and epicardial contour. Annotated structures were the right ventricle and the endocardial and epicardial contours of the left ventricle. The model was initialised manually.

Further work will include larger training sets to increase accuracy and multi-slice multi-phase models striving towards a full-volume, full-cyclic statistical model of the human heart. Main challenges herein are occasional higher morphologic complexity (presence of papillary muscles) and lower contrast besides the general increase in memory requirements and computational complexity.

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