Fast Registration of Cardiac Perfusion MRI

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MR scanners. Changes in image intensity during the bolus passage are modelled by an Active Appearance Model augmented with a cluster analysis of the training set. Preliminary validation carried out using five subjects showed acceptable segmentation accuracy produced very rapidly (below 40 ms per image).

Introduction

Within the last decade magnetic resonance imaging has been proven able to assess myocardial perfusion. However, the required amount of manual post-processing renders the method prohibitive to clinical practice. Most work is spent marking up of points of correspondence on the myocardium, thus registering the perfusion sequence. We propose a replacement of this tedious and error prone labour, which provides a structured manner of collecting and applying expert knowledge given by medical doctors.

Data

The data material comprises 250 myocardial perfusion, short-axis, magnetic resonance images. For each of five subjects, 50 sequential images were selected before, during and after the bolus of contrast (Gd-DTPA). Breath-hold was not used and the time-gap between images was approximately three seconds. Registration relative to the heart-cycle was obtained using ECG-gating. Matrix size was 128x128 pixels. Endocardial and epicardial contours of the left ventricle (LV) were annotated using 66 landmarks. To fixate in-plane rotation, the right ventricle (RV) was annotated using 12 landmarks.

Methods

The proposed method builds on the Active Appearance Models (AAMs) [1], which recently has proven very successful in many different medical applications [2]. AAMs establish a compact parameterisation of object variability, as learned from a training set. The modelled object properties are shape and pixel intensities (texture). From these quantities new images similar to the training set can be generated. Objects are annotated by marking up each example with points of correspondence over the set by hand or by automated methods. Using a learning-based optimisation scheme, an AAM can rapidly be registered to unseen images.
Contrary to sequences of perfusion images, AAMs traditionally deal with single images. However, texture variability could be modelled as one observation per sequence providing a more specific model. Regrettably, to model this behaviour properly, far more training sequences would be required compared to taking each frame as an observation. Consequently, given the low number of sequences, we treat each image in a sequence as an observation. Circumventing the need for large training sets unfortunately violates the assumption in AAMs, that the texture variation is well modelled by a multivariate Gaussian. Due to the radical changes in intensity during contrast uptake this is clearly not the case. Fig. 1 (left) shows the two most significant texture parameters in an AAM, for 200 images in the data set. Here it is verified that the expected clustering is very conspicuous. Modelling these textures with a multivariate Gaussian gives rise to several problems. The resulting model is not very specific and can easily generate textures that are not plausible to occur during a perfusion bolus passage. In order to model the distribution of textures above we propose an unsupervised learning approach that model texture variation using an ensemble of linear subspaces. We have chosen a standard *k*-means classification combined with a Monte Carlo simulation scheme where several classifications are carried out, based on different initial random class centres. The obtained classification of the data set, using five classes, is shown in Fig. 1 (middle). From this classification, a set of AAM texture models is obtained with corresponding parameter update matrices following [1]. As changes in texture over the sequence is assumed to be uncorrelated with shape, building a joint shape model from all sequences yields the best estimate of an inter- and intra-subject shape variability. We call this joint model a *Cluster-aware AAM* (CAAM). Fitting a CAAM to unseen images now involves choosing the appropriate texture model. Model selection is performed by exhaustively trying all models, then selecting the model producing the best fit. Finally, the fact that changes in pose and shape are uncorrelated with the change of texture is used to initialise and constrain the model fitting process. In the stable period after the bolus passage a prior model of the shape pose is estimated. This model is subsequently applied before and during the bolus passage to stabilize the CAAM search.

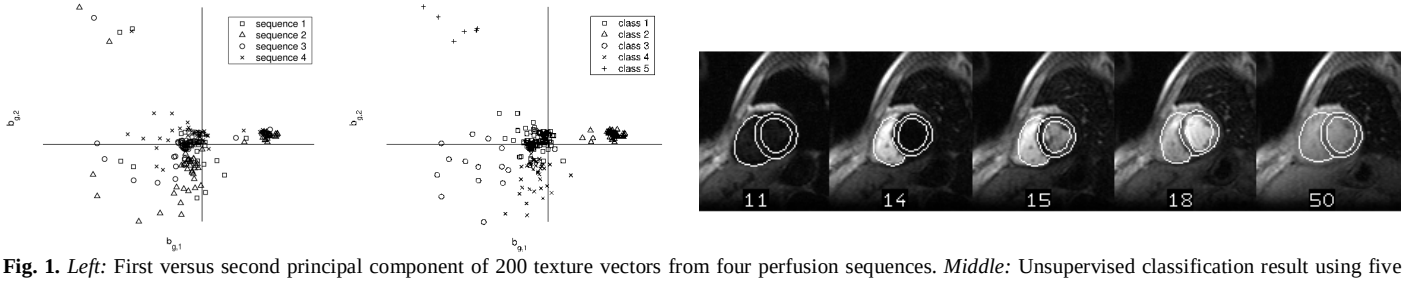

Fig. 1. *Left:* First versus second principal component of 200 texture vectors from four perfusion sequences. *Middle:* Unsupervised classification result using five classes. *Right:* Segmentation results before, during and after the bolus passage.

Results

To evaluate the proposed method a Cluster-aware AAM using five classes was built on four perfusion sequences of 50 frames each. The stable period was manually set to the last 25 frames of each sequence. Using hold-out evaluation the model was tested on the fifth sequence. The mean landmark error for LV and RV was 1.25 pixel (distance from landmark to ground truth contour) using 1.7 second of CPU time on a standard PC. Selected frames are shown in Fig. 1 (right).

Discussion

We have described a novel, data-driven method for registration of cardiac perfusion MRI. Very few assumptions concerning the data content have been made. Almost all parameters are estimated from training data, rather than being hard-coded into a computer framework. We believe this to be a very fruitful approach, as the method easily adapts to new expert knowledge. Preliminary validation of the method, showed high segmentation accuracy, considering the small number of subjects available. We anticipate a substantial increase in accuracy as more training data becomes available. Typically, cardiac perfusion images are acquired for several slices in the apex-basal direction. An extension of our method is straightforward to implement by concatenating texture vectors to obtain one joint multi-slice model. The running time of the method is below two seconds for a 50-frame perfusion sequence and can easily be sped up. Thus, the method provides means for segmentation in an on-line setting, e.g. for live motion-compensation in MR scanners.

References

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