Automatic segmentation of LV volumes in murine cine MR data using an EM-MRF algorithm with partial volume correction

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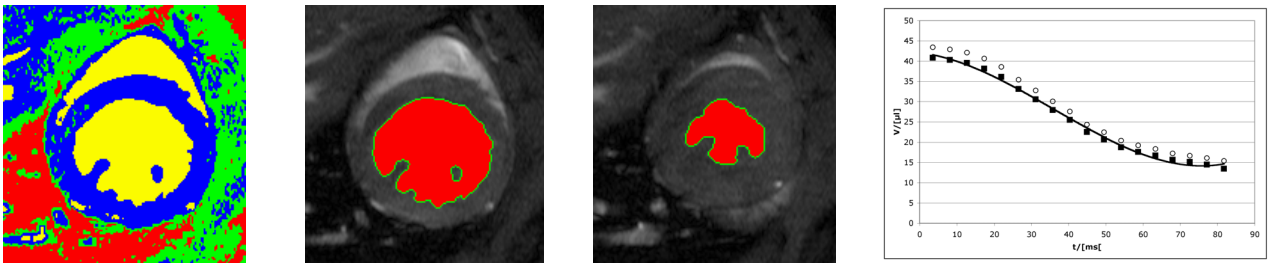
Introduction: Genetically modified mice are commonly used as models for human cardiac disease, and high-resolution cine magnetic resonance imaging has been applied successfully to quantify myocardial mass and function in mice (e.g. (1, 2)). However, left ventricular end-diastolic (EDV) and end-systolic volumes (ESV) have to be segmented in the respective cine frames in 6-10 short axis slices to determine cardiac function, which involves a considerable amount of user-input and time. Various methods – model-driven or model-free – have been proposed in the past for functional analysis of human cardiac MR images (see (3) for a review). We developed a novel approach based on an expectation-maximization (EM) algorithm, combined with a Markov random field (MRF) model and partial volume correction, and applied it to murine cardiac cine images.

Methods: The algorithm can be divided into three steps:

- Different tissue types, corresponding to a range of image intensities, are modelled as Gaussian distributions each of which is characterised by the parameter vector $x_i=(\mu_i,\sigma_i)$ (with μ_i: mean and σ_i: variance). The probability of a pixel belonging to one of the tissue types can be calculated using Bayes' theorem and a two-step EM-algorithm is then used to iteratively fit the model parameters (μ_i,σ_i) to the data.
- A Markov random field model is incorporated into the EM-algorithm in order to take spatial information of each pixel into consideration.
- Partial volume effects are corrected based on a linear combination of Gaussian distributions for combined image intensities in one pixel (4, 5).

The algorithm was applied to stacks of murine 2D cine-MR-data obtained at 11.7 T covering the entire heart with a spatial resolution of 0.1×0.1×1 mm and a temporal resolution of 4.6 ms (20-30 frames per heart beat).

Results:



(a) (b) (c) (d)

Fig. 1a shows the result of the statistical classification of a murine mid-ventricular end-diastolic frame in short-axis orientation based on the EM algorithm. Tissue intensities were modelled with four Gaussian distributions (red: 5.4±3.2; green: 23.7±8.3; blue: 39±13; yellow: 112±30; mean±variance). Fig. 1b and 1c shows short-axis images through the same mouse heart with the EDV and ESV of the left ventricle segmented (areas in red, boundaries in green). Note that the papillary muscle – although isolated inside the cavity – is still classified correctly. The overall EDV and ESV obtained by the automated segmentation compared well with values obtained manually (difference: 11±3% for EDV and 6±4% for ESV, respectively, n=3). Fig. 1d shows a time-volume curve for the entire left ventricle of the mouse with (filled symbols) and without (empty symbols) correction of the partial volume effect. Fitting this curve (line in Fig. 1d) allows for determination of the contractility of the left ventricle ((dV/dt)=-0.57 µl/ms for the example shown).

Discussion & Conclusion:

The aim of our work was to establish a method that can be routinely used to analyse the increasing amount of functional data obtained from mouse hearts *in vivo*. Our initial results for EDV and ESV of the left ventricle using the automated segmentation agreed well with data obtained manually. In particular, this approach allowed for constructing a time-volume curve for the left ventricle (in (6) it is calculated for a single slice only). We are currently extending our algorithm to overcome the problem of signal voids, caused by flowing blood in the relaxation phase of the heart. This will allow for the measurement of relaxation and contractility of the heart and therefore maximise the physiological information available. Further work is also required to characterize the method in respect to stability, robustness and dependence on signal-to-noise ratio.

Acknowledgement: This work was funded by the British Heart Foundation (BHF). We would like to thank Dr. J. Saunders for his programming skills.

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