

Infarct Segmentation of the Left Ventricle Using Graph-Cuts

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Abstract. Delayed-enhancement magnetic resonance imaging (DE-MRI) is an effective technique for imaging left ventricular (LV) infarct. Existing techniques for LV infarct segmentation are primarily threshold-based making them prone to high user variability. In this work, we propose a segmentation algorithm that can learn from training images and segment based on this training model. This is implemented as a Markov random field (MRF) based energy formulation solved using graph-cuts. A good agreement was found with the Full-Width-at-Half-Maximum (FWHM) technique.

Keywords: Segmentation, Delayed-enhancement MRI, Left ventricle, Graph-cuts.

1 Introduction

Acute and chronic infarction in the myocardium has important prognostic implications in patients suffering from heart diseases. There is growing evidence suggesting that the use of Cardiovascular Magnetic Resonance CMR using DE-MRI sequences can be considered the gold-standard modality for assessment of infarct. However, the optimal technique for quantifying DE in DE-MRI is still debatable. An excellent survey and evaluation of these techniques can be found in [1]. The two highly used techniques, owing to their ease of implementation and simplicity, is the FWHM and standard-deviation (SD) techniques. The latter fixes infarct to be a certain number of standard deviations from healthy myocardium, and the former defines infarct to be above half of the maximal signal within infarct. Although there is now strong evidence that the FWHM technique is highly reproducible [1] and at least one body of work establishing correlation with histology studies [2], it still remains unclear why the chosen half of the maximal signal in FWHM would universally conjure the right quantification for infarct in DE-MRI.

In this work, we present a segmentation method for the data provided as part of the MICCAI challenge on ventricle DE-MRI data from humans and animals.

It is based on a probabilistic tissue intensity model of DE-MRI data, which is derived both from training and the unseen data. The algorithm uses a Markov random field (MRF)-based energy formulation that is solved using graph-cuts [3]. The method of graph-cuts has shown high accuracy, simultaneous ROI detection, and scalability to three dimensions in segmenting structures [4]. It has been applied in a wide variety of segmentation problems arising in computer vision and medical image processing [5,6,7]. It is used in this work to efficiently solve the MRF model. The main advantages of employing the graph-cut technique in ventricle DE-MRI quantification are the following: 1) Uses a training model and thus the algorithm can be trained prior to suit to the quality of enhancement in the test cohort, and 2) Regions of infarct segmented are generally continuous and free from *salt-and-pepper* holes commonly encountered in thresholding techniques such as FWHM and SD.

2 Methods

The segmentation of infarct from DE-MRI can be described as assigning a label $f_p \in \{0, 1\}$ to every voxel p in the search space of the image. The search space for infarct is myocardium and a binary segmentation is assumed to be readily available. Voxels representing infarct tissue are assigned the foreground class label $f_p = 1$ and non-infarct or healthy tissues are assigned background class label $f_p = 0$. Given the observed intensities in the search space of the image and prior knowledge about infarcts, the segmentation problem can be solved using a probabilistic framework where the maximum *a posteriori* (MAP) estimate is computed using Bayes' theorem:

$$\arg \max_{\mathbf{f}} P(\mathbf{f}|\mathbf{I}) = \frac{P(\mathbf{I}|\mathbf{f})P(\mathbf{f})}{P(\mathbf{I})} \quad (1)$$

where \mathbf{f} is the total label configuration and \mathbf{I} are all observed intensities within the search space. The image likelihood $P(\mathbf{I}|\mathbf{f})$ describes how likely is the observed image given a label configuration \mathbf{f} . The prior $P(\mathbf{f})$ encodes any prior knowledge of the tissue class labels (i.e. healthy and infarct tissue classes).

The MAP estimate allows to determine the most likely label configuration \mathbf{f} , given the observed intensities \mathbf{I} . To make numerical computation more convenient, the MAP formulation is transformed to one involving only summations. This is possible by taking the negative logarithm of Eq. 1:

$$\hat{\mathbf{f}} = \arg \min_{\mathbf{f}} \{-\ln P(\mathbf{I}|\mathbf{f}) - \ln P(\mathbf{f})\} \quad (2)$$

where $\hat{\mathbf{f}}$ is the optimal labelling. The prior probability $P(\mathbf{I})$ can be ignored as it is independent from the labelling \mathbf{f} . Note that the segmentation problem is now an energy minimization problem, following from (2):

$$\hat{\mathbf{f}} = \arg \min_{\mathbf{f}} \{\lambda E_{\text{data}}(\mathbf{f}) + E_{\text{prior}}(\mathbf{f})\} \quad (3)$$

The weighting term λ weighs the relative contribution of the energy terms: E_{data} is the data term which measures the disagreement between a prior probabilistic (i.e. training) model and the observed data, and E_{prior} is a smoothness term penalizing any discontinuities within a tissue class. It achieves this by penalizing discontinuities between adjacent voxel pairs in a neighbourhood system. Eq. 3 is commonly represented in existing literature as an energy function over the entire image as:

$$E(f) = \lambda \sum_{p \in \mathcal{P}} D_p(f_p) + \sum_{\{p,q\} \in \mathcal{N}} V_{p,q}(f_p, f_q) \quad (4)$$

Here D and V are terms corresponding to E_{data} and E_{prior} respectively of Eq. 3.

For MRF-based energy functions such as the one in Eq. 4, global optimization methods are computationally inefficient to be applied to medical image segmentation, especially with 3D free-breathing images. Other optimization schemes such as the Iterated Conditional Modes (ICM), widely applied in medical image segmentation, is well known to suffer from local minima trapping. The graph-cut method employed in this work, is now a widely used technique for minimizing context-dependent MRF problems as the one suggested here.

In the graph-cut implementation of [3], a close approximation of the global minimum is guaranteed and this is most desirable in DE-MRI we seek a global optimal solution (i.e. segmentation of infarct) based on the observed and training data. Indeed, a locally optimal solution would yield regions with inconsistent segmentations. In the graph formulation, the MRF-based energy function in Eq. 4 is coded into the edge-weights. The cost of the graph *cut*, partitioning the graph into two sets of nodes each belonging to a separate class: scar or healthy, is equal to the total energy of the corresponding segmentations. The problem is thus to find the cut with the least cost thus yielding the optimal segmentation.

2.1 Integration of Information in Edge-Weights

In the graph-cut method, the graph constructed from the infarct search space (i.e. region of myocardium) contains t -links and n -links. The t -links connect each voxel in the image to the tissue label classes namely healthy and infarct. The n -links are links between adjacent voxels that enforce smoothness in a local neighbourhood. The t and n -links correspond to the data term E_{data} and smoothness terms E_{prior} of Eq. 3 respectively. The t -links are the major contributing term and is what drives most of the segmentation process. It is sensible that the weights assigned to these links are derived from a tissue prior such as a probabilistic model of healthy and infarct tissues.

Tissue Intensity Prior: For integrating prior knowledge about healthy and infarct tissues, tissue intensities are modelled in each class. In the healthy tissue (i.e. non-infarct) class, tissue intensities are modelled from the unseen image. As the segmentation of myocardium is assumed to be available, tissues

lying outside myocardium are modelled using a multi-modal Gaussian mixture model. The number of modes is left variable as it is often unclear what would be the ideal and optimal number of tissue modes within the healthy class.

For infarct tissue class, the *enhancement ratio* of the mean intensity of infarct to blood-pool is modelled from the training data. These can be readily obtained from manually segmented infarct images. The ratio is modelled with a uni-modal Gaussian distribution. The data term of Eq. 3 and thus the t -link in the graph-cut is obtained from the aforementioned intensity distributions: $P(I_p|f_p = 1)$ for infarct and $P(I_p|f_p = 0)$ for healthy, and thus before we insert this information as edge-weights we must have:

$$D_p(f_p) = -\ln P(I_p|f_p) \quad (5)$$

Tissue Continuity Prior: The smoothness term V in Eq. 3 ensure that segmented regions remain smooth and continuous. Neighbouring adjacent voxels with similar intensities incur an exponentially high *cut* cost if they are classified into separate tissue classes. The Lorentzian error norm [6] is employed, which is a robust metric for measuring intensity differences within a neighbourhood:

$$\varphi(p, q) = 1 + \frac{1}{2} \left(\frac{|I_p - I_q|}{\sigma} \right)^2 \quad (6)$$

The implementation of the graph-cut algorithm used is the one found in [8].

3 Results

3.1 Challenge Data

The data provided as part of this challenge was acquired using a standard 1.5T scanner and a 32 -channel coil (Philips Healthcare, Best, Netherlands). These were both from human ($n = 10$) and pig ($n = 10$). In the human set, the pixel resolution was reconstructed to $1.3 \times 1.3 \times 2 \text{ mm}^3$. For the animal data, the resolution of the images provided were $1.7 \times 1.7 \times 6 \text{ mm}^3$. Segmentation of the myocardium was also provided for each scan. These were manually annotated by a clinical expert. Also a set of training data ($n = 5$) were provided for both the patient and animal cohorts. This included expert segmentations of infarct within the myocardial contour. A sample of the datasets provided can be seen in Fig. 1.

3.2 Comparison with Gold-Standard

The FWHM is now established as a gold-standard for quantifying infarct in DE-MRI scans of the ventricle with good correlation shown against histology studies [2,1]. Results from the proposed algorithm were evaluated quantitatively against segmentations from the FWHM technique. Details on the implementation of

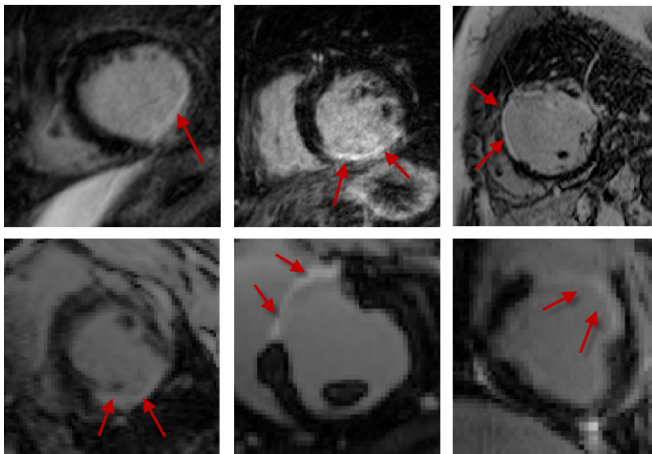


Fig. 1. Sample of the human (top row) and animal pig (bottom row) DE-MRI data provided to participants as part of the challenge. Red arrows indicate areas of enhancement.

FWHM can be found in [2]. Infarct was defined as signal intensities T where: $T > 0.5 \times T_{\max}$, here T_{\max} is the (mean) peak signal intensity within myocardium.

Infarct was quantified using both FWHM and the proposed algorithm. For comparison, the amount of infarct detected represented as percentage of myocardium was determined in both the methods. These comparisons are shown in the Bland-Altman plots of Fig. 2 for the human data set and 3 for the animal data set. In these plots, the percentage difference (vertical axis) is plotted against the average (horizontal axis) of the two techniques. Furthermore, the two techniques are also compared using the Dice overlap measure [9] in Table 1. We see good agreement in both human (Mean difference in measurements = -0.9%) and animal (Mean difference = -1.4 %) datasets. Note that a negative percentage indicates under-estimation of infarct by the proposed algorithm. There was also good pixel-by-pixel correlation in both human (Mean dice = 93/100) and animal (Mean dice = 87/100) datasets.

3.3 Performance

The human DE-MRI images were segmented in all but 1 case successfully using the proposed graph-cut algorithm. Segmentations were evaluated both qualitatively and quantitatively. A successful segmentation was defined as one where the algorithm was able to produce a result *and* had good correlation (Dice > 0.7) with FWHM. See Fig. 4 for a sample of the segmentations generated by the algorithm. The segmentations were computed in less than 5 seconds on a 2.5 Ghz PC. There was no operator input during the entire segmentation process. However, it is essential that a correct segmentation of the myocardium is provided as this defines its search space.

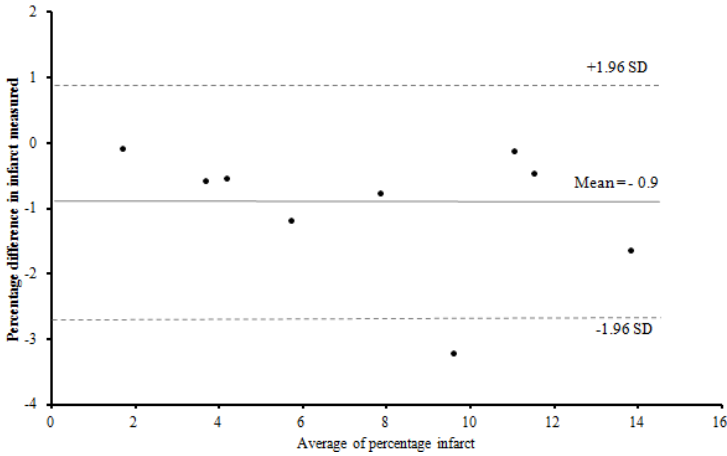


Fig. 2. Patient data-set: Bland-Altman plot showing difference in measurements (infarct detected as percentage of myocardium) in FWHM and proposed algorithm. A negative percentage indicates under-estimation of infarct by the proposed algorithm.

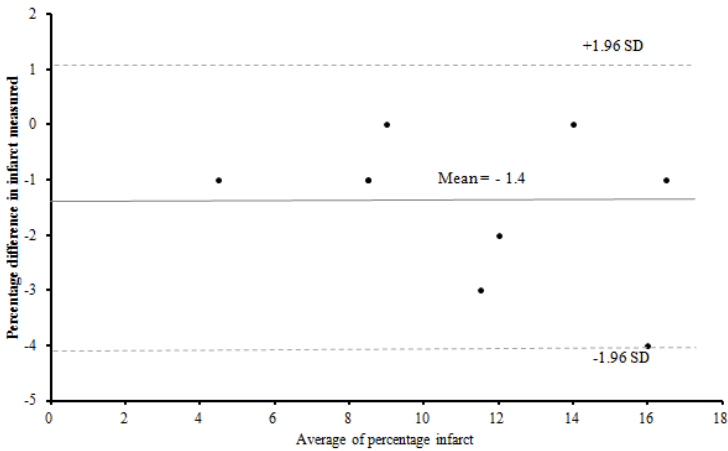


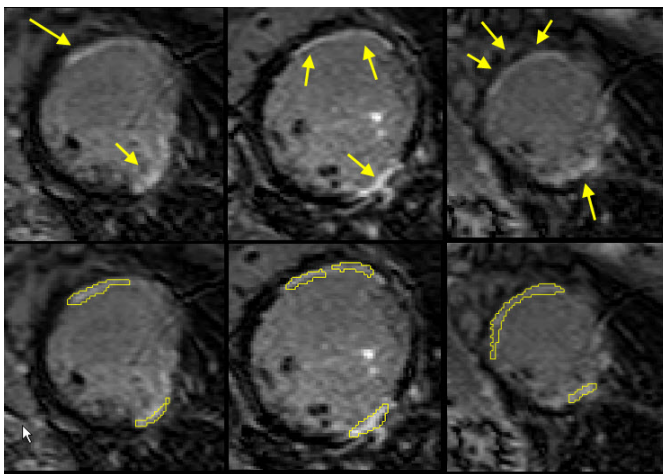
Fig. 3. Animal data-set: Bland-Altman plot showing difference in measurements (infarct detected as percentage of myocardium) in FWHM and proposed algorithm. A negative percentage indicates under-estimation of infarct by the proposed algorithm.

In the animal DE-MRI images, segmentations were obtained in all but 2 cases successfully. Similar to the human data, segmentations were computed in less than 5 seconds with no operator input. Fig. 5 shows a sample of the output generated by the algorithm.

Table 1. Dice overlap comparison with FWHM technique

No.	Human	Animal
1	80	90
2	90	95
3	91	98
4	95	92
5	93	95
6	98	75
7	92	89
8	95	77
9	94	72
10	97	50
Mean	93 (5)	87 (10)

The Dice overlap between FWHM and the algorithm for human and animal data sets. The Dice ranges between 0 and 100 where 100 represents perfect overlap.

**Fig. 4.** Patient data: Original DE-MRI scans (top row) and their corresponding graph-cut segmentations (bottom row)

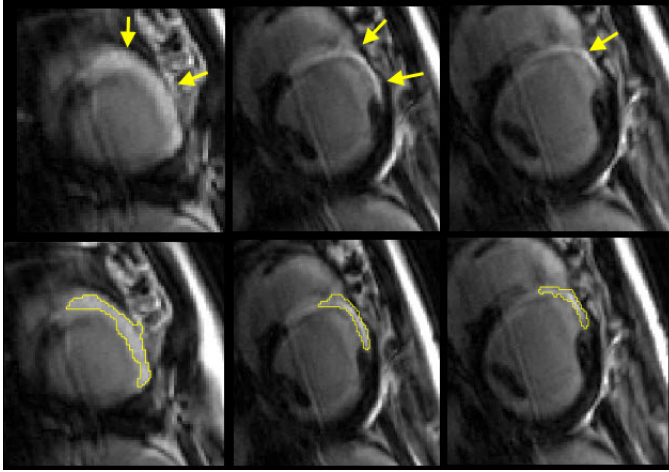


Fig. 5. Animal data: Original DE-MRI scans (top row) and their corresponding graph-cut segmentations (bottom row)

3.4 Conclusions

The proposed work employs a graph-cut implementation to maximize the MAP estimate and obtain the most likely (i.e. optimal) segmentation for infarct, given the observed and training data. The algorithm was tested on both patient and animal DE-MRI by utilizing the training data from each separately. Results from the algorithm were verified by a clinician qualitatively and were deemed suitable for clinical applications. Furthermore, quantitative validation with FWHM, currently the gold-standard in infarct quantification, shows good agreement.

Quantification of acute and chronic infarction in the myocardium is a challenging problem and has important prognostic implications in patients suffering from heart-related illnesses. Existing techniques rely on setting a standard cut-off intensity value for infarct and it is yet not clear why fixing a global intensity value would generate accurate segmentations. Given the quality of images obtained in clinical practice and as seen in the mix provided within this challenge, it is becoming clear that techniques which exploit local information are more likely to generate accurate segmentations. Furthermore, any quantification algorithm intended to be used in clinical practice must be tested against multi-center studies. Future work will further include a more detailed quantitative evaluation with ground-truth information.

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