

MORPHOLOGICAL-BASED 3D SEGMENTATION METHOD OF CARDIAC MRI DATA

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Introduction

We present a morphological-based segmentation scheme for the extraction of the left ventricular blood pool in cardiac MRI images. Extraction and quantification of this feature is an important stage in the diagnosis of cardiovascular diseases [Frangi, 2001]. Our method, based on reconstruction by dilation, is controlled using dynamic thresholds and constrained with a prior shape model that prevents over-segmentation. Our approach has been tested on 33 3D+time datasets and compared against manual annotations.

Method

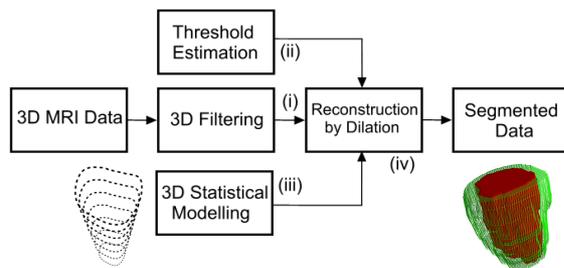


Figure 1: Overview of segmentation algorithm

Figure 1 illustrates the stages of the segmentation algorithm, and each computational component is outlined below.

(i) Prior to segmentation, the datasets are subjected to 3D filtering to reduce noise and improve the homogeneity of the blood pool.

(ii) Dynamic thresholds are used to control growth in stage (iv). The thresholds are driven by statistical image information local to the solution, and are updated at every iteration.

(iii) Learned statistical models are used to constrain solution expansion in stage (iv), limiting over-segmentation and convergence outside the endocardium wall. Models are trained from manual annotations that have been validated by a physician.

(iv) The weighted interaction between the estimated thresholds and the 3D statistical model drives the evolution of the solution. The algorithm is applied until convergence is reached.

Results

The algorithm has been tested against thirty-three short-axis MRI cardiac datasets of patients under the age of 18. The datasets are composed of 20 temporal 3D volumes over one cardiac cycle. Resolution of the datasets in the xyz plane ranges from $256 \times 256 \times 8$ to $256 \times 256 \times 15$ pixels. Further details can be found in [Andreopoulos, 2008].

Automatic segmentations are compared against manual annotations. Segmentation accuracy is quantified using the point-to-curve error measurement. The average error across datasets is: 6.04 ± 3.30 pixels.

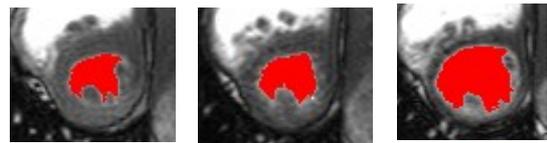


Figure 2: Example segmentations (shown in red) of the blood pool. These results illustrate the exclusion of the papillary muscles from the solution.

Discussion

The evaluation results are promising considering the intensity and anatomical variation in these datasets. Errors are mainly due to under-segmentation, since this is a conservative algorithm, and could be improved with a more sophisticated constraint scheme. The proposed algorithm is useful for fast localisation of the left ventricular blood pool and compares favourably against state-of-the-art methods. Future work will be directed to extension of the proposed approach to 3D+time segmentation.

Acknowledgements

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References

- Andreopoulos et al, Medical Image Analysis, 12:335-357, 2008.
- Frangi et al, IEEE Transactions on Medical Imaging, 20:2-25, 2001