

Multi-Object and N-D Segmentation of Cardiac MSCT Data Using SVM Classifiers and a Connectivity Algorithm

J Fleureau¹, M Garreau¹, AI Hernández¹, A Simon¹, D Boulmier^{1,2}

¹INSERM U642, Laboratoire Traitement du Signal et de l'Image, Rennes, France

¹Université de Rennes 1, LTSI, Campus de Beaulieu, Rennes 35042 Cedex France

²Centre Cardio-Pneumologique, CHU Pontchaillou, Rennes, France

Abstract

In this paper we present a new technique for general purpose, semi-interactive and multi-object segmentation in N-dimensional images. This method associates supervised classification methodologies with a region growing algorithm coupled with a connectivity approach. These concepts are combined in a competitive context implemented via a distributed real-time technology which allows multi-object detection. This approach is original by its atypical multi-object extraction, a rapidity of execution and the facility to introduce a priori information by the selection of a limited number of seed points inside the objects of interest. We apply this new method for the segmentation of cardiac structures observed in Multislice Computed Tomography (MSCT) imaging. First results obtained on real 3D data reveals the good behaviour of the method, considering segmentation accuracy while minimizing user interaction and computational load.

1. Introduction

With the increasing number of cardiovascular diseases, obtaining new knowledge on the different structures and mechanisms involving in cardiac activities becomes more and more important. Several ways can be considered to reach that goal but one very interesting stays in non invasive methods and especially imaging approaches [1]. MSCT imaging provides today the means to observe quite accurately the heart and all of its subparts, at specific instants or during one cardiac beat. Nevertheless, the development of help diagnosis tools requires a first step: the extraction of the heart components from the entire CT volume. This step of segmentation is actually hard to perform by the nature of the obtained image. In fact, similar intensities of two different structures present in the same part of the image, the fuzziness and the complexity of their borders, the artefact of reconstruction or even physiological problems like the inhomogeneous dispersion of contrast

product, lead to difficult problems to consider in a segmentation process.

Such an algorithm should answer to at least three requirements: being able to take advantage of the image information with very few preprocessing, being able to provide a result in very limited computing time, but also being as ergonomic as possible that is to say being able to accept a priori information from the user. The segmentation problem in image analysis has been widely considered in the litterature, but we can focus our comparative study on three main kinds of methods. Fuzzy Connectedness [2] is a fuzzy approach which associates interactively selected seed points with each object to segment and then builds a connectivity map which symbolizes the strengthness of the link (connectivity) between each pixel of the map and the seed point. Such a method seems powerful but can require the introduction of user-parameters or a preprocessing step. Graphcuts [3] can be an interesting alternative. The user has to select one region of the object and one region of the background for the hard initialization. After this interactive step, a method based on an energy minimisation by graph-cut algorithm is applied. Such a method needs very few parameters but multi-object detection is not yet proposed. Level Set methods or deformable models [4] have been developed, in which regions evolve by iterative evaluation of local and global energetic criteria, but often infers difficulties in the process with a quite crucial step of initialization.

2. Methods

We propose an alternative way to perform the segmentation process, a way which could satisfy to both multi-object approach, simplicity, rapidity and accuracy. To face this difficult optimization problem, meta-heuristics used in our approach are relevant from swarm intelligence, specifically from ant colony algorithms, with the development of a distributed and self-organized system coupled with adaptive memories or maps. The main point of what we

propose here is to perform segmentation through the interactions of several Basic Agents (BAs). It is important to precise that our method is not considered as a Multi-Agent System associated to a more complex and cognitive behavior, but some similar concepts can be found in the definition of Basic Agents and their associated strategy. Data segmentation is the result of competitions and collaborations between several processes symbolized by those BAs.

The global algorithm could be described as follows. A BA is interactively associated with one Object of Interest (OOI) by the selection of one seed point in the image by the user. Several BAs can be assigned to the same OOI. If two BAs are associated to the same object, they are labeled “partners; otherwise they are identified “competitors”. Once they are placed in the image, each BA first acquires knowledge of its image territory by locally learning its characteristics in terms of intensity and texture. Each BA is then able to recognize if a new local part of the image presents similarities (or not) with its territory.

Secondly, each BA applies its exploratory strategy on the image to contribute to the formation of a “Segmentation map”. In fact, each one of those entities can be viewed as a conqueror which explores their connected neighbors (or image spels) and tries to recognize if the new area encountered could be its own or not. If it is the case and if the new area hasn’t been already engaged, the new territory is acquired. In the opposite case, an interaction with the current owner happens. The different BAs can adopt several behaviors and the interactions are consequently varied. When no more extension by propagation of BAs in the image is possible, the final territory of each agent match with the OOI we would like to segment initially.

Learning of texture and intensities

Each Basic Agent begins by learning about its territory. We have thus introduced new 2D vectors, called “Transition Vectors” (TV) that symbolize local transitions of intensity in N-D data. They are basically built by the simple aggregation of the intensity of two connected spels (voxels in 3-D images). They need no computation and no prior knowledge about the distributions. They present an interesting point: the set of TV linked to an OOI have a typical shape in the intensity plane, which is therefore learnt through a supervised classifier (Figure 1).

More precisely, once the user has selected a seed point for each BA, the local N-D neighborhood of this seed point is normally representative of the OOI and the associated set of TV is also representative of this OOI in terms of intensity and texture. Therefore, by considering the TVs’ sets of each BA in the intensity plane, we are faced with an unlinear multi-class supervised classification problem that we can solve through Support Vector Machine (SVM) [5]. With the combination of clustering algorithms and SVM

it is therefore possible, for each BA, to learn simply and quickly, the image characteristics of their territory.

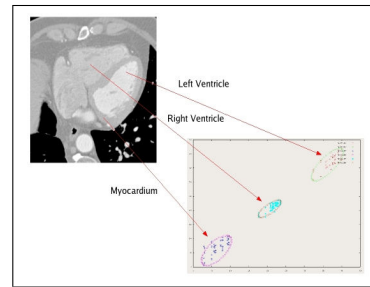


Figure 1. Transitions Vectors in the intensity plane

Interaction between BAs

We now focus on the step of propagation of each BA. During their connected extension, each BA tries to maximize its territory. Nevertheless they necessary meet other BAs which are evolving on this image map. This “meeting” is available through two channels of communications: the “Segmentation Map” itself (which is in fact the original image segmented) and also a crucial “Travel Map” which informs, for a given spel, the length of the path browsed by the current owner to acquire it. A “short path” is equivalent to a quite natural territory acquisition, whereas a “long and sinuous path” inside the image illustrates a not so much natural extension.

Two kinds of interaction can be encountered. One BA meets a partner: a step of cooperation is started (Travel Map updating and share of knowledge, mainly) but the label of the territory cannot be changed. If one BA meets a competitor: the BA which arrived with the shortest path to the current spel wins the competition (Figure 2). So, acquired territories are not static and they can always be reviewed. This competition is one of the essential parts of this algorithm: it improves the segmentation results by facing the different OOI to each others.

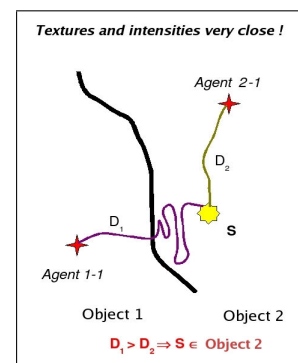


Figure 2. Competition between BAs

Different behaviors

A last point we would like to highlight here concerns the intrinsic BAs' behavior. We have introduced two different kinds of BA. The first one, called "Main BA" is associated to an OOI and tries to maximize its territory as we described before. But another kind of BA was also introduced. It is very common to observe leaks in some structures or even connected structures and one BA can consequently spread into the whole image (as we don't suppose any preprocessing step or any prior model). We have consequently introduced "Inhibitor BAs" associated to "Competitor Objects" (CO). Inhibitor BAs have a specific role: they try to inhibit main BA propagation in some critical configurations and they consequently allow the user to bring some a priori knowledge to the segmentation.

3. First Results

This framework has been applied to cardiac MSCT data acquired on a GE Lightspeed with 16 detectors rings. Our goal was to extract different regions of the heart from the whole database. We focus our interest, in particular, on the left ventricle (LV), the left atrium (LA), the right ventricle (RV) and the myocardium (MY) surrounding the left ventricle. We also try to highlight the improvement due to the use of inhibitor agents associated to "Competitor Objects". We provide first qualitative and quantitative results that show the right behavior of the algorithm. The machine used for the test was a P4 3GHz with 1Go of physical memory.

Integration of prior knowledge with competition

In this first example we show how the notion of competition can lead to improvement in terms of multi-objects segmentation. In MSCT data it is often difficult to differentiate left ventricle and atrium because of their connexity and their perfect similarity in terms of intensity and texture. We show how here (Table 1 and Figure 3), in 3D, by defining one group of BAs for the left ventricle and one other group of BAs for the left auricle, that the competition between each territory leads to quite good results of segmentation. Finally, few interactions with the user are needed as just a limited number of seed points chosen on one slice are selected.

Table 1. Segmentation characteristics for the first example

| Database | | GE Lightspeed | | |
|-------------------|---------|-----------------|----|----|
| Volume Dimensions | | 512 × 512 × 350 | | |
| Computing Time | | 1 mn 30 s | | |
| Segmented Objects | | RV | LA | LV |
| Nb of Seeds | Slice 1 | 4 | 2 | 3 |

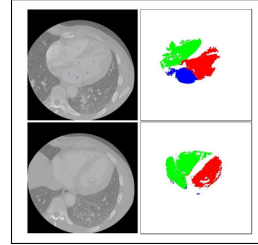


Figure 3. 3D segmentation of LA, LV, RV structures: Visualisation of results in two slices

Integration of prior knowledge with inhibitor agents

We are going now to illustrate a way to face with a priori information: the use of inhibitor agents. In the following situation, we try, in 3D, to segment at the same time the left ventricle (grouped with the left atrium), the right ventricle (grouped with the right atrium) and the myocardium around the left ventricle cavity. The major problem comes here from the myocardium. In fact the myocardium appears, on MSCT images, very similar in intensity and connected to one part of the background. So, if we try to segment it directly by just associating agents to this part, the agent spreads in the whole region associated to the myocardium but also to one part of the background (Figure 4).

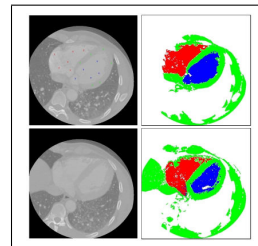


Figure 4. 3D segmentation of myocardium without inhibitors: Visualisation of results in two slices

If we now add prior information by defining a new object associated to a part of the background (anatomical parts not directly interesting), we see how the competition can lead to expected results (Table 2 and Figure 5).

Table 2. Characteristics of the segmentation of myocardium with inhibitors

| Database | | GE Lightspeed | | | |
|-------------------|---------|-----------------|----|----|----|
| Volume Dimensions | | 512 × 512 × 350 | | | |
| Computing Time | | 4 mn | | | |
| Segmented Objects | | VG | VD | MY | CO |
| Nb of Seeds | Slice 1 | 5 | 5 | 7 | 9 |
| | Slice 2 | 3 | 3 | 6 | 14 |

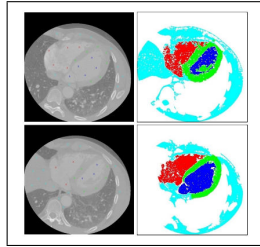


Figure 5. 3D Segmentation of myocardium with inhibitor: Visualisation of results in two slices

We can finally present the 3D segmented structures through a more visual point of view. We can build, from the final segmentation map, three-dimensional shapes by using marching cube algorithm. We thus obtain a more concrete geometric representation of the different segmented organs (Figure 6). We also precise that those figures have been obtained without any other treatment (just a marching cube step) which prove the quality of the raw-based results obtained from the proposed method.

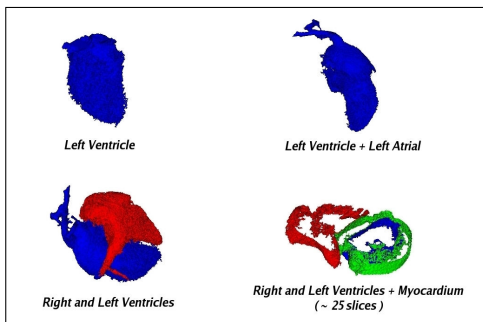


Figure 6. Segmented organs visualized in 3D

Extraction of quantitative clinical parameters

We present here quantitative results and especially volume variation of the LV along the cardiac cycle which can be obtained from the 3D extracted structures. The histogram of the different volumes of the left ventricle was obtained on one reference database (Figure 7). We precise that those volumes concern only the left ventricle and not the left atrium (which has been removed thanks to an adapted inhibitor agent, as we presented before). The continuity of the different volumes through the cycle and the time evolution of the histogram seem to validate quite accurately our methodology: higher volumes are correctly encountered for end-diastolic phase (around 0%) and the smaller ones for the end-systolic phase (around 45%).

4. Conclusion and perspectives

The proposed framework, based on its distributed approach and the only use of seed points is fast and ergonomic. It needs no preprocessing, is applicable to N-D

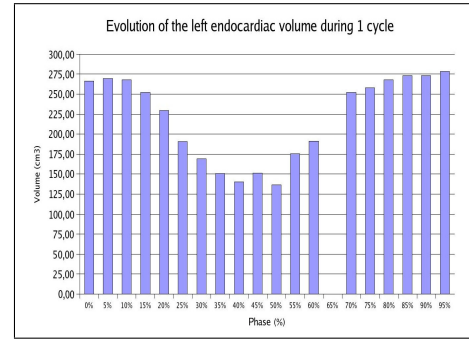


Figure 7. Left ventricle volume during one cycle

rough data with few computation (multi-threaded implementation and use of dynamical programming) and also allows an easy introduction of prior information through specific BAs. The presented results show the potential of this method by providing encouraging outcomes. A deeper validation is of course necessary (tests on more data, comparison with manual segmentation, extraction of more physiological parameters) and will be our next work.

Acknowledgements

This work is supported by the IPECA ALFA project between Europa and South America.

References

- [1] Frangi A, Niessen W, Viergever M. Three-dimensional modeling for functional analysis of cardiac images: A review. *IEEE Trans on Medical Imaging* 2001;20(1):2–25.
- [2] Udupa J, Samarasekera S. Fuzzy connectedness and object definition: Theory, algorithms, and applications in image segmentation. *Graphical Models and Image Processing* 1996;58(3):246–261.
- [3] Boykov YY, Jolly MP. Interactive graph cuts for optimal boundary & region segmentation of objects in n-d images. *Computer Vision 2001 ICCV 2001 Proceedings Eighth IEEE International Conference on* 2001;1:105–112.
- [4] McNerney T, Terzopoulos D. Deformable models in medical image analysis : A survey. *Medical Image Analysis* 1996; 1(2):91–108.
- [5] Smola AJ, Scholkopf B. On a kernel-based method for pattern recognition, regression, approximation, and operator inversion. *Algorithmica* 1998;22(1/2):211–231.

Address for correspondence:

INSERM U642, Laboratoire Traitement du Signal et de l'Image
 Université de Rennes 1, LTSI, Campus de Beaulieu, Rennes
 35042 FRANCE
 julien.fleureau@gmail.com