

# AN EXPLORATION FRAMEWORK FOR SEGMENTATION PARAMETER SPACES

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## ABSTRACT

Segmenting 3D images is critical in medical imaging but the parameterization of segmentation algorithms is difficult due to their computation heaviness and complex interactions between the parameters. This paper targets the exploration of deformable-model-based segmentation parameter spaces to search for salient ranges. We propose a framework exploring the parameter space with a genetic algorithm and interactively clustering the segmentation results. The framework only requires a limited number of parameters, it does not make any assumption on the segmentation algorithm and it does not require any ground truth or gold standard. Results obtained on a 3D image of the heart show that the proposed method has good robustness capabilities and that it is able to efficiently exhibit interesting parameter ranges.

**Index Terms**— Image segmentation, clustering methods, genetic algorithms.

## 1. INTRODUCTION

The segmentation of 3D medical images is involved in several procedures such as building anatomical models or extracting quantitative clinical parameters from patient data [1]. Generally, segmentation algorithms have an important amount of parameters and their tuning requires significant expertise. Besides, 3D segmentations can take several minutes on a PC, which makes parameterization a cumbersome process.

To facilitate parameterization some works use parallel computing to explore the parameter space in a reasonable time. In general exhaustive searches are conducted through parameter sweeps [2] and are complemented with some experiment design [3]. These methods are efficient but produce little information on the characteristics of the parameter space which is our main concern in this work. Moreover they often rely on a reference segmentation (e.g. expert), which is seldom available for medical images.

The problem here is to explore the segmentation parameter space to identify ranges where the behavior of the algorithm is singular. Ultimately our goal is to design a sys-

tem providing assistance to progressively identify parameter ranges of interest. These may include ranges producing a “good” segmentation or leading to some unique behavior.

The proposed framework combines a genetic algorithm with a k-medoid clustering to explore the parameter space. The segmentation algorithm is seen as a black-box for which only the input parameters and results are exposed. A computing grid is used to sustain the required computing power. The framework is presented in section 2 and experiments are shown on 3D images in section 3.

## 2. METHOD

Figure 1 shows an overview of the framework.  $N^0$  is a fixed parameter denoting the total number of segmentations to be computed at iteration 0. It is used to uniformly sample the considered parameter ranges ( $R_1, \dots, R_n$ ). Segmentations are then computed in parallel. Once all results are available, a dissimilarity matrix is built from pairwise-computed Dice coefficients without any expert reference. This matrix is used to cluster segmentation results using k-medoid. Then the user decides to continue or to interrupt the exploration process. In the first case, he/she selects the cluster of interest from which new parameter combinations are generated using a genetic algorithm. The following sub-sections detail these steps.

### 2.1. Parameter sampling

Both decimal and integer parameters are considered. Let  $t$  be the number of integer parameters and  $n - t$  be the number of decimal parameter. Given  $N^0$  (fixed according to the available computing power),  $N_{R_i}$  samples are uniformly taken from each range  $R_i$  so that  $\prod_{i=1}^n N_{R_i} = N^0$ . If  $i \leq t$  (integer parameters) then:

$$N_{R_i} = \min(|R_i|, \lfloor \sqrt[n-t]{N^0} \rfloor)$$

, where  $|\cdot|$  is the cardinality operator and  $\lfloor \cdot \rfloor$  is the floor function. If  $i > t$  (decimal parameters) then:

$$N_{R_i} = \lfloor \sqrt[n-t]{\frac{N^0}{\prod_{j=1}^t N_{R_j}}} \rfloor.$$

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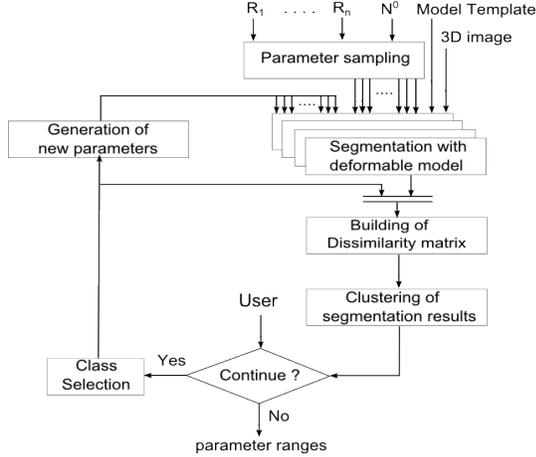


Fig. 1. Overview of the proposed framework.

## 2.2. Segmentation

The segmentation algorithm is seen as a black box taking as input numerical parameters varying in ranges  $R_i$ , a 3D image to be segmented and a model template to be deformed. It produces meshes that are voxelized to produce labeled images with the same size as the input image.

## 2.3. Building of dissimilarity matrix

The similarity measure used to compare two segmentation results is derived from the Dice coefficient. Given two segmentation results  $I_i$  and  $I_j$  represented as equal-sized images labeled from  $m$  elements of  $L = \{l_1, l_2, \dots, l_m\}$  and given  $F \subset L$  the labels of interest for the study, then the similarity between  $I_i$  and  $I_j$  is defined as:  $\widehat{dice}(I_i, I_j, F) = \frac{2|I_i \cap I_j|_F}{|I_i|_F + |I_j|_F}$ . The elements of the dissimilarity matrix are defined as  $d(I_i, I_j) = 1 - \widehat{dice}(I_i, I_j, F)$ . Note that  $1 - \widehat{dice}$  is not a distance since it does not verify the triangular inequality. At iteration 0, only segmentations obtained from the initial parameters are used to build the dissimilarity matrix (the matrix is of size  $(N^0)^2$ ). At iteration  $i > 0$ , the matrix is built both from segmentations produced by the generated individuals and from the segmentations in the cluster selected by the user at iteration  $i - 1$  (see section 2.5).

## 2.4. Clustering of segmentation results

Let  $I$  be the set of segmentation results to cluster into  $k$  clusters.  $k$ -means require to compute average segmentations, which is not suitable. Instead, we use  $k$ -medoids to extract class representatives from individuals. The problem is to find the  $k$ -tuple of medoids  $(m_1, \dots, m_k)$  subset of  $I$  so that:

$$(m_1, \dots, m_k) = \underset{(m_1, \dots, m_k) \in I^k}{arg \min} \sum_{i=1}^k \sum_{I_j \in C_i} d(I_j, m_i)$$

and  $C_i = \{I_j \in I, \forall l \neq i, d(I_j, m_l) < d(I_j, m_i)\}$

Exhaustive search can be employed for the minimization. This guarantees that the global minimum is found but it becomes highly compute-intensive when  $k$  or  $|I|$  increases. In this case the heuristic presented in [4] is used. Statistics on the parameters of the cluster elements are also computed.

## 2.5. User input

Instead of optimizing the segmentation process towards some reference, the framework can focus on any interesting parameter space region. For instance, if a particular structure of the image is not properly segmented it can be interesting to precisely identify which regions of the parameter space lead to this problem. At each iteration the user decides to stop or to continue the exploration process. In the second case he/she has to select the cluster in which the exploration will be refined. The selection is done by visualizing the cluster medoid.

## 2.6. Generation of new parameters

The exploration is refined within the selected cluster. In our case genetic algorithms seem well adapted to such generation since they make no assumption on the behavior of the segmentation algorithm. Two steps are involved: (i) a selection of parent pairs and (ii) a crossover between parents to generate new individuals. For now no random mutation is introduced. The individuals are composed of the segmentation parameters and are encoded with real values.

Parents are ordered by increasing value of their fitness function defined from their distance to the cluster medoid: for individual  $I_i$  in cluster  $C_k$ ,  $fitness(I_i) = d(I_i, m_k)$ . Non-overlapping pairs of consecutive parents are then selected.

The crossover uses weighted arithmetic averages of the parents' parameters [5]. To increase diversity, we randomly choose two weights  $\alpha_1$  and  $\alpha_2$  from a uniform distribution (0,1) and then consider  $\beta_1 = \frac{\alpha_1}{\alpha_1 + \alpha_2}$  and  $\beta_2 = \frac{\alpha_2}{\alpha_1 + \alpha_2}$  ( $\beta_1 + \beta_2 = 1$ ). Two new individuals are generated by combining the parents' parameter values:  $W_1 = \beta_1 V_1 + \beta_2 V_2$  and  $W_2 = \beta_2 V_1 + \beta_1 V_2$ , where  $V_i = [v_i^1, \dots, v_i^m]$ ,  $i \in \{1, 2\}$ , are the parameter vectors of the two parents and  $W_i = [w_i^1, \dots, w_i^m]$ ,  $i \in \{1, 2\}$  are the parameter vectors of the two generated individuals. Note that  $w_1^j$  and  $w_2^j$  are in  $[\min(v_1^j, v_2^j), \max(v_1^j, v_2^j)]$ . Finally the generated individuals are appended to the parents to construct the new population.

## 3. EXPERIMENT AND RESULTS

This experiment assesses the ability and the robustness of the framework to find relevant ranges in a large parameter space.

### 3.1. Experiment conditions

The target application is the segmentation of cardiac 3D magnetic resonance images. We consider a synthetic image of the

heart for which the behavior of the segmentation algorithm is easily interpreted. This image was built by voxelizing a 253x206x148 bounding box of a cardiac mesh. We concentrate on the segmentation of the left-ventricular cavity (LV) which is used, e.g., to quantify the ejection fraction.

The segmentation algorithm considered here is based on deformable elastic template and is described in [6]. We focus on 7 parameters of the deformation step: (1) the external force factor (FF) applied to the template (the magnitude of the model deformation is proportional to this parameter), (2 and 3) two Young moduli ( $Y_0$  for the left ventricular and  $Y_1$  for the right ventricular) controlling the template stiffness, (4 and 5) two Poisson coefficients ( $P_0$  and  $P_1$ ) describing the model compressibility, (6) the number of geometrical iterations  $NQ$ , related to the template relaxation during the deformation process and (7) the number of quadratic iteration  $NG$ , i.e., the number of non linear iterations in the deformation step.

For the exploration, we use  $N^0 = 288$ ,  $k = 2$  and the following parameter ranges:  $FF \in [0.1, 0.9]$ ,  $Y_0 \in [1, 10]$ ,  $Y_1 \in [1, 10]$ ,  $P_0 \in [0, 0.5]$ ,  $P_1 \in [0, 0.5]$ ,  $NQ \in \llbracket 0, 2 \rrbracket$  and  $NG \in \llbracket 0, 5 \rrbracket$ . Three iterations are conducted. The k-medoid problem is solved by exhaustive search.

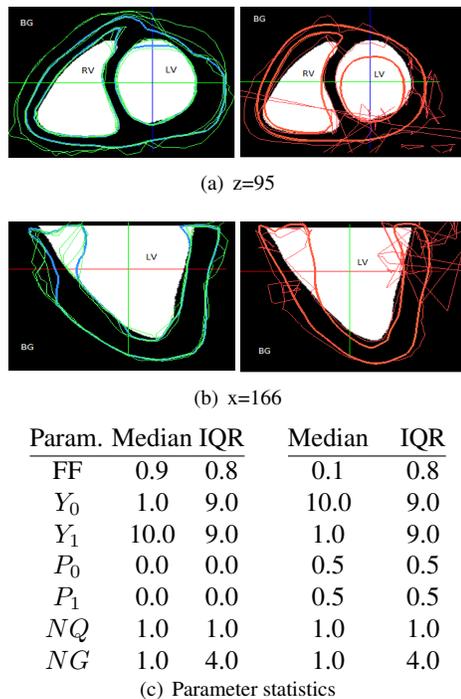
The computing infrastructure was the biomed Virtual Organization of the EU-Grid Infrastructure<sup>1</sup>. The “virtual lab for medical imaging” [7] is used to deploy the framework.

### 3.2. Results

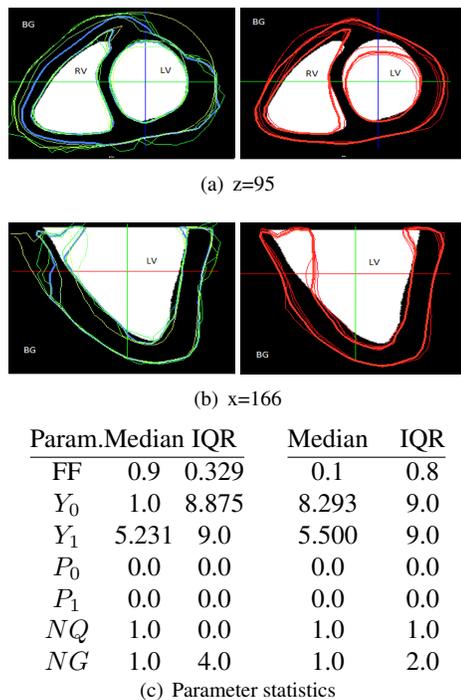
Results are shown on figures 2, 3 and 4 (generated using the CardioViz3D software © INRIA 2008). Mesh intersections with 2 orthogonal image planes ( $z=95$  and  $x=166$ ) are shown. The two columns represent clusters produced by the clustering. Five individuals are shown for each cluster: the medoid (in bold), the furthest individual from the medoid, and the individuals corresponding to the first, second and third quartiles defined by the distance to the medoid. The cluster represented on the left column is the one that was selected by the user focusing on the segmentation of the left-ventricular cavity (section 2.5). The cluster represented on the right column was left out. Medians and inter-quartile ranges (IQR) of the segmentation parameters used to generate cluster individuals are also reported. Overall these 3 iterations represented a total computing time of 116 hours that were executed in 32 hours on the computing platform.

## 4. DISCUSSION AND CONCLUSION

Results show that the proposed framework has good ability to steer the exploration towards the parameter space region of interest. In this experiment the region under study was the left-ventricular cavity ; we can see on figures 2, 3 and 4 that the medoid of the cluster selected by the user (thick line

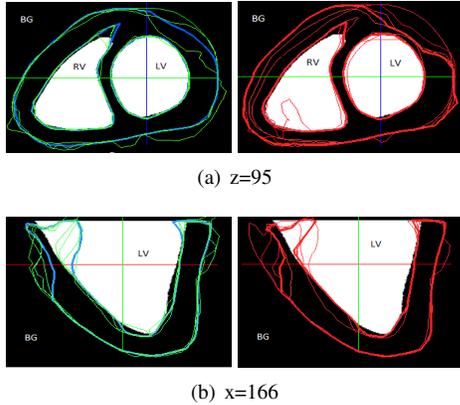


**Fig. 2.** Clusters obtained at iteration 0 ( $N^0 = 288$ ). Left: selected cluster ; right: left out. Cluster medoids in bold.



**Fig. 3.** Clusters obtained at iteration 1 ( $N^1 = 105$ ).

<sup>1</sup><http://wiki.healthgrid.org/LSVRC:Biomed>



Param.	Median	IQR	Median	IQR
FF	0.9	0.244	0.9	0.367
$Y_0$	5.231	8.199	2.914	5.951
$Y_1$	0.1	2.278	5.467	9.0
$P_0$	0.0	0.0	0.0	0.0
$P_1$	0.0	0.0	0.0	0.0
$NQ$	1.0	0.0	1.0	0.0
$NG$	5.0	1.0	1.0	4.0

(c) Parameter statistics

**Fig. 4.** Clusters obtained at iteration 2 ( $N^2 = 105$ ).

of the left column) converges towards the surface of the left ventricular cavity.

This experiment also shows that the framework is able to cope with outliers that are very far from the average segmentation. For instance, in the cluster left out at iteration 0 (figure 2 - right column) it is clear that the segmentation algorithm was completely misbehaving for some parameter sets. However the exploration framework was still able to identify two clusters, filtering out the outliers for the subsequent iterations. This shows the good robustness of the framework.

Statistics show that the IQR of the selected cluster decreases with the iteration number. This gives an indication on the stability of the framework. Besides, high IQRs mean that the parameter does not characterize the cluster, which is for instance the case for  $Y_0$  at iteration 2.

Overall our exploration framework is a robust tool to study the parameter space of segmentation algorithms based on deformable models. The clustering and genetic evolution enable a rapid identification of the parameter ranges of interest, which is a cumbersome task when exhaustive searches are conducted. Using an exhaustive search to identify the parameter regions found in the experiment requires to compute 2,500 segmentations while only 398 were needed here. The method requires no ground truth nor gold standard and it makes no assumption on the implementation of the segmentation algorithm. It has only 4 parameters: the image to segment, the template model, the cardinality of the initial population and the ranges of the studied parameters. It is

parallel by nature, which makes it able to exploit distributed computing resources.

Studying the impact of mutation in the genetic algorithm could be an interesting future work which would further increase the range of the studied region of the parameter space. The generation of new individuals could also use historical information to avoid repeating already computed configurations. Besides, the clustering method could be improved to dynamically detect the appropriate number of clusters in the segmentation results. Finally the genericity of the exploration framework suggests that other problems involving large parameter spaces could be addressed with the same method.

## 5. ACKNOWLEDGMENT

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## 6. REFERENCES

- [1] J. Montagnat and H. Delingette, "4D deformable models with temporal constraints: application to 4D cardiac image segmentation," *Medical Image Analysis*, vol. 9, no. 1, pp. 87–100, 2005.
- [2] S. Specovius, R. Siewert, J. Doege, D. Schnapauff, T. Denecke, and D. Krefting, "Grid based evaluation of a liver segmentation method for contrast enhanced abdominal MRI," in *Proceedings of HealthGrid 2010*, 2010, pp. 159–170.
- [3] C. Ding-Horn and S. Yung-Nien, "A self-learning segmentation framework—the taguchi approach," *Computerized Medical Imaging and Graphics*, vol. 24, no. 5, pp. 283 – 296, 2000.
- [4] S. Weiguo and L. Xiaohui, "A hybrid algorithm for k-medoid clustering of large data sets," in *Evolutionary Computation, 2004. CEC2004. Congress on*, June 2004, vol. 1, pp. 77–82.
- [5] X Wu, Y Zhu, J Dai, and Z Wang, "Selection and determination of beam weights based on genetic algorithms for conformal radiotherapy treatment planning.," *Phys Med Biol*, vol. 45, no. 9, pp. 2547–58, 2000.
- [6] Y. Rouchdy, J. Pousin, J. Schaerer, and P. Clarysse, "A nonlinear elastic deformable template for soft structure segmentation: application to the heart segmentation in MRI," *Inverse Problems*, vol. 23, pp. 1017–1035, 2007.
- [7] Sílvia D. Olabariaga, Tristan Glatard, and Piter T. de Boer, "A virtual laboratory for medical image analysis," *IEEE TITB*, vol. 14, pp. 979–985, July 2010.