SEGMENTATION OF MULTIMODAL MEDICAL VOLUMES USING EVOLUTIONARY CLUSTERING

F. MASULLI[1,2], A.M. MASSONE[1], and A. SCHENONE[3]

(1) *Istituto Nazionale per la Fisica della Materia*
Via Dodecaneso 33 - 16146 Genova (Italy)
(2) *DISI - Dipartimento di Informatica and*
Scienze dell'Informazione - Università di Genova
Via Dodecaneso 35 - 16146 Genova (Italy)
(3) *Istituto Nazionale per la Ricerca sul Cancro*
Largo R. Benzi 10, 16132 Genova (Italy)
masulli@ge.infm.it, massone@ge.infm.it, schenone@cisi.unige.it

ABSTRACT

The Evolutionary Clustering (EC) algorithm presented in this paper is based on a (μ, λ)-Evolution Strategy where the object variables of genotypes are the centers of clusters. In the experimental section we compare the segmentation obtained by the application of C-Means (CM) algorithm and two variants of EC to a simple data set consisting of a multimodal transverse slice from a MRI head acquisition volume. EC obtains more stable solutions than CM, and, as it can take into account the cardinality of clusters, dramatically improves the quality of segmentation results.

KEYWORDS: Evolution Clustering algorithm, multimodal medical volumes, segmentation through clustering.

INTRODUCTION

The aim of multimodal medical volumes (MMV) segmentation is to aggregate voxels with similar properties (corresponding to the different anatomical and/or pathological tissues) in the different diagnostic imaging volumes. The application of clustering algorithms to this task has been shown to be very robust to noise and able to process complementary information carried by each volumetric image [3]. Moreover, the used

clustering method itself must be well grounded in statistics and must be not limited by intrinsic problems. Moreover, many biasing effects (due, e.g., to heterogeneous clusters and to partial volume effect during acquisition) must be taken into account in selecting a clustering algorithm for the segmentation of medical images.

In [7, 4, 8] an extensive comparison of clustering algorithms, when applied to MMV segmentation, has been presented. The companions concerned the Hard C-Means (CM) [5] and some algorithms based on fuzzy set theory, such as the Fuzzy C-Means algorithm [2], the Deterministic Annealing [10], the Possibilistic C-Means [6], and some of their variants. Fuzzy clustering methods can be considered as different ways of application of regularization approach to the problem of multiple local optima in CM [9]. Nevertheless, it is worth to point out fuzzy methods are not able to give a solution to the *global versus local search dilemma in clustering*.

In order to try to find the global minima of the clustering cost function, in this paper we apply a novel clustering algorithm, alternative to the fuzzy-regularization techniques, using a global search technique based on Evolution Strategies (ES) that are methods for continuous parameter optimization problems founded on the model of organic evolution [11, 1].

The proposed Evolution Clustering (EC) algorithm will be detailed in the next Section. In the experimental results presented in following Section, we compare the quality of segmentations obtained by the application of CM and EC algorithms to a simple data set consisting of a multimodal transverse slice. As remarked in the Section of Conclusions, the EC algorithm is able to obtain more reproducible solutions than CM in terms of the positions of centroids and of clusters extension in the feature space. We present also a version of EC taking into account the cardinality of clusters that significantly improves the quality of segmentation results.

EVOLUTION CLUSTERING ALGORITHM

In order to overcome the limits of C-Means, a (μ, λ)-Evolution Strategy [1] can be used to find the global optimum of the CM *global error function* J_w defined as the expectation of the squared local cost function [2]:

$$J_w \equiv < D^2 > = \sum_{k=1}^{n} \sum_{j=1}^{c} u_{jk} D_j^2(\mathbf{x}_k) \tag{1}$$

where u_{jk} is the membership value of pattern $\mathbf{x}_k$ ($k = \{1, ..., n\}$) to cluster $j - th$ with center $\mathbf{y}_j$ ($j = \{1, ..., c\}$), and the distortion $D_j(\mathbf{x}_k)$ can be defined as the *Euclidean distance* $|| \mathbf{x}_k - \mathbf{y}_j ||$.

Tab. 1 illustrates the Evolution Clustering (EC) algorithm. Each genotype is a list $\mathbf{a} = (\mathbf{y}_1, ..., \mathbf{y}_c, \sigma_1, ..., \sigma_c)$ containing the object variables (i.e. the centers of clusters $\mathbf{y}_j$) and the strategy parameters σ_j.

After parameters setting (step 1), the population is initialized in the following way (step 2): Centers of clusters (i.e. object variables) are initialized at random in

[1] (μ, λ)-**ES** are particularly useful in our problem, as they enable the search algorithm to escape from local optima [11, 1].

Table 1: Evolution Clustering algorithm.

1. *assign μ, λ, the number of clusters, and the threshold ϵ;*
2. *initialize the population;*
3. *evaluate J_w for each individual (Eq. 1);*
4. **do until** $\Delta J_w^{best}/J_w^{best}$ *is greater than ϵ;*
5. **count1**=*0;*
   (a) **while count1** *less then μ;*
      i. **count1**++*;*
      ii. *select by rank two individuals for mating;*
      iii. *order consistently the centers of clusters in both selected individuals using algorithm RI;*
      iv. *crossover object variables (discrete recombination);*
      v. *crossover strategy parameters (intermediate recombination);*
      vi. *mutate individual;*
   (b) **end do***;*
   (c) *evaluate J_w for each individual (Eq. 1);*
   (d) *select the μ fittest individuals for next population;*
6. **end do**.

the d-dimensional hyperbox $\mathbf{I} = \Pi_{i=1}^{d} [min_k(x_{ik}), max_k(x_{ik})]$ ($\mathbf{I} \subset \mathbf{R}^d$), while strategy parameters are initialized at random in the range $[0, \alpha]$, where α is order of $1/10$ the side of $\mathbf{I}$.

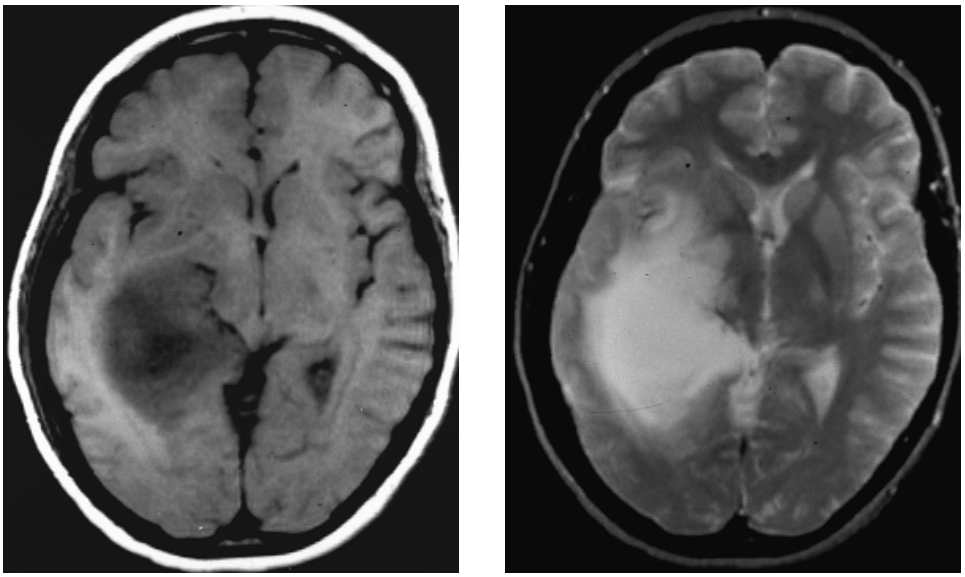
The remaining steps are quite standard for a (μ, λ)-**ES**, with the exception of Step 5(a)iii, as object variables of parents (centers of clusters), before mixing using discrete recombination crossover, must be reindexed, in such a way centers with same index are likely to stay in the same region of $\mathbf{I}$.

The reindexing algorithm (RI) used is modified from the RL algorithm proposed in [12]. Besides, the stop condition (Step 4)

$$\frac{\Delta J_w^{best}}{J_w^{best}} < \epsilon \tag{2}$$

is based on the ratio of normalized difference of objective function J_w evaluated on the fittest individual of two successive generations.

It is worth noting that it is easy to make variants to the basic EC. For instance, in order to the interference of big blobs to the localization of the centers of small clusters, it is straightforward to change in the algorithm J_w with the following *scaled global error function* J_s:



(a) (b)

Figure 1: T1-weighted (a) and T2-weighted (b) MRI images of a patient with glioblastoma multiforme in the right temporal lobe.

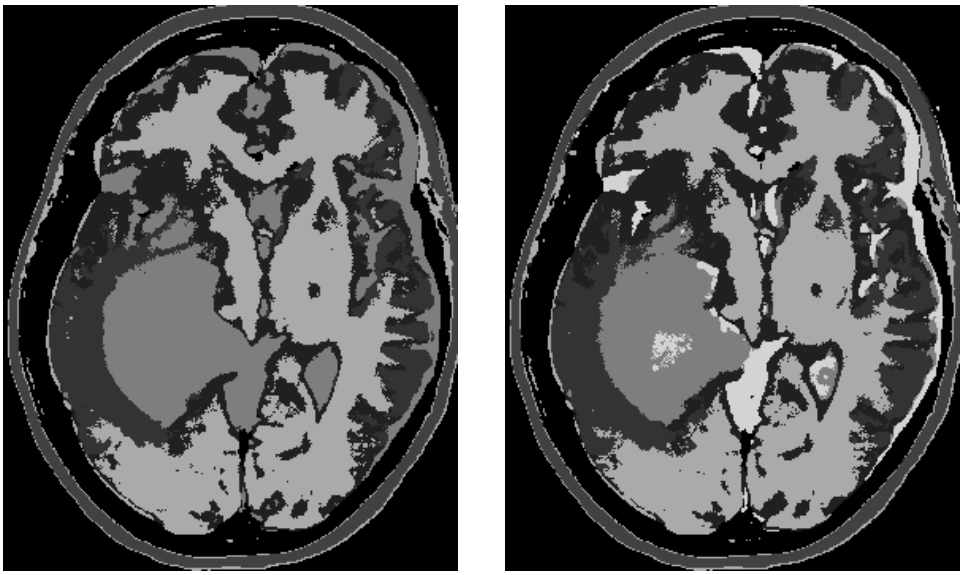
$$J_s \equiv \sum_{j=1}^{c} \frac{1}{C_j} \sum_{k=1}^{n} u_{jk} D_j^2(\mathbf{x}_k), \tag{3}$$

where C_j is the cardinality of cluster $j - th$.

EXPERIMENTAL ANALYSIS

Data set

Let we consider a simple data set consisting of a multimodal transverse slice of the head (Fig. 1) composed by spatially correlated T1-weighted and T2-weighted MRI images from a head acquisition volume of an individual with glioblastoma multiforme. The images are 288 x 362 with 256 gray levels. The tumor is located in the right temporal lobe and appears bright on the T2-weighted image and dark on the T1-weighted image. A large amount of edema surrounds the tumor and appears very bright on the T2-weighted image. The lower signal area within the mass suggests tissue necrosis. Each pixel in the above defined two-modal slice is associated to an array of two intensity values (T1 and T2). Therefore, each of these couples of pixel intensity is represented by a point in a 2D feature space, whose coordinates represent the intensity values in that pixel of each modality belonging to the multimodal set. The segmentation task consists in finding the main classes in this feature space and in associating each pixel in image to one of this classes. The main classes in the data set are: white matter, gray matter, cerebro spinal fluid (CSF), tumor, edema, necrosis, scalp. A slight misregistration between images may be responsible of some misclassification errors in final results.



(a) (b)

Figure 2: Segmentations obtained by the EC algorithm with 7 clusters and using J_w (a), or using J_s (b).

Methods

According to the $\mu/\lambda = \mathbf{1/7}$ rule, we selected $\mu = 10$ and $\lambda = 70$. Moreover, we initialized $c = 7$, $\epsilon = .005$, and the centers of clusters at random in $\mathbf{I}$. We implemented the selection by rank using a linear probability distribution with negative slope, while the intermediate recombination is implemented as the average of components of parents. Using the stop condition of Eq. 2, the EC ends in about 15 iterations.

Results and Discussion

The unsupervised segmentation obtained using the standard C-Means CM algorithm almost correctly defines scalp and white matter. Nevertheless it produces mistakes in classification of gray matter and edema in the left side of brain, and especially is not able to separate tumor, necrosis and CSF. Similar results are obtained by the basic EC with the standard cost function J_w (Fig. 2a).

From an extensive testing, EC results to be largely more reproducible concerning the positions of centroids and the extension of clusters in the feature space.

By using the *scaled global error function* J_s to take into account the cardinality of clusters, the quality of EC results dramatically improves (Fig. 2b). Moreover, we can notice that, in comparison with CM and the first version of EC, the second version of EC correctly distinguishes between tumor and CSF, and within the tumor region is able to find the necrosis region. Correct definition of scalp and white matter and misclassification in the left side of the brain of CM are unchanged.

CONCLUSIONS

Evolution Clustering (EC) algorithm is based on the application of Evolution Strategies (ES) [11, 1] to the search for the global minimum of the C-Means [5].

In the experimental results presented in the paper, we have compared the segmentation obtained by the application of CM, EC using J_w and EC using J_s to a simple data set consisting of a multimodal transverse slice MRI from a head acquisition volume of an individual with glioblastoma multiforme.

The two implementations of EC give more stable solutions than CM concerning the positions of centroids and the extension of clusters in the feature space. In particular, the EC using J_s dramatically improves the quality of segmentation results, as is able to take into account the cardinality of clusters.

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