Image Thresholding Based on Bacterial Foraging and Pareto Multiobjective Optimization

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Abstract–**Social foraging behavior of Escherichia coli bacteria has recently been explored to develop a novel algorithm for distributed optimization and control. This paper exploits the metaphor of natural foraging of bacteria in the context of image segmentation. We adapt the bacteria chemotaxis multi-objective optimization algorithm to optimize simultaneously two segmentation criteria (Between-class variance criterion and entropy criterion) to improve the quality of the segmentation. The proposed method was evaluated on various types of images. The obtained results show the robustness of the method, and its non dependence towards the kind of the image to be segmented.**

Keywords: **Bacterial foraging, Image segmentation, Image thresholding, Multiobjective optimization, Pareto approach**.

I. INTRODUCTION

Nature ecosystems have always been the rich source of mechanisms for designing artificial computational systems to solve difficult engineering and computer science problems. The increasing interest of these systems is motivated by two basic aspects [7]:

- Traditional methods have proven to be unable to adequately handling complex problems, characterized by the lack of complete mathematical models and the manipulation of a large number of variables.
- To a variety of engineering problems there is a similar version in nature.

In the optimization domain, researchers have been inspired by biological processes to develop some effective stochastic techniques that mimic the specific structures or behaviors of certain creatures. For examples, genetic algorithms (GA), which represent a fairly abstract model of Darwinian evolution and biological genetics, ant colony optimization (ACO) which is based on foraging behaviors of ant colonies and particle swarm optimization (PSO) which is inspired by the choreography of a bird flock.

Recently, search and optimal foraging of bacteria (chemotaxis) have been used for solving optimization problems. Bacterial chemotaxis multiobjective optimization algorithm (BCMOA) [8] is a novel algorithm to solve multiobjective optimization problem (MOP) which is based on bacterial chemotaxis and communication exchange in bacterial colonies. Some benchmark optimization problems were used to demonstrate the effectiveness of BCMOA in finding the solutions close the Pareto optimal front, and its performance compared to NSGA-II [6] regarding convergence and diversity.

In this work, we treat one of the central problems in computer vision and pattern recognition witch is the image segmentation. We exploit the flexibility of multiobjective fitness functions and the power of a Bacterial chemotaxis multiobjective optimization algorithm (BCMOA) to propose a new image thresholding method that allows to optimize several segmentation criteria simultaneously, in order to improve the quality of the segmentation.

The organization of the paper is as follows: the Sections 2, we introduce the problem of multi-level image thresholding as a multiobjective problem. We expose in Section 3, the multiobjective optimization approaches in image thresholding. In Section 4, the bacterial chemotaxis as optimization process is reviewed. In Section 5, the mathematical formulation of the different criteria is given in the first part of this section, in the second part, we present the proposed algorithm based on Pareto multiobjective optimization. In Section 6, we illustrate the obtained results through the proposed image thresholding algorithm. Finally, Section 7 concludes the paper.

II. IMAGE THRESHOLDIN

Image thresholding is an important technique for image segmentation [18, 26] that can be classified as bi-level thresholding and multilevel thresholding. Bi-level thresholding classifies the pixels of an image into two classes, one including those pixels with gray-levels above a certain threshold, the other including the rest. Multilevel thresholding divides the pixels into several classes. The pixels belonging to the same class have gray-levels within a specific range defined by several thresholds. Thresholding is widely used in many image processing applications such as optical character recognition [1], automatic target recognition [10, 13], inspection applications [24] and medical image applications [15].

Various parametric and non-parametric thresholding methods and criteria have been proposed in order to perform

bi-level thresholding [22, 23]. They are extendable to multilevel thresholding as well, however, for optimal multilevel thresholding, existing algorithms are being trapped by an exhaustive search of all possible threshold subsets. To overcome this problem, several techniques have been proposed [9]. Some of them are designed especially for computation acceleration of a specific objective function, such as the Otsu's function, while other techniques are designed to be used with a general purpose. Among the last category, we can find dichotomization techniques, iterative schemes, reduction strategies and the meta-heuristic techniques.

In the literature several criteria to regularize the segmentation problem are presented [22, 23]. However, there is no single criterion able to regularize the segmentation problem for all kinds of images. Then, in order to have a good segmentation on more kinds of images, some criteria are used simultaneously. To optimize simultaneously these criteria, the multiobjective optimization (MO) techniques are used in image thresholding problem.

III. Multiobjective optimization in image segmentation

In multiobjective optimization problems, we have two or more objective functions to be optimized at the same time, instead of having only one. As a consequence, there is no unique solution to multiobjective optimization problems, but instead, we aim to find all of the good trade-off solutions available (the so-called Pareto optimal set) [20].

Several bio-inspired optimization techniques have been developed for MO problems, the most known are genetic algorithms (AGs). The nondominated sorting genetic algorithm II "NSGA-II" [6] is the most popular genetic algorithm for solving MOP.

Another interesting biological process that has been already implemented as a multi-objective optimization technique is the bacterial chemotaxis [8]; this algorithm uses fast nondominated sorting procedure [6], communication between the colony members and a simple chemotactical strategy to change the bacterial positions in order to explore the search space to find several optimal solutions.

The use of multi-objective problem approaches has been found in image segmentation methods [3] with clustering and histogram thresholding methods. There is also an attempt of using multi-objective approaches for evaluation of image segmentation methods. As compared to multi-objective clustering approaches, there is limited research endeavour of using methods with MO in classical histogram thresholding methods.

The use of MO in image segmentation with thresholding techniques has been dominated by Nakid et al. [15,16]. They have proposed to find the optimal thresholds that allow to optimize a set of criteria as the objective functions. The aim is to increase the information on the positions of the optimal thresholds to obtain the correct segmentation.

IV. Bacterial chemotaxis as optimization process

Bacteria have the tendency to gather to the nutrient "rich areas" by an activity called chemotaxis. This process is achieved through swimming and tumbling [4, 5]. Depending upon the rotation of the flagella in each bacterium, it decides whether it should move in a predefined direction (swimming) or an altogether different direction (tumbling), in the entire lifetime of the bacterium.

Based on this concept, Passino proposed an optimization technique known as the bacterial foraging optimization algorithm (BFOA) [19]. This novel algorithm considers not only the chemotactical strategy but also other stages of bacterial foraging behavior as swarming, reproduction and elimination and dispersal; besides communication between bacteria acquires great influence on the entire process, getting closer to the concept that foraging is a phenomenon of a bacterial colony rather than an individual behavior.

Since its advent in 2002, BFOA has attracted researchers from diverse domains of knowledge. This has resulted in a few variants of the classical algorithm as well as many interesting applications of the same to the real-world optimization problems. Tang et al. [25] proposed a bacterial foraging behavior in varying environments. Li et al. proposed a modified bacterial foraging algorithm with varying population (BFAVP) [14].

Amos et al. [2] exposed the potential of implementing bacterial chemotaxis as a distributed optimization process, recognizing that in natural colonies, it is the interaction and communication between bacteria the mechanism that enables them to develop biologically advantageous patterns.

Guzman et al. [8] proposed the first extension of the chemotaxis strategy for solving multi-objective problems.

V. Proposed approach

Suppose that an image I having N pixels with $L+1$ gray levels $L = \{0, 1, ..., L\}$, is to be classified into $k+1$ classes $(C_0, C_2,..., C_k)$ with the set of k thresholds $T=\{t_1, t_2,..., t_k\}$. To optimize M segmentation criteria simultaneously and to obtain the Pareto front and then the optimal Pareto solution (optimal threshold values for image segmentation), we adapt the Bacteria Chemotaxis Multiobjective Optimization Algorithm *BCMOA* [8] that consists in using a colony of S bacteria $Bac = (X_j^1,..., X_j^i,..., X_j^S)$ that are located initially at random positions. $X_j^i = (x_{j,1}^i,..., x_{j,p}^i,..., x_{j,k}^i)$ is the i^{th} bacterium at j^{th} chemotactic step. $x_{j,p}^i$ is the p parameter of the bacterium X_j^i, such that $x_{j,p}^i \in [0, L-1]$ and $x_{j,p-1}^i < x_{j,p}^i < x_{j,p+1}^i$.

For each bacterium X_j^i in the initial location (*j*=o), the objective function values $J_l(X_j^i)$ *; l*= 1,…, *M*, are calculated. Applying a fast nondominated sorting procedure [5] the bacteria whose locations represent nondominated solutions, are classified in a list $POF1_j$, and all dominated bacteria are stored in a list $Bacdom_j$.

Each strong bacterium in $POF1_j$, apply the flowing chemotactical equation for position update:

$$X^{i}_{j-current} = X^{i}_{j-prev} + C(i)\frac{\Delta(i)}{\sqrt{\Delta^T \Delta(i)}} \quad (1)$$

Where: Δ^i_j is a random vector generated by the strong bacterium *i*, in which each element $\Delta^i_{j,p}$, $p = 1, 2, \ldots, K$, is a random number on [-1,1] and *C(i*) is the size of the step taken in the random direction specified by the tumble (run length unit).

Making use of its temporal-space memory, the strong bacterium compares its current objective function values $J_l(X^i_{j-current})$ with the previous $J_l(X^i_{j-prev})$; *l*=1…*M*, using nondomination concept. As a result of the comparison each strong bacterium reacts with any of these possible movements: if one of the locations previous X^i_{j-prev} or current $X^i_{j-current}$ dominates the other, the bacterium moves to the nondominated location and from there, takes a very small tumble *ST* in a random direction (short tumble), according to (2) or (3). On the other hand, if any of the locations previous X^i_{j-prev} and current $X^i_{j-current}$ dominates the other, from its current location the bacterium takes a bigger tumble *LT* in a random direction (long tumble), according to the (4).

$$x^i_{j+1,p} = x^i_{j-prev,p} + ST_{j,p}\Delta^i_{j,p} \quad (2)$$

$$x^i_{j+1,p} = x^i_{j-current,p} + ST_{j,p}\Delta^i_{j,p} \quad (3)$$

$$x^i_{j+1,p} = x^i_{j-current,p} + LT_{j,p}\Delta^i_{j,p} \quad (4)$$

Each weak bacterium X^i_j in $Bacdom_j$ randomly selects a strong bacterium, moves to a location near the strong bacterium selected and keeping the same direction, takes a step (swim) besides the rich location. The new position X^i_j of weak bacterium after tumbling is given by:

$$x^i_{j+1,p} = x^{strong}_{j,p} + x^{strong}_{j,p} \times r1_p + SW_{j,p} \quad (5)$$

Where: $r1_p$ is a random number on [-0.1, 0.1].

After the application of the chemotactical strategy for every bacterium in the colony, a complete chemotactical step was executed.

The long tumble, short tumble and swim sizes for each parameter *p* are automatic updated during the process and are defined by (6), (7) and (8), respectively:

$$ST_{j,p} = 0.1 \times Lt_{j,p} \quad (6)$$

$$LT_{j,p} = \frac{1}{S} FAC_j(\max(POF1_j)_p - \min(POF1_j)_p) \quad (7)$$

$$SW_{j,p} = FAC_j(x^{strong}_{j,p} - x^{weak}_{j,p}) \quad (8)$$

Where: $x^{strong}_{j,p}$ is the parameter *p* of strong bacterium location at j^{th} chemotactic step. $x^{weak}_{j,p}$ is the parameter *p* of a weak bacterium location at j^{th} chemotactic step. $\max(POF1_j)_p$ *is* the maximum values for the parameter *p* within the set of nondominated solutions *POF1* at j^{th} chemotactic step. $\min(POF1_j)_p$ is the minimum values for the parameter *p* within the set of nondominated solutions *POF1* at j^{th} chemotactic step. FAC_j is a factor, which decreases linearly from one to zero at every chemotactic step and given by:

$$FAC_j = (CHS_{\max} - j) / CHS_{\max} \quad (9)$$

Where: CHS_{max} is the maximum number of chemotactic steps.

When a bacterium hits the boundary the boundary of the solution space in one of the *p* parameter dimensions, its location is pulled back to the allowed solution space in that dimension (strategy of Absorbing Walls) [21].

In order to stimulate the diversity of solutions, the density parameter proposed in [12] was applied; when the size of the *POF1* is above 50% the size of the colony, density parameter is calculated for all strong bacteria in order to be sorted in non-descending order according to this value. To select its strong bacterium to apply the chemotactical strategy, each weak bacterium must select from the 25% top part of that strong bacteria sorted list.

A. Segmentation Criteria

In this approach, we use two threshold criteria witch can be described as follows: let there be *N* pixels in a given image, with gray-level range over *[0..L]* and n_i denote the occurrence of gray-level *i*, giving a probability of gray-level *i* as:

$$p_i = \frac{n_i}{N} \quad (10)$$

A1. Between-class variance criterion

The Otsu's method [17] is based on the discriminant analysis. It consists in the maximization of the between-class variance of the thresholded image as:

$$J_1(t_1,t_2,...,t_k)=\omega_0\omega_1(\mu_0-\mu_1)^2+\omega_0\omega_2(\mu_0-\mu_2)^2+\omega_0\omega_3(\mu_0-\mu_3)^2+...+\omega_0\omega_k(\mu_0-\mu_k)^2+\omega_1\omega_2(\mu_1-\mu_2)^2+\omega_1\omega_3(\mu_1-\mu_3)^2+...+\omega_1\omega_k(\mu_1-\mu_k)^2+...+\omega_{k-1}\omega_k(\mu_{k-1}-\mu_k)^2 \quad (11)$$

Where:

$$\omega_n=\sum_{i=t_n}^{t_{n+1}-1} p_i \ , \ \mu_n=\sum_{i=t_n}^{t_{n+1}-1}\frac{i\times p_i}{\omega_n} \quad \text{and} \quad 0\le n\le k$$

The optimal segmentation threshold vector $(t_1^*,t_2^*,...,t_k^*)$ makes the total variance maximum:

$$(t_1^*,t_2^*,...,t_k^*)=Arg\max_{0<t_1<t_2<...<L} J_1(t_1,t_2,...,t_k)$$

A2.Entropy Criterion

The Kapur's method [11] is based on the entropy theory. It consists in the maximization of the sum of entropies for each class, as follows:

$$J_2(t_1,t_2,...,t_k)=H_0+H_1+...+H_k \quad (12)$$

Where:

$$H_0=-\sum_{i=0}^{t_1-1}\frac{p_i}{\omega_0}\ln\frac{p_i}{\omega_0} \ , \ \omega_0=\sum_{i=0}^{t_1-1}p_i$$

$$H_1=-\sum_{i=t_1}^{t_2-1}\frac{p_i}{\omega_1}\ln\frac{p_i}{\omega_1} \ , \ \omega_1=\sum_{i=t_1}^{t_2-1}p_i$$

$$H_2=-\sum_{i=t_2}^{t_3-1}\frac{p_i}{\omega_2}\ln\frac{p_i}{\omega_2} \ , \ \omega_2=\sum_{i=t_2}^{t_3-1}p_i$$

$$H_k=-\sum_{i=t_k}^{L}\frac{p_i}{\omega_k}\ln\frac{p_i}{\omega_k} \ , \ \omega_k=\sum_{i=t_k}^{L}p_i$$

The optimal segmentation threshold vector $(t_1^*,t_2^*,...,t_k^*)$ is that maximizing the total entropy:

$$(t_1^*,t_2^*,...,t_k^*)=Arg\max_{0<t_1<t_2<...<L} J_2(t_1,t_2,...,t_k)$$

B. Proposed Algorithm

The proposed Thresholding using Pareto Bacteria Chemotaxis Multiobjective Optimization algorithm "*TPBMO"* consists in the optimization simultaneously of the functions: the between-class variance and the total entropy. Then, the optimal threshold vectors *X* correspond to the Pareto solution. The *TPBMO* algorithm is summarized below:

- **Initialization**
  1) Input the parameters: *S*, *CHS*max, *k*, M.
  2) Generate the first positions (*j*=0) of the threshold values randomly for a population *Bac* of bacteria;
- For j=0 to CHS_{max}
  1) For each bacterium X_j^i in *Bac* ; *i*= 1,…, *S*, calculate the objective function values $J_l(X_j^i)$; *l*= 1,…, *M* , using (11) and (12).
  2) Classify the location *Bac* of all bacteria using nondomination concept on $J_l(X_j^i)$; *l*= 1,…, *M*;
  3) Store each bacterium that was classified as nondominated in a list $POF1_j$ and store all dominated bacteria in a list $Bacdom_j$.
  4) Calculate the density parameter den_j for all strong bacteria.
  5) If $den_j > 50$ Then
     Sort the list $POF1_j$ in non-descending order
  6) Calculate the parameters of steps sizes *ST, LT and SW*, using (6), (7)and (8) respectively.
  7) For each bacterium X_j^i in $POF1_j$
     a) Generate a random vector $\Delta_j^i \in \Re^k$
     b) Apply the chemotactical equation for position update, using (1)
     c) Calculate the objective function values $J_l(X_{j-current}^i)$; *l*= 1,…, *M*, using (11) and (12).
     d) Apply nondomination concept to calculate the new location using (2), (3) or (4).
     e) Apply strategy of Absorbing Walls
     f) Store the location in the list *Bac*
  8) For each weak bacterium X_j^i in $Bacdom_j$
     a) If $den_j > 50$ then
        Select a strong bacterium from the 25% top part of $POF1_j$
        Else
        Randomly select a strong bacterium X_j^{strong} from $POF1_j$.
     b) Calculate the new location of the weak bacterium by using (5).
     c) Apply strategy of Absorbing Walls
     d) Store the location in the *list Bac.*

     End For
- Return the results: the threshold values and segmented image.

VI. Experimental results

To evaluate the performance of the proposed *TPBMO* algorithm, we present some experiments with two selected images among the images usually used to test the segmentation algorithms. These experiments are performed on a computer having Intel Core 2 Duo processor (3 GHZ) and 2 GB memory.

The parameters used in all tests were: the number of bacteria (*S)* was 200, the maximum number of chemotactical

steps was 100 and the number of objective functions (*M*) was 2.

The figures Fig. 1 and Fig. 2 present the obtained results of the images Screws (into two and three classes) and Peppers (into four and five classes). From a visual point of view, the segmentation of the image Screws is of good quality. Furthermore, the borders of the Screws are protected well. In the case of results of the images Peppers (into four and five classes), we notice that the objects, in these images, are globally well extracted from the background.

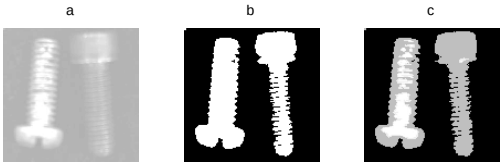

Fig. 1. Thresholding Results of Screws image: (a) Original, (b) Segmentation into 2 classes threshold t = 188, (c) segmentation into 3 classes thresholds t = (190, 240).

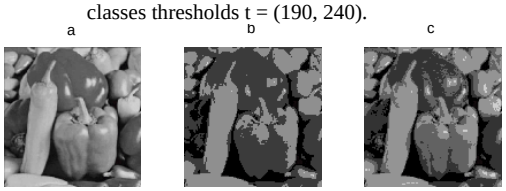

Fig. 2. Thresholding Results of Peppers image: (a) Original, (b) Segmentation into 4 classes thresholds t= (54, 133, 213), (c) segmentation into 5 classes thresholds t = (46, 90, 139, 206).

In order to measure the performance of the segmentation, we used the criterion of Peak Signal to Noise Ratio "*PSNR*", which is used as a quality measurement between the original image and the thresholded image, the value is normally expressed in decibels (dB). The higher the *PSNR*, the better the quality of the thresholded, or reconstructed image. The *PSNR* is defined as:

$$PSNR = 20\log_{10}\left(\frac{255}{RMSE}\right) \tag{13}$$

Where *RMSE* is the root mean-squared error, which is defined as:

$$RMSE = \sqrt{\frac{1}{M \times N}\sum_{i=1}^{M}\sum_{j=1}^{N}\left(I(i,j) - \hat{I}(i,j)\right)^2}$$

Where I and $\hat{I}$ are the original and the thresholded images, and $M \times N$ are the dimensions of the image.

In order to show the quality of the thresholded results in segmentation based on the simultaneous optimization of some criteria and their results when these criteria used separately, a comparison of *PSNR* values for the proposed *TPBMO* method and Otsu's, Kapur's methods with exhaustive search is presented in TABLE 1.

TABLE 1 COMPARISION OF PSNR VALUES FOR METHODS UNDER EVALUATION

Images	Otsu	Kapur	TPBMO
Screws (two classes)	8.13	8.71	8.74
Screws (three classes)	10.34	10.03	10.42
Peppers (four classes)	13.29	13.11	13.35
Peppers (five classes)	16.49	16.64	16.68

From the results presented in TABLE 1, it can be seen that the proposed *TPBMO* algorithm gives the highest value of *PSNR* value for almost all the segmented images, this performance is due to the inclusion of several criteria in the segmentation process.

The figures Fig. 3 and Fig. 4 illustrate, in two dimensions, the Pareto fronts in the case of segmentation of the images Screws (into three classes) and Peppers (into four classes). These results are the average of 25 successive executions of the *TPBMO* algorithm. Every point in the front corresponds to a segmentation result.

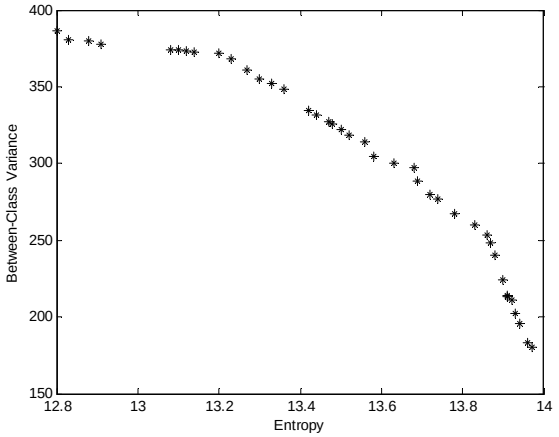

Fig. 3. Pareto front found by *TPBMO*, in the case of segmentation into 3 classes for image Screws.

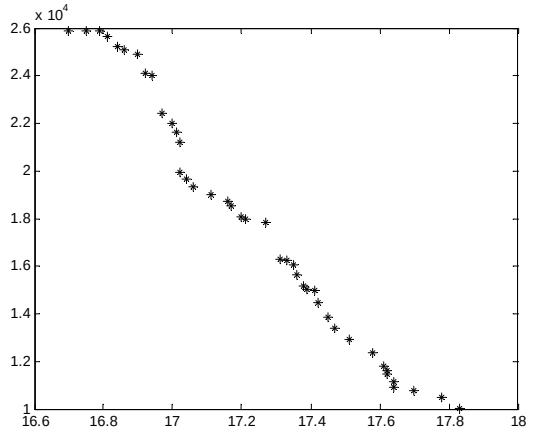

Fig. 4. Pareto front found by *TPBMO*, in the case of segmentation into 4 classes for image Peppers.

The average computational cost on our configuration is around 2 s , 7s , 15s and 27s, in the case of two classes, three classes, four classes and five classes respectively.

IV. Conclusion

In this paper, we have presented a supervised thresholding approach *TPBMO* based on Pareto multi-objective optimization and the bacterial chemotaxis. We have adapted the *BCMOA* algorithm by changing the size of the initial population and the number of generations, and by adding a simple strategy to handle constraints for each bacterial location in order to sort the parameters of bacterial, in descending order, and not to hit the boundary of the solution space. This approach enables to determinate the optimal thresholds of two criteria: the between-class variances criterion and the entropy criterion**.** The proposed method is validated by illustrative examples; comparison with the exhaustive search Otsu's, and Kapur's methods showed the robustness of the proposed method and its non dependence towards the kind of the image to be segmented, and also showed that image segmentation based on the simultaneous optimization of some criteria gives satisfactory results and increases the ability to apply one same technique to a wide variety of images.

In the future work, we will improve this approach by adding other segmentation criteria which allow highlighting the textures within the image, and by using the GPU (Graphics Processing Unit) to accelerate the segmentation process.

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