

Object localization in medical images using genetic algorithms

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Abstract—We present a genetic algorithm application to the problem of object registration (i.e., object detection, localization and recognition) in a class of medical images containing various types of blood cells. The genetic algorithm approach taken here is seen to be most appropriate for this type of image, due to the characteristics of the objects. Successful cell registration results on real life microscope images of blood cells show the potential of the proposed approach.

Keywords— Genetic algorithms, object registration, pattern recognition, blood cell microscope images

I. INTRODUCTION

ONE of the most frequently arising problems in the processing of (still) images is that of object registration. It arises in images containing objects, possibly overlapping, against a more-or-less uniform background. Objects may belong to one or more types or classes. Class identifying differences typically refer to the object morphology or shape, dimensions, color, opaqueness, surface texture and location / direction characteristics, [1], [5]. The aims of digital processing of an object image are numerous: Object detection, localization, recognition and classification constitute major goals. Furthermore, more detailed object characterization in terms of size, color, direction, scaling, shift or rotation might be of interest for specific applications. Finally, search of an image for the existence or not of a specific object prototype (under a given degree of flexibility as to the similarity level required in the match) is often of importance, [1].

Common in all the problems mentioned above is the processing of the images digitally, through an appropriate software package, either general-purpose or custom developed for the application at hand. Digital image processing is a mature field that offers to the researcher a variety of approaches. Given a field application, however, choice of the most suitable method or approach has not yet been fully automated.

In the present paper we present an application of the genetic algorithms approach to the problem of localization of objects in medical images of blood cells, taken via a microscope. The problem arises invariably in all blood or serum analysis medical contexts, and as such it has early received an intense research interest. Although there certainly exist automated

solutions, the issue of quality along with the critical nature of the results, often necessitate manual / visual treatment by the human expert on a microscope.

We propose the genetic algorithms approach here, because, as it will become clear through the results obtained, it was seen to be well suited to the morphology of the objects in the images treated.

A genetic algorithm is a non-linear optimization method that seeks the optimal solution of a problem via a non-exhaustive search among randomly generated solutions. Randomness is controlled through a set of parameters, thus turning genetic algorithms into exceptionally flexible and robust alternatives to conventional optimization methods. Genetic algorithms suffer a few disadvantages: they are not suitable for real time applications and take long to converge to the optimal solution. Convergence time cannot be predicted either. Nevertheless, they have become a strong optimization tool, while current research focuses on their combination with fuzzy logic and neural network techniques, [2].

Genetic algorithms imitate natural evolutionary procedures for the production of successive generations of a population. In a technical context, each generation is a candidate solution for evaluation. An evaluation function is necessary to “guide” the evolution process towards improved generations (solutions), [3], [4]. If we assume that the solution to a given problem can be expressed as a set of vectors (e.g., a set of points on the 2-D plane), then this set of vectors is called a “generation” and each vector is called a “chromosome,” while the vector elements are called “genes”. Of course they may represent practically any physical quantity. The set of all possible generations forms a “population”. The first generation is generated randomly. Each “parent” generation is evaluated through an evaluation function that yields a “grade.” The next generation is created so as to get a higher grade, i.e. to represent a better solution.

In its simplest form, a genetic algorithm consists of three (3) mechanisms: (i) *parent selection*, (ii) *genetic operation* for the production of descendants (offspring), and (iii) *replacement of parents* by their descendants, [2]. *Parent selection* process follows one of the selection processes of roulette, classification, constant situation, proportional forms or elitist choice. The *genetic operations* of (i) crossover and (ii) mutation combine parents to produce offspring of improved characteristics (getting higher grade by the evaluation function). *Parent replacement* strategies include (i)

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generational replacement and (ii) steady state reproduction.

II. THE PROPOSED METHOD

A. Problem description

Blood cell microscope images, such as the sample shown in Fig. (1), show cells of two different classes (possibly overlapping) against a uniform background. Class A is represented by bigger and usually more deformed cells whereas class B is represented by cells looking generally more normal and more uniform in shape and size. Cell color or grayscale can also be exploited; yet it is unreliable by itself, due to the various cell coloring techniques usually applied on the sample before it is placed in the microscope. In the present context, we will not go into the medical interpretation of the image, i.e. the diagnosis of certain pathologies connected to the presence or count or percentage of class A or class B cells, as this does not affect the technical problem addressed – although it renders the obtained results critical.

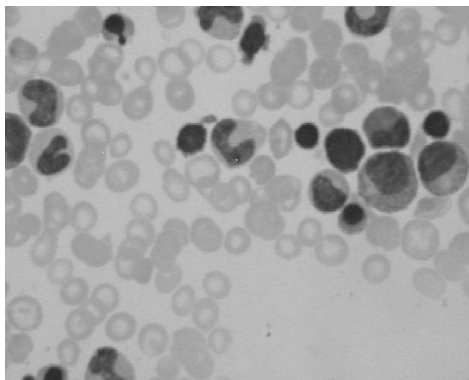


Fig. 1: Sample blood cell microscope image showing two classes of cells in a uniform background.

Referring to Fig.1, we aim to address the following problems in ascending order of importance:

- 1) Detection of class A cells,
- 2) Percentage of the class A cells surface in the image, and
- 3) Registration of class A cells (coordinates and size).

Although this could be treated as an image segmentation problem, [1], we claim that the genetic algorithms approach taken here is far more efficient in terms of processing time, while it yields high correct recognition scores.

B. Image preprocessing

The histogram of the grayscale image is employed in order to obtain a grayscale threshold value Th , below which fall class A cells only. The sample histogram, shown in Fig. (2a), exhibits three major areas of grayscales, corresponding – from darker to lighter scale – to: (i) class A cell pixels, (ii) class B cell pixels and (iii) background pixels. Threshold value Th is set to the local minimum of the histogram curve, lying between the first two peaks mentioned above. The image is thresholded by Th , thus producing a binary (black and

white) image, as in Fig. (2b).

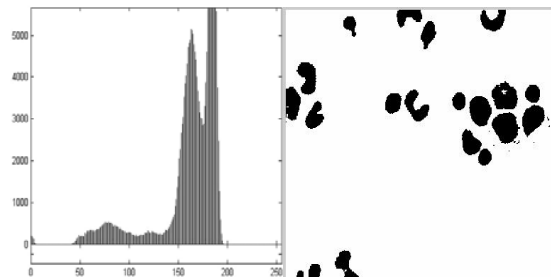


Fig. 2: (a) Histogram of the grayscale image in Fig.(1), (b) Binary version of Fig. (1) with threshold $Th=110$.

The first two problems (detection of class A cells and calculation of their % area in the image) are straightforward if we use the binary image. We next focus on the third problem, for which we employ a genetic algorithm method.

C. The proposed genetic algorithm approach

The genetic algorithm is repeatedly applied to the image as many times as the number of class A objects (bigger than a threshold area of TB pixels) it contains. Of course, an appropriate stopping rule is necessary, because the number of class A objects is originally unknown.

Within each of the above repetitions, the genetic algorithm generates a succession of T generations, each consisting of N chromosomes. Each chromosome contains three (3) genes, namely, the 2-D plane coordinates of the center of an object (circle) and the radius of it. The first generation is generated randomly, whereas every next one is based on the following choices:

- (i) Chromosomes are binary encoded, with 9, 10 and 4 bits for the 1st, 2nd and 3rd gene, respectively.
- (ii) Parent pairs are selected by the roulette rule.
- (iii) The genetic operations include 3-point crossover for the 1st and 2nd gene and 1-point crossover for the 3rd gene, with crossover probability Pc and arithmetic (bit) mutation, uniform across genes, with mutation probability Pm .
- (iv) Generalized replacement is employed, combined with an elite strategy using a number of Pe elite chromosomes directly copied to the next generation.
- (v) No schema theory is employed.

Once a new generation is produced, its N binary chromosomes are decoded and evaluated by the fitness function. This function assigns a numerical “grade” to each chromosome, which is used for the parent selection and genetic operations of the next generation. When the T -th generation is reached, iteration stops and the chromosome of the T -th generation with the highest grade is considered as a solution (localized circular object).

As mentioned earlier, a stopping rule is necessary: Repetition stops when the area of the image designated by such a solution is found to contain less than 40% of class A pixels – meaning that essentially there remain no more

significant class A objects.

Critical for the success of the genetic algorithm is the choice of the evaluation (fitness) function, [3]. Indeed this is the only means of communication between the genetic evolutionary process and its environment (i.e., the problem it seeks to solve). When chromosomes of the current generation are graded by the fitness function, the genetic algorithm gains feedback from the environment so as to adjust its evolution towards an improved next generation, [4]. For the problem at hand, we have employed the straight-forward option of a fitness function which counts the class A pixels contained in the area of the original image designated by the (center, radius) pair of a given chromosome. In that sense, chromosomes (circular objects) highly overlapping with class A objects in the image get a higher grade.

III. EXPERIMENTAL PART

In Section II it became clear that the both the efficiency and the success of the method depend critically on a number of parameters, like Th , TB , T , N , Pm , Pc , Pe , etc. These should be adjusted using prior information about the specific family of images, for optimal performance. In this Section we investigate the effect of these parameters on the overall method performance.

A sample blood cell image with superimposed results is shown in Fig. (3). Circular objects localized by the genetic algorithm are marked with a white circle. This is a particularly successful experiment, as 20 out of 20 (100%) class A objects are localized. Major parameter choices are $N=50$ chromosomes, $T=50$ generations, $Pc = 80\%$, $Pm = 8\%$ and number of elite chromosomes $Pe = 5$.

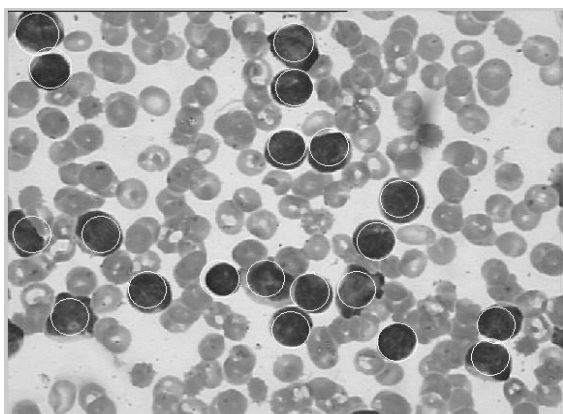


Fig. (3): Original image with superimposed genetic algorithm results marked with a white circle. 20 out of 20 (100%) of class A objects are localized correctly.

However, not all parameter choices yield analogous results. We have therefore varied the set of parameters according to Table I, and examined results for a set of 16 images of the same family.

In order to reduce the number of all possible parameter combinations, we have used the set of parameters mentioned

for the Fig. (3) experiment, namely, [$N=50$ chromosomes, $T=50$ generations, $Pc = 80\%$, $Pm = 8\%$ and number of elite chromosomes $Pe = 5$], as the default, and varied one parameter only at a time, while the others retained their default values.

TABLE I
GENETIC ALGORITHM PARAMETERS VARIATION

Nr.	Parameter	Range
1	T	[10, 50, 90]
2	N	[10, 50, 70]
3	Pc	[10%, 50%, 80%]
4	Pm	[4%, 8%, 50%]
5	Pe	[1, 5, 20]

Due to the random initialization of the genetic algorithm (random gene values in the first generation of chromosomes), convergence of the algorithm to the same local minimum in successive iterations is not guaranteed. Therefore each experimental setup is run four (4) times, and results are averaged.

Out of the set of all experiments performed, we present here results obtained on the sample image of Fig. (1), for:

- (i) a highly successful parameter choice of $N=70$, localizing 17 out of the 18 objects included (results in Fig. (4)),
- (ii) a least favorable parameter choice of $N=10$, localizing 8 out of the 18 objects included (results in Fig. (5)).

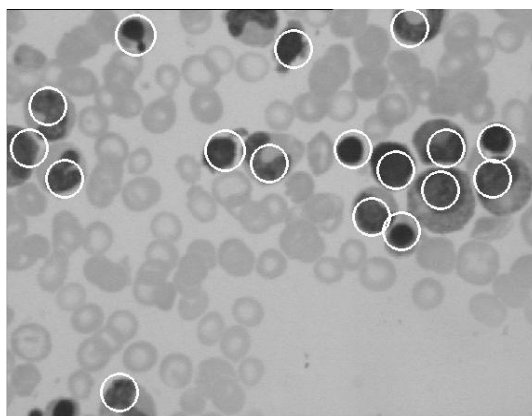


Fig. 4: Successful localization of 17/18 objects [$N=70$].

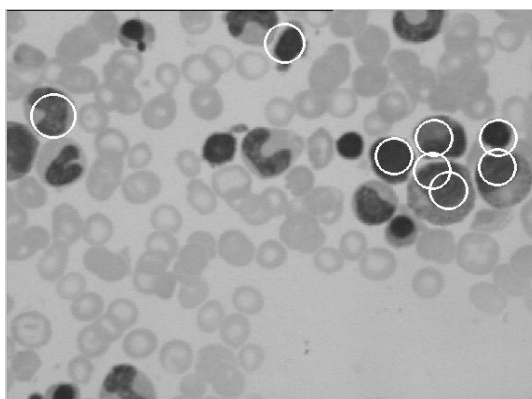


Fig. 5: Unsuccessful localization of 8/18 objects [$N=10$].

Comparison of Figs. (4) and (5) shows the critical role of the number of chromosomes N : Solution improves as N increases, but processing load and time increase rapidly with N , as well!

The results obtained in the performed set of experiments show that solution improves as:

- 1) T increases; yet a this picture is reversed if T increases incommensurately with the N .
- 2) N increases, which is an expected result. Moreover, for high values of N convergence to the same optimal solution is achieved for all iterations.
- 3) P_c increases, as far as it does not exceed 80% approximately, and as far as a few elite chromosomes are copied directly to the next generation.
- 4) P_m remains close to a medium value of around 10%. A lower P_m does not allow "luck" to play some role in the procedure, whereas a higher P_m randomizes considerably the procedure.
- 5) P_e remains around a medium value of around 5 (in a population of about 50), as lower values eliminate promising candidates, whereas higher values do not allow for enough innovation.

As it has become clear from the experiments performed, the relation between T and N values is critical for the overall performance of the genetic algorithm. In light of that observation, we have experimentally obtained a empirical function $N = f(T)$. This function can be expressed as the ratio of two first order polynomials of T , whose coefficients vary according to a set of selections. Fig. (6) shows the plot of the empirical function $f(T)$, for three different coefficients (selections).

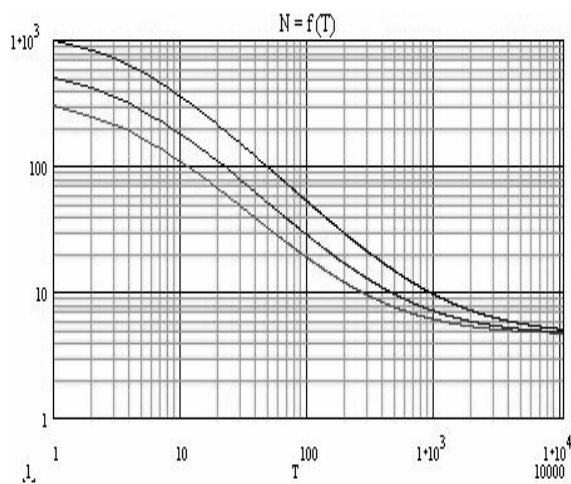


Fig. 6: Plot of function $N = f(T)$ for 3 different coefficients (selections): [300, 500, 1000] (lower to upper curve).

The plot in Fig. 6 may be used as a rule of thumb for the selection of the number of chromosomes N appropriate for a given number of generations T . For example, if we use the

middle curve, $T=50$ produces the choice of $N=50$. This choice has already been seen to produce excellent results in Fig. (3).

As a last comment, let us note that, as Fig. (7) "zooms" in a part of Fig. (3), it reveals that localization of physical shapes by ideal circles can only be approximate. The evaluation function yields a grade for each solution, based on the pixel count of the area over which real object and the genetic algorithm circle overlap. If the grades given by the evaluation function to each solution are summed up, then this total can serve as a type of error, i.e., as an objective measurement for the overall quality of the solution.

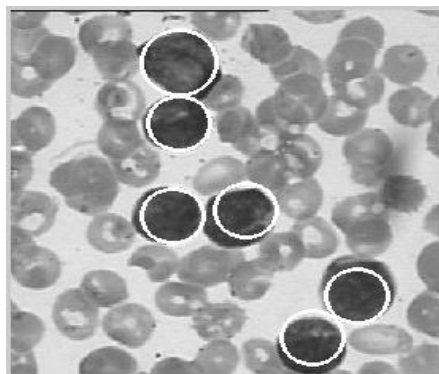


Fig. 7: A zoom into the upper central part of Fig. (3) reveals the approximate nature of the localization results.

IV. CONCLUSION

We have applied a genetic algorithm approach to the problem of localization of objects belonging to a certain class, in blood cell microscope images. Thanks to its non-exhaustive nature, the proposed approach is far more efficient than conventional image processing solutions, such as image segmentation. Experiments on real field images yield strongly encouraging correct localization results, rising up to 94% (17 over 18 objects) or even 100% (18 over 18 objects), for appropriate choice of the genetic algorithm parameters. Furthermore, an empirical function is obtained, as an aid to the choice of the two major parameters among them.

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