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A nuclei segmentation method based on Butterfly Algorithm for H& Estained images

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Abstract*: Nuclei segmentation in H&E strained images plays a vital role in diagnosis of various diseases. Huge research is being carried out by various researchers in developing computerized methods for automatic segmentation of nuclei. These computerized methods played vital role in minimizing human intervention in diagnosis of various diseases. In this paper, we have proposed a new nuclei segmentation method which uses Butterfly Algorithm for avoiding local optima for Histopathological images. The algorithm is based on food foraging strategy of butterflies, as they use their sense of sight, taste, smell, touch and hearing to determine the position of food and mating partner. Histopathological images data set of TNBC patients has been taken. The performance measure of the proposed method is evaluated bases on Accuracy, F1 score and Aggregated Jaccard Index.

***Index Terms*: Butterfly Algorithm, Histopathological Images, Nuclei Segmentation.**

I. INTRODUCTION

Digital pathology is the technique used to analyze digitally scanned histology images of high resolution, which can then take advantage of computer tools and algorithms. Analysis and interpretation of these images plays a vital role in the automated prognosis and diagnosis of cancer and multiple chronic diseases. Accordingly, the interpretation and analysis of these H&E stained images over the past decade gains a lot of attention. In order to detect nuclear-level changes, pathologists visually examine hundreds of slides per day under the microscope within the human eye limitation such as differentiate between hue and image intensity. Automated nuclei segmentation algorithms help the pathologists in the process and overcome the above said limitations. Hence, Segmentation of nuclei from the digital images becomes the most challenging task and requires a highly skilled workforce and best clustering algorithm for better segmentation[2].

An image is divided into multiple segments in image segmentation based on the different features such as set of pixels, color and intensity values[3]. This paper discusses the method of image segmentation based on pixels involving the selection of initial seed points. To partition the image into multiple groups, the similar set of pixels is grouped together. Pixel intensity values can sometimes decrease segmentation performance when the histopathological images have a highly complex background and foreground. Therefore, histopathological images such as stained Hematoxylin and Eosin (H&E), clustering is one of the most widely used methods.

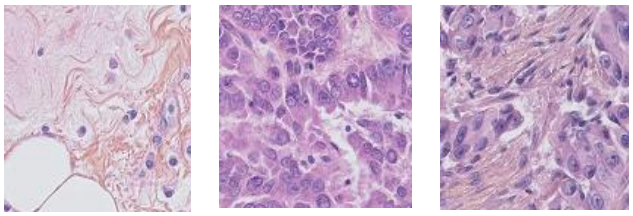

Fig.1. Representative histopathological Images [7].

Even though, some attempts for this nuclei segmentation based on clustering have found in literature[4]-[6], It has been identified that the methods are suffering with stick to local minima. To overcome the problem, we have used meta-heuristic method namely Butterfly Algorithm which guides the clustering to skip from local minima. Butterfly Algorithm[1] is recently proposed meta-heuristic method to find the optimal clustering within histopathological images. In this paper, a novel nuclei segmentation method of histopathological images based on clustering is presented using the butterfly algorithm to obtain the optimal clusters.

The rest of the paper is organized as follows: the Butterfly Algorithm is detailed in Section II. The proposed method of nuclei segmentation is discussed in Section III. Section IV and Section V explains experimental results and conclusions respectively.

II. BUTTERFLY OPTIMIZATION ALGORITHM

Butterfly Optimization Algorithm [1] is based mainly on food foraging strategy of butterflies, as they use their sense of sight, taste, smell, touch and hearing to determine the position of food and mating partner. These senses are useful for the butterflies to migrate from one place to other places, escaping from predators and laying eggs in safe places. Smell is the most important sense among all the senses used for searching food even from long distances. A male butterfly is ready to spot the female butterfly through her pheromone that are scent secretions emitted by the female butterfly to cause specific reactions. Butterflies are search agents in this optimization. A butterfly generates fragrance with specific intensity which is based on fitness function. This fragrance travels over distances where other butterflies can sense it.

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If a butterfly can able to sense the other butterfly fragrance it will travel towards it and this phase is termed as Global search .When a butterfly doesn't sense any fragrance from the surrounding then this butterfly moves randomly and this phase is called as local search. Every butterfly is supposed to generate and emit some fragrance as it enables other butterflies to attract each other. Every butterfly moves randomly or towards its best butterfly emitting more fragrance.

The whole butterfly algorithm is divided in to 3 phases namely initialization, iteration and termination. In initialization phase a random number of initial butterfly population is generated which remains fixed through the execution and butterflies position is randomly assigned in the search phase and fitness values and fragrance is calculated. In Iteration phase every butterfly in a search space move towards new position and generates fragrance using the Equation (1).

$$F = KI^{a} \quad (1)$$

Mainly, the butterfly can move to global search phase or local search phase. In Global search phase the butterfly move towards the fittest butterfly and is represented by Equation (2).

$$y_i^{t+1} = y_i^t + \left(k^2 \times x^* - y_i^t\right) \times F_i \quad (2)$$

Here y_i^t defines the solution vector y_i for ith butterfly in iteration number t, x^* represents current best solution among all the solutions found in the current iteration, F_i defines the fragrance of ith butterfly and k is random number lies between [0,1].

When a butterfly doesn't sense any fragrance from the surrounding then this butterfly moves randomly and this phase is called as local search .Local search phase is represented by Equation (3).

$$y_i^{t+1} = y_i^t + \left(k^2 \times y_j^t - y_k^t\right) \times F_i \quad (3)$$

Here y_j^t and y_k^t represents the j^{th} and k^{th} butterflies from the solution space which belongs to some swarm. F_i defines the fragrance of ith butterfly and k is random number lies between [0,1].

Iteration phase is continued till the stopping criteria is not matched and stopping is maximum number of iterations and in final phase it outputs the best solution found with the best fitness. The pseudo code is explained in the Algorithm 1.

III. PROPOSED SEGMETATION METHOD

For Segmentation of Nuclei, one of the efficient methods is Clustering. In this paper, a novel approach of clustering based on Butterfly Optimization algorithm has been presented for the segmentation of Nuclei. The proposed method takes H&E stained image and number of clusters as an input and we pass these to Butterfly Optimization Algorithm ,The algorithm outputs the optimal cluster center positions and best score. We initialized these optimal cluster center to K-means. The K-means calculates the distance from the clusters centers to the all other objects using the Euclidian distance formula and assign objects to the nearest cluster and finally, we create the images that segment the nuclei by color. In the Butterfly Optimization Algorithm, the objective function used to minimize the compactness in the clusters is given by Equation (5).

$$\underset{k_1, k_2, .. k_p}{Arg\min} \sum_{i=1}^{n} \sum_{j=1}^{m} u_{ij}^{\ 2} \left\| y_i - k_j \right\|^2 \quad (5)$$

Where $\{k_1, k_2 \ldots\ldots, k_p\}$ are the cluster centers and y_i is the cluster member and u is degree of belongingness and is given by Equation (6).

$$u_{ij} = \frac{1}{\sum_{r=1}^{t} \left(\frac{\left\| y_i - k_j \right\|}{\left\| y_i - k_r \right\|} \right)^2} \quad (6)$$

ALGORITHM 1: BUTTERFLY ALGORITHM[1]

1: Initialize the population(p) with the random number, max iterations with random value
2: Define the sensory modality k,power exponent a, switch probability p and Stimulas intensity.
3: Initialize the postion of each particle L_i in population with some random value.
4: While the stopping criteria is not met do
5: Calculate fragrance of each butterfly which is correlated with Objective function and find the best search agent.
6: for each butterfly Li in population do
7: Generate the random number r from [0, 1]
8: if r<p then
9: Move towards the best butterfly using Equation (2)
10: else
11: Move randomly using Equation (3)
12: End for
13: Update the value of a
14. End while
15.Return the best solution.

In H&E stained histopathological images nuclei are the dark regions, the segmented nuclei is the region of cluster centers with smallest pixel values. The detailed procedure of the Butterfly based segmentation is depicted in Algorithm 2.

ALGORITHM 2 : BOA based Nuclei Segmentation Method

Input: Let I be the H&E Strained Image
Output: Segmented Nuclei
1: Convert input image from RGB color space to CIELAB color space
2: Find the optimal cluster centoids using Butterfly Optimization Algorithm.
3:Perform clustering using the optimal cluster centroids obtained in step2.
4: Label every pixel in the image using the results from clustering.
5: Create the Images that segment the H&E images by color.
6: Segment the Nuclei in to separate image.

IV. EXPERIMENTAL REASULTS

The proposed method is tested on the H&E strained Histopathology images dataset taken from the TNBC (Triple Negative Breast Cancer), which consists of mainly three colors namely pink, white and blue ignoring the variations in the Brightness. So, we have taken number of clusters as 3 and segmented the image in to 3 optimal cluster regions. As we know, In H&E stained images, the nuclei region is represented with blue color, finally segmented the Nuclei using the same color. The dataset consists of 11 slides which consist of multiple images.

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We have taken at least one image from each slide for experimental results. Figure 4 depicts some sample images with their respective Ground Truth. We have taken three performance parameters namely Accuracy, F1 score and AJI (Aggregated Jaccard Index value) in to consideration. Accuracy represents how close the segmented image is with Ground truth image. Precision means the measure of exactness and whereas the Recall means measure of completeness which is nothing but sensitivity.F1 score is the harmonic mean of precision and recall. AJI is a quantitative measure of segmentation. We also implemented Generic Algorithm based nuclei segmentation method for comparison. The comparative analysis of genetic algorithm based segmentation method and Butterfly Algorithm based segmentation method is depicted in Table I.

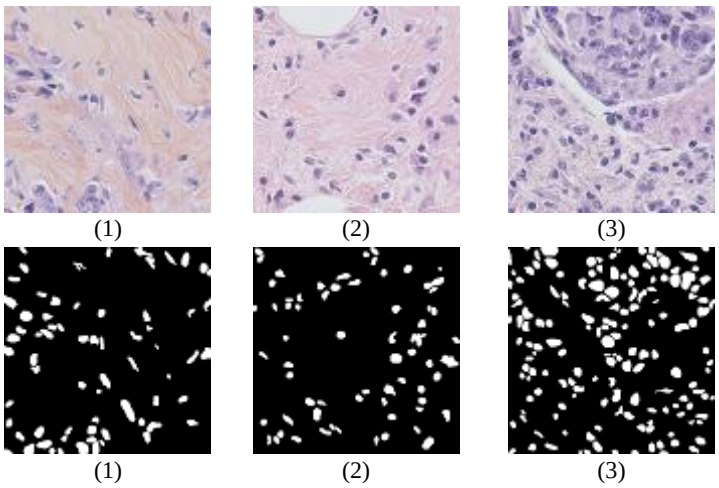

Figure 2. Representative histology images along with their Ground Truth

	MEASURE	ACCURACY		F-SCORE		AJI	
	ALGORITHM	GA BASED	BOA BASED	GA BASED	BOA BASED	GA BASED	BOA BASED
IMAGES	Image1	0.93	**0.95**	0.52	**0.75**	0.35	**0.60**
	Image2	0.83	**0.84**	0.67	**0.71**	0.51	**0.55**
	Image3	0.98	**0.98**	0.65	**0.67**	0.48	**0.50**
	Image4	0.96	**0.97**	0.7	**0.78**	0.55	**0.64**
	Image5	**0.91**	0.90	0.55	**0.61**	0.38	**0.44**
	Image6	0.89	**0.93**	0.43	**0.72**	0.27	**0.56**
	Image7	0.85	**0.87**	0.7	**0.70**	0.53	**0.53**
	Image8	0.81	**0.78**	0.66	**0.68**	0.49	**0.51**
	Image9	0.89	**0.90**	0.68	**0.71**	0.51	**0.56**
	Image10	0.9	**0.90**	0.69	**0.72**	0.53	**0.57**

Table I. Comparative analysis of Genetic Algorithm based and BOA based segmentation methods

Table I contains the segmentation accuracy of the BOA based and GA based methods over 10 representative images in terms of accuracy score, F-score and AJI. To have better segmentation, we must get high value. Thus, from the table, it can be observed that Accuracy score is above 0.9 for more than 70% of the images and the maximum accuracy score is 0.98 for the proposed method. F-score is above 0.7 for more than 80% of the images and the maximum accuracy F-score is 0.78 for the proposed Method. Similarly, AJI value of BOA based method outperforms the GA based method with respect to AJI.

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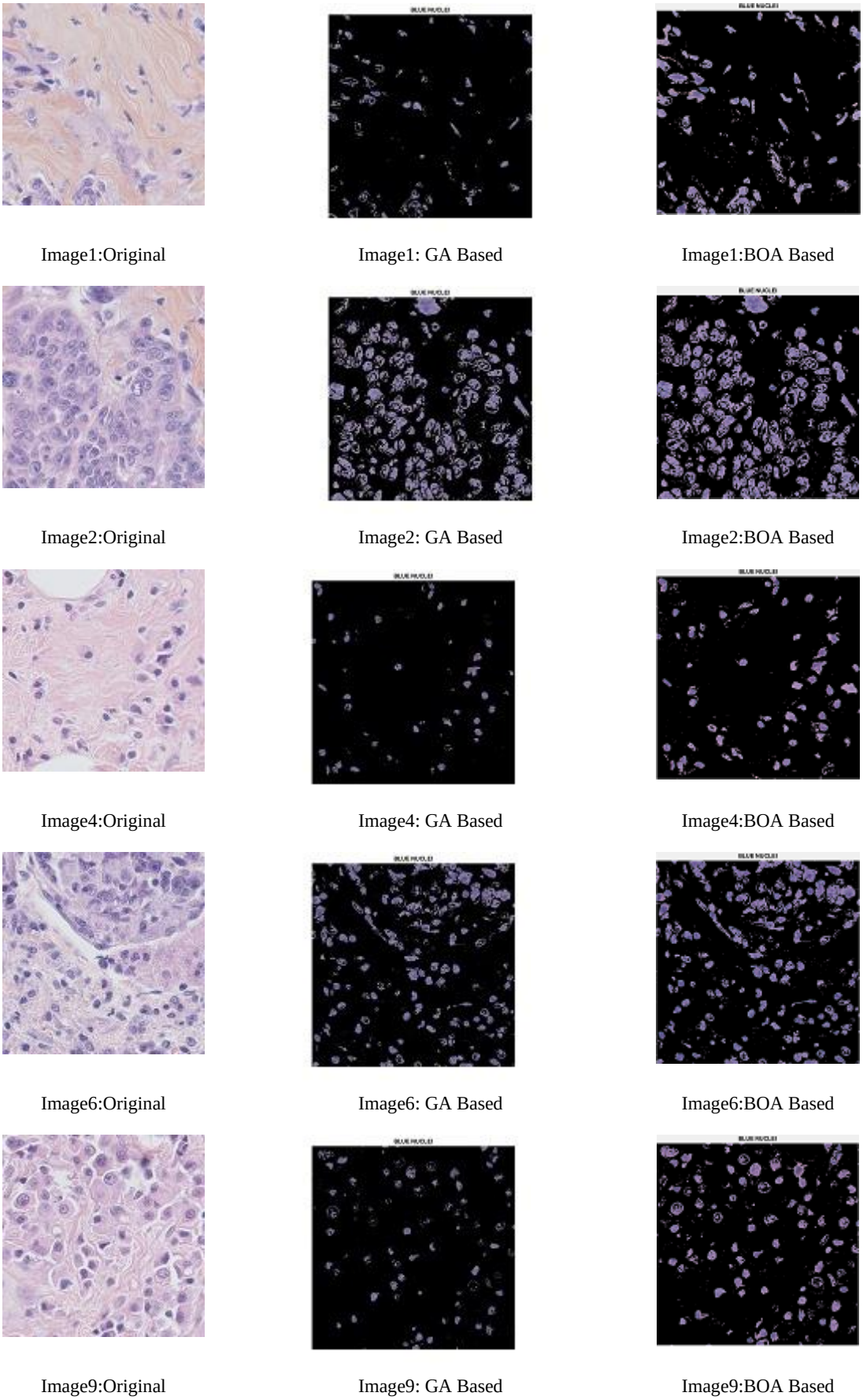

Image1:Original | Image1: GA Based | Image1:BOA Based

Image2:Original | Image2: GA Based | Image2:BOA Based

Image4:Original | Image4: GA Based | Image4:BOA Based

Image6:Original | Image6: GA Based | Image6:BOA Based

Image9:Original | Image9: GA Based | Image9:BOA Based

Figure 3. Segmentation results of GA based and BOA based methods

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V. CONCLUSION

In this paper, a new clustering method based on butterfly algorithm has been proposed which is further used for automated segmentation of nuclei in histopathological images. In the proposed method, the butterfly algorithm outputs the optimal cluster centers. The cluster centroid with the minimum value is identified and the corresponding cluster is considered as the nuclei region. The experimental validation of the proposed method, is performed mainly on H&E stained Triple Negative Breast Cancer patient images, is performed by the publicly available histopathological image dataset. The experimental evaluation shows that the proposed method comparatively divides the nuclei better than the previous methods. However, various histopathological images can be used for the presented method.

In this paper, a novel nuclei segmentation method based on Butterfly optimization algorithm is proposed and compared with a nuclei segmentation method based on Genetic algorithm. In the proposed method, the butterfly algorithm is used to find optimal cluster centers for the segmentation process which will help to avoid local minima. The experimental validation of the proposed method, is performed mainly on H&E stained Triple Negative Breast Cancer patient images, is performed by the publicly available histopathological image dataset. The experimental evaluation shows that the proposed method comparatively divides the nuclei better than the GA based segmentation method.

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