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Chromosomal Edge Detection using Modified Bacterial Foraging Algorithm

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Abstract

This paper proposes a modified bacterial foraging algorithm with a probabilistic derivative approach to detect edges in chromosome images. Chromosomal Edge Detection is fundamental for automatic karyotyping for noise reduction and getting useful messages from the edges. Subjected to staining and other imaging constraints, chromosomal banding patterns lack in resolution, contrast and suffer from noise. For this reason, chromosomal edge detection is highly preferred prior to the segmentation and classification of chromosomes. When the chromosomes occlude or overlap, edge detection becomes extremely difficult. Edge detection is highly challenging and this paper presents a Modified Bacterial Foraging Algorithm (MBFA) based on a probabilistic derivative methodology based on Ant Colony Optimization (ACO) for the detection of edges in chromosomes. Bacterium searches for the nutrients in the direction decided by a probabilistic derivative approach derived from ACO and the edge pixels are identified and traversed. The study reveals that MBFA gives the most promising results in detecting chromosomal edges, greatly reducing the computation time and memory requirements. Acceptable values of parameters for performance evaluation like Kappa (K) and Entropy (E) are achieved with the proposed algorithm in comparison to the other conventional methods of edge detection.

Keywords: *Ant Colony Optimization (ACO), Banding patterns, Chromosomes, Edge detection, Entropy, Karyotyping, Kappa, Modified Bacterial Foraging Algorithm, Probabilistic derivative*

1. Introduction

The efficacy of automatic karyotyping depends on the resolution of the chromosome banding patterns [1]. Due to laboratory processing conditions like cell culture and staining, the banding patterns are subjected to noise and other kinds of distortion that leads to poor edge connectivity, contrast and digital quantization. Figure 1a shows a single chromosome and Figure 1b shows the chromosomes spread in a Metaphase stage, stained with the Giemsa stain that enhances the visibility of the chromosomes in the metaphase stage of cell division. Edges are fundamental features in an image, containing valuable information about the direction, step characteristics, shape and lot of other useful factors [2]. Edge detection and extraction is highly crucial to recuperate information on the shape, structure, and other vital characteristics of the image. Edge detection is conventionally performed using algorithms such as Sobel, Prewitt, Laplacian, Gaussian and other edge detection operators [3]. However,

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these techniques perform high pass filtering that is not suitable to detect chromosome edges because both the noise and edge possess high frequency characteristics. Also, the conventional edge detectors require a huge search space for edge detection. For instance, for a given image of dimension 512*512, the search space is $2^{512*512}$, extremely huge, consuming a lot of time and memory.

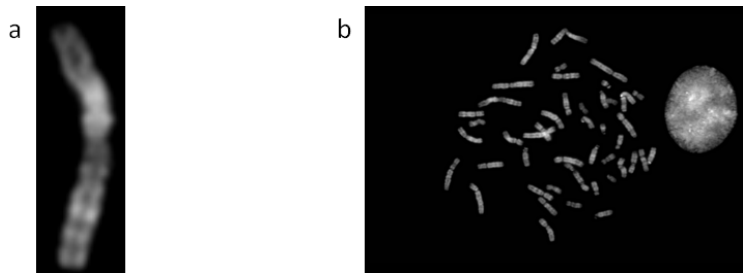

Figure 1. a) Single chromosome b) Giemsa Stained chromosomes in a Metaphase stage

This paper proposes a novel approach for detecting chromosome edges using Bacterial Foraging Optimization as proposed by [4], combined with a probabilistic derivative approach to detect the chromosomal edges. The probabilistic derivative strategy is derived from the Ant Colony Systems [5] and the foraging behavior of the bacteria *Escherichia Coli* is hypothetically modeled here as an optimization procedure. Bacterial Foraging Algorithm find diverse applications in modeling control systems, estimation of harmonics, reducing transmission loss, intelligent learning in automated machines, design of active filters, enhancement of color images and other areas related to engineering design [6–10]. A swarm of bacteria searches for the nutrients in the search space in such a manner that they maximize their energy in unit time spent in foraging that drives all the bacteria to traverse through the edge pixels. The probabilistic derivative approach helps in finding the optimal direction of movement for these bacteria and the derivative rules are defined to make sure that the intensity variation due to noise is neglected. This paper presents a qualitative and quantitative analysis of the performance of a Modified Bacterial Foraging Algorithm (MBFA) and the other conventional methods of edge detection in terms of Kappa (K) and Entropy (E) measures. The initial values of the parameters of MBFA on detecting the edges are also elaborated.

2. Bacterial Foraging Technique

Passino [4] developed a novel bacterial-derivative based technique to exploit the foraging behavior of the bacteria *Escherichia Coli* for function optimization and this paper employs the Passino's algorithm, modified with a probabilistic derivative approach for edge detection in chromosome images. Bacterial Foraging technique is an optimization procedure where the bacteria tend to maximize their energy in unit time spent in searching and exploiting the nutrients. Edge detection is analogous to tracing the nutrients and the bacterium exhibits a tumbling or swimming on its way to traverse the edge pixels. A random movement in any direction is preferred in the classical theory where all the directions are preferred equally. This paper exploits the probabilistic derivative approach, inherited from the Ant Colony Systems. In this way, the bacterium will move in that direction where there is the highest probability of finding the nutrients, *i.e.*, the edge pixels. The derivative approach easily distinguishes between the local variations due to noise and image structures. Bacterial

Foraging technique is a noise-protected operation that combines the strategy of noise cancellation and edge detection in a single framework.

The proposed MBFA technique together with a probabilistic derivative approach for determining the optimal direction of movement for the bacterium takes a small set of data as input, making computations simpler, faster and more memory-efficient. In this way, MBFA outperforms all the existing, conventional methods of edge detection. Bacterium exhibits tumbling and running movement on its way to trace the nutrients. With every tumble, the bacterium moves at a random direction and the running movement results in the bacterium moving in a straight line path, the run modulation depending on the strength of the nutrients. With tumbling and moving, the bacterium finally converges to the most favorable point in the search space.

Chemotactic movement is the principle motivation behind the foraging behavior of the *Escherichia Coli* Bacteria [11]. A chemotactic encompasses several runs with a tumble. With every chemotactic step, the bacterium updates its position in accordance to equation (1). Let 'Σ_i^t' presents the position of the 'i'th bacterium in the 't'th chemotaxis step, 'C(i)', the step length during the 'i'th chemotaxis, 'α(i)', a unit vector which for the direction of swim following the tumble. The current position, 'Σ_i^{t+1}' of the bacterium is given by equation (2), where 'τ_i' is a randomly produced vector with the same dimension of the problem:

$$\Sigma_i^{t+1} = \Sigma it + C(i)\alpha(i) \quad (1)$$

$$\alpha(i) = \frac{\tau_i}{\sqrt{\tau_i{}^T \tau_i}} \quad (2)$$

Reproduction occurs for every chemotactic step and the bacteria are arranged in the decreasing order of their nutrient concentration, procured in the earlier chemotactic steps. The bacteria with the highest nutrient concentration are allowed to reproduce where they split into two of equal size and are placed in the same location. The residual bacteria in the population will die so that the size of the population remains unaltered after the reproductive procedure. The reproductive step simulates the natural concept of human reproduction and only the bacteria with the highest nutrient concentration will survive and reproduce, ensuring the possible optimal solutions are searched efficiently.

In nature, the environmental changes have a considerable impact in the population behavior. For instance, an abrupt change in the concentration of the nutrient will cause the bacteria to starve to death or shift to other possible locations [12]. An Elimination-Dispersal event will stimulate these actions and will occur after every reproductive step. A random number lying in the range (0, 1) is generated for every bacterium and the bacteria will be eliminated if the value is less than 'P_{ed}', the probability of elimination-dispersal. A new bacterium will be generated. The number of elimination-dispersal events varies for the MBFA technique and the algorithm ends with the completion of the elimination-dispersal event. The looping operation among chemotaxis, reproduction and elimination-dispersal continues until convergence is achieved.

3. Probabilistic Derivative Approach

The probabilistic derivative approach helps in finding the concentration of the nutrient and the most appropriate direction for the bacterium to move so that the edge pixels are efficiently traced. Figure 2(a) shows the pixel (x, y) with its 8-connected neighborhood and Figure 2(b) shows the pixels to be considered for the edge in the North east-South West Direction.

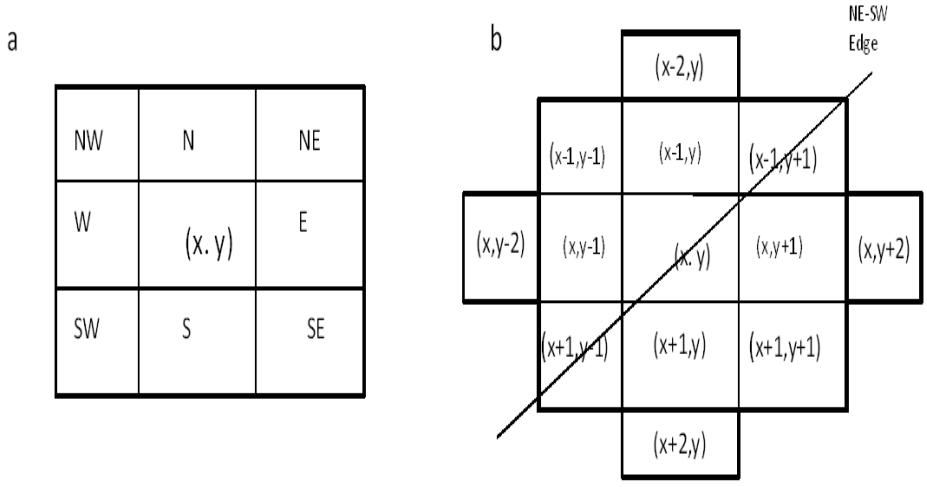

Figure 2. a) Pixel (x, y) with its 8-connectivity b) The pixels to be considered for the edge in NE-SW direction

The derivative at a pixel (x, y) in the N-W direction is given by equation (3) as

$$\mathfrak{d}_{(x,y)}^{NW} = \text{I (x-1, y-1)} - \text{I (x, y)} \quad (3)$$

where 'I (x,y)' is the pixel intensity at (x, y). An edge is considered to pass through the pixel (x, y) in the NE-SW direction and the values of the derivatives in the direction perpendicular to the edge for the pixels at positions (x, y), (x + 1, y - 1) and (x - 1, y + 1) will be having a high value. The average value of the derivates in all possible directions including N-S, W-E, NW-SE and SW-NE, passing through the pixel (x, y) is determined. The concentration of the nutrient at the pixel point (x, y) will be a function of this derivative and hence by equation (4),

$$\eta_i = \mathfrak{d}_{(x,y)} \quad (4)$$

where 'η_i' is the concentration of the nutrient for the 'i'th bacterium.

A direction probability matrix is then computed [5] that accurately locate the edge pixel for the bacterium to relocate from the current pixel value. There are eight possible directions of movement and the next possible direction is identified by using the transition matrix, which a function of pheromone discharged by ants on their path of travel and a special factor, called the heuristic factor, inspired from the Ant Colony Systems. The transition probability matrix at position 'I' and the probability of moving along a given direction 'i' to 'j' are given by equation (5):

$$\rho_{ij} = \frac{\mathbb{I}([\tau_j(t)]\mathbb{I}^{\alpha})\mathbb{I}([N_j]\mathbb{I}^{\beta})}{\sum_{j\in allowed j}\mathbb{I}([\tau_j(t)]\mathbb{I}^{\alpha})\mathbb{I}([N_j]\mathbb{I}^{\beta})} \quad (5)$$

$$\rho_{ij} = \frac{[\eta_j]}{\sum_{j\in allowed j}[\eta_j]} \quad (6)$$

The Bacterium moves in a random direction with 'ρ_{ij}' being the probability of selecting the direction from 'i' to 'j', given by equation (6). If the current location of the bacterium is given by (x, y), with a unit step size 'C(i)', the bacterium will move to the location [x+1, y+1] if the SE direction is selected at random.

4. Results

The performance of an edge detection operator can be evaluated based on the accuracy in edge detection and the amount of useful information obtained in the form of meaningful edges. The accuracy is determined in this work, using the Relative Grading Method [13]. Conventional edge detection operators like Canny, Sobel, Robertz, Prewitt and Laplacian of Gaussian are used and a Majority Image (M) is found using the results of these edge detection operators. The output of the proposed MBFA technique is compared to that of the true images in pixel-by-pixel manner. An edge pixel is identified in the Majority image, if most of the conventional edge detection methods claim to have an edge pixel in its neighborhood. Figure 3 shows the results of edge detection operation on a single chromosome. Figure 4 shows the results of the edge detection operation using Roberts, Sobel, and Majority image (M) obtained using the relative grading method and the proposed MBFA technique. Figure 5 shows the Original chromosome image spread in the metaphase stage and the results of the edge detection operators including Canny, Laplacian of Gaussian and Prewitt. Figure 6 shows the results of edge detection operations on the chromosome spread image using Roberts, Sobel, Majority Image (M) obtained using the relative grading method and MBFA.

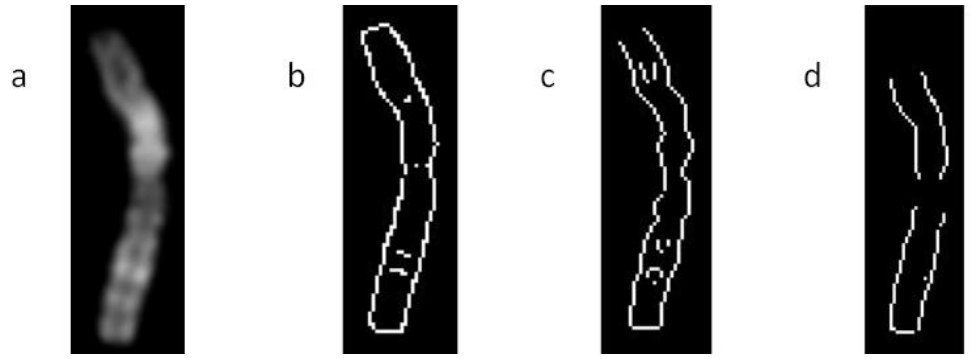

Figure 3. a) Original Single Chromosome Image b) Canny Edge c) Log Edge d) Prewitt Edge

Figure 4. a) Roberts Edge b) Sobel Edge c) Majority Image (M) d) Proposed MBFA

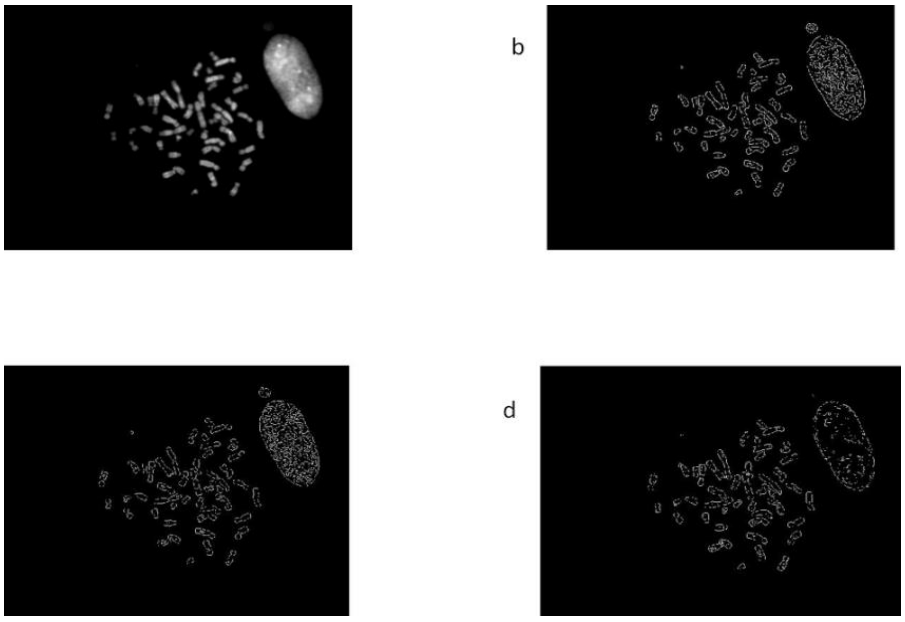

Figure 5. a) Original Chromosome spread in Metaphase stage b) Canny Edge c) Laplacian of Gaussian Edge d) Prewitt Edge

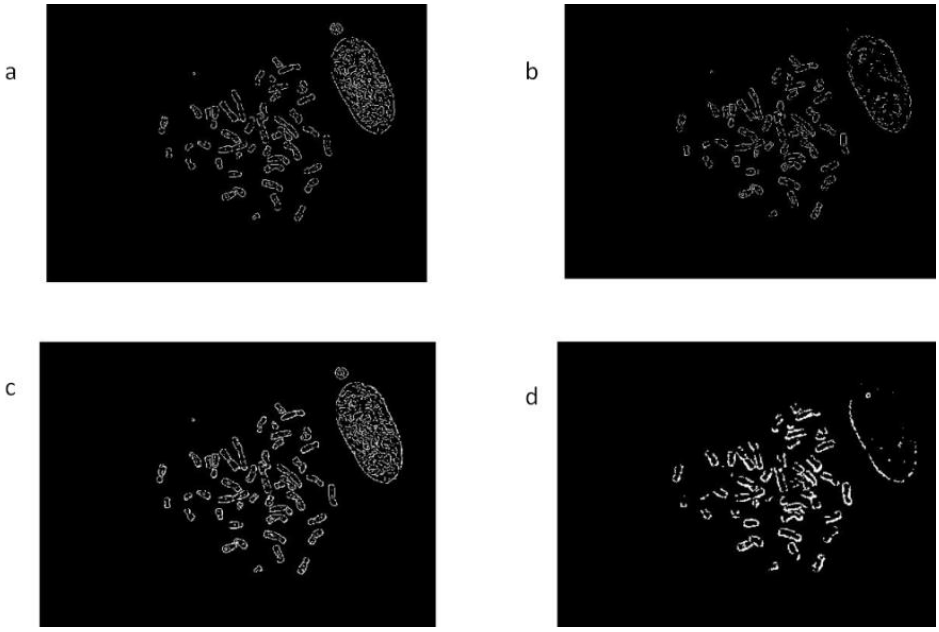

Figure 6. a) Roberts Edge b) Sobel Edge c) Majority Image (M) d) MBFA

A Majority image obtained from the edge detection methods including Canny, Sobel, Roberts, Prewitt and Laplacian of Gaussian are named as M (Canny, Sobel, Roberts, Prewitt, Laplacian of Gaussian). Cohen proposed a parameter called Kappa that measures the accuracy in performing pixel-by-pixel comparison of two images 'J_1' and 'J_2', denoted by 'k $[J_1,J_2]$' [14]. Shannon measured the amount of information in an image using an entropy

function that gives the degree of uncertainty in an image [15]. The entropy of an image 'J' is given by equation (7).

$$H(J) = \sum_{-i=0}^{L} P_i \log P_i \quad (7)$$

Where 'J' is the input image, 'P_i' is the frequency of the pixel with intensity 'i'.

5. Performance Evaluation

The chromosome images are obtained from the standardized chromosome database, made available [16] at the BIOIMLAB, Laboratory of Biomedical Imaging, Department of Information Engineering, University of Padova, Italy [17]. The MBFA technique is compared in its performance to the other conventional edge detector operators like Canny, Sobel, Roberts, Prewitt and Laplacian of Gaussian. The operations are performed using Matlab Image Processing Toolbox. The initial values of the parameters of MBFA are chosen as: S = 800, S_r = 0.5S, N_S = 20, P_{ed} = 0.95, N_{ed} = 20, N_{re} = 1, N_c = 200. The bacteria traverses through the edge pixels and the edges are observed white in a black background. The proposed MBFA technique detects the edges accurately however the edges are incomplete due to the constraints imposed on the Maximum value of the length of swim for a given bacterium. Also, the bacteria moves parallel to the edges that makes the edges appear thick in comparison to that of the results obtained with the other conventional edge detection operators. Table 1 shows the values of Kappa (K) for the conventional edge detection operators and the MBFA technique. Column 2 of Table 1 shows the K (M (Canny, Sobel, Roberts, Prewitt, Laplacian of Gaussian), MBFA). Column 3 in Table 1 shows the ratio between the M of Canny and that of MBFA, (*i.e.*) K (M (Canny, Sobel, Roberts, Prewitt, Laplacian of Gaussian), Canny)/ K (M (Canny, Sobel, Roberts, Prewitt, Laplacian of Gaussian), MBFA). The ratios owing to the other conventional edge detection operators are shown in the other columns of the table. The proposed MBFA method outperforms the other conventional edge detection operators for the given set of input chromosome images. Table 2 shows the value of Entropy (E) for the output of the conventional edge detection operators on the input set of images. Sobel operator gives the least value of entropy for the set of input chromosome images and gives the most appropriate edges.

Table 1. Kappa (K) values for conventional edge detectors and the proposed MBFA

Image	Majority Image	Canny/MBFA	Sobel/MBFA	Robertz/MBFA	Prewitt/MBFA	Laplacian of Gaussian/MBFA
1.bmp	0.483	0.271/0.4459	0.291/0.446	0.415/0.463	0.336/0.529	0.321/0.513
2.bmp	0.462	0.381/0.4615	0.401/0.463	0.473/0.499	0.453/0.517	0.466/0.524
3.bmp	0.433	0.363/0.4814	0.396/0.481	0.418/0.559	0.477/0.512	0.453/0.536
4.bmp	0.496	0.382/0.5412	0.386/0.551	0.422/0.555	0.461/0.622	0.472/0.616
5.bmp	0.541	0.352/0.5736	0.362/0.592	0.394/0.616	0.433/0.632	0.428/0.629

Table 2. Entropy (E) values for the conventional edge detectors and the proposed MBFA

Image	Canny	Sobel	Roberts	Prewitt	Laplacian of Gaussian	Proposed MBFA
1.bmp	0.8560	0.6244	0.6083	0.6280	0.7691	0.8457
2.bmp	0.8064	0.5261	0.5712	0.5265	0.6219	0.6451
3.bmp	0.7111	0.4861	0.5669	0.4685	0.5752	0.6274
4.bmp	0.6496	0.5423	0.5681	0.5479	0.6351	0.8452
5.bmp	1.0512	0.6495	0.4504	0.6237	0.8647	0.8913

Table 2 shows that Sobel and Prewitt operators are found to have comparably less value of entropy to the other edge detection operators. The edge detectors of Laplacian of Gaussian and the proposed MBFA have a comparable performance but Canny performs poorer in comparison to the other edge detection methods. It is obvious from the table that the proposed MBFA finds significant edges in the majority of images.

6. Effect of variation of MBFA parameters

Entropy (E) and Kappa (K) are considered as measures to evaluate the variation of parameters of MBFA. The parameters are said to have an optimum value if they yield low E and high K value. Table 3 (a-g) shows the variation in Kappa and Entropy for the varying values of the parameters of the MBFA namely the number of bacterium (S), Split Ratio (S_r), Chemotactic Steps (N_c), Swim Length (N_s), Reproduction steps (N_{re}), Elimination/Dispersal steps (N_{ed}), and probability of elimination/dispersal (P_{ed}) respectively.

Table 3. a) Variation in Kappa (K) and Entropy (E) for the values of the number of bacterium 'S' b) Variation in Kappa (K) and Entropy (E) for the values of Split Ratio 'S_r' c) Variation in Kappa (K) and Entropy (E) for the values of Chemotactic steps 'N_c'

a

S	K	E
100	0.55	0.8
200	0.4	0.81
300	0.48	0.83
400	0.53	0.85
500	0.51	0.83
600	0.49	0.81
700	0.47	0.8

b

S_r	K	E
0.1S	0.45	0.45
0.2S	0.47	0.92
0.3S	0.48	0.87
0.4S	0.5	0.84
0.5S	0.51	0.82

c

N_c	K	E
5	0.5	0.85
10	0.51	0.83
15	0.49	0.79
20	0.5	0.83
25	0.51	0.81
30	0.49	0.8

Table 4. a) Variation in Kappa (K) and Entropy (E) for the values of Swim Length 'N_s' b) Variation in Kappa (K) and Entropy (E) for the values of Reproductive Steps 'N_{re}' c) Variation in Kappa (K) and Entropy (E) for the values of Elimination/Dispersal steps d) Variation in Kappa (K) and Entropy (E) for the values of Probability of Elimination/ Dispersal 'P_{ed}'

a

N_s	K	E
10	0.49	0.8
20	0.48	0.81
30	0.46	0.79
40	0.45	0.78
50	0.42	0.76
60	0.46	0.75
70	0.44	0.73
80	0.43	0.71

b

N_{re}	K	E
2	0.5	0.82
4	0.49	0.81
6	0.5	0.8
8	0.5	0.81
10	0.5	0.82
12	0.48	0.8
14	0.5	0.81
16	0.5	0.82

c

N_{ed}	K	E
2	0.5	0.81
4	0.51	0.82
6	0.52	0.83
8	0.53	0.85
10	0.54	0.9
12	0.38	0.56
14	0.4	0.62
16	0.46	0.71

d

P_{ed}	K	E
0.5	0.4	0.63
0.6	0.45	0.72
0.7	0.47	0.73
0.8	0.5	0.8
0.9	0.45	0.67
1.0	0.32	0.42

Table 3c and Table 4b shows that the results are not affected by the variations in 'N_c' and 'N_{re}'. Constant values of Kappa (K) and Entropy (E) are thus observed. Table 4a shows that the value of 'K' and 'E' decreases with increase in the value of 'N_s'. Table 3b shows that the variation in 'E' is significant, when compared to 'K', as the Split Ratio (S_r) is varied. The 'E' value drops after N_{ed} = 10 that is observed from the Table 4c. The value of 'K' increases with the value of 'S', but there is no significant change in the 'E' value, as observed from Table 3a. An optimum value of P_{ed} = 0.9 can be chosen for the Table 4d shows that the value of 'K' and 'E' are forming a parabola, centered at a value of 0.8. Increase in 'S' is always favorable but it adds more computation burden. Thus an optimal trade-off has to be explored between performance and computation time. Figure 7 shows the result of edge detection operation using the proposed MBFA for a value of S=100 and S=800. Figure 8 shows the results with the value of $S_{r\,=}$ 0.2S and $S_{r\,=}$ 0.4S.

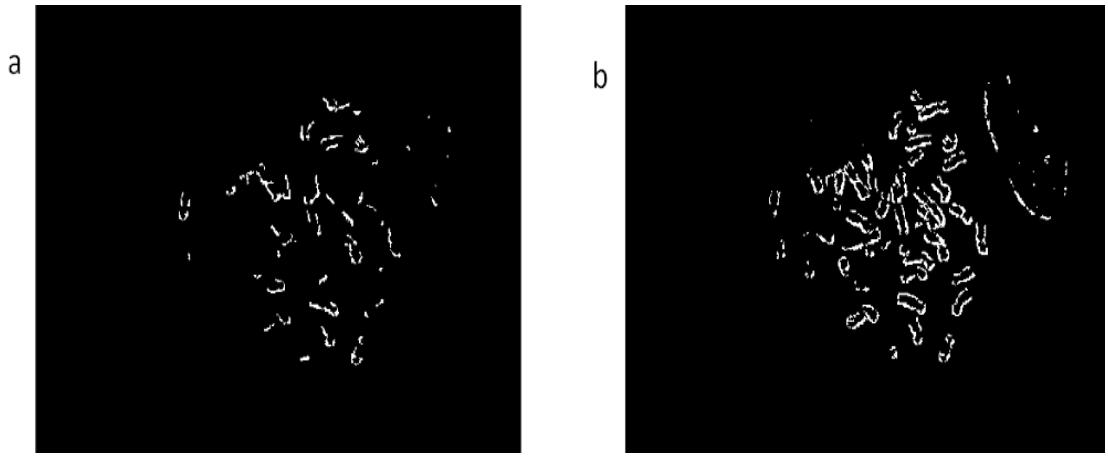

Figure 7. a) Size of the Bacteria 'S' = 100 b) Size of the Bacteria 'S' = 800

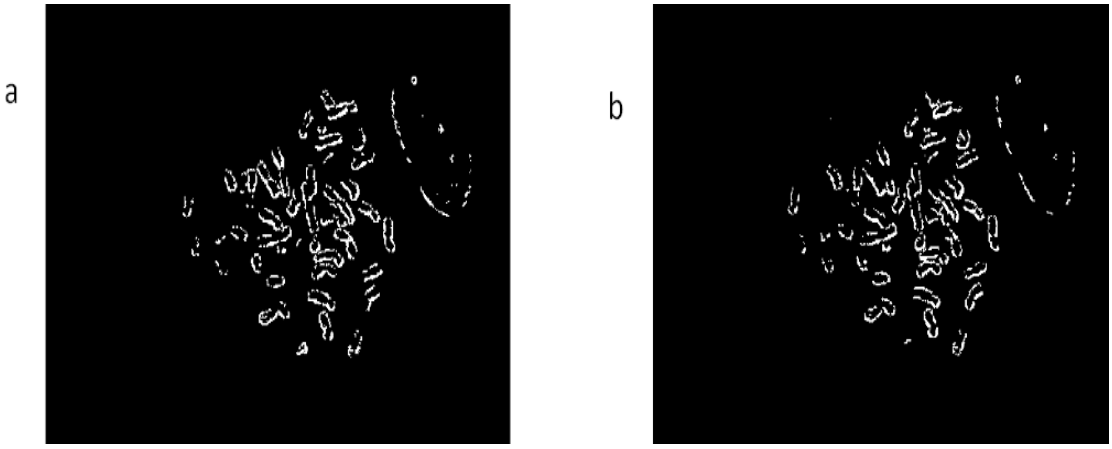

Figure 8. a) Bacteria Split Ratio 'S_r' = 0.2S b) Bacteria Split Ratio 'S_r' = 0.4S

7. Conclusion and Future Work

Image enhancement and edge detection are extremely crucial for accurate segmentation that facilitates efficient classification of chromosome and diagnosing genetic disorders. Image enhancement is done with multi-scale differential operators and MBFA algorithm with a probabilistic derivative approach is employed to detect the chromosome edges. The algorithm finds edges even under intense noise conditions. The computational time incurred in finding the chromosomal edges with the MBFA algorithm is considerably good in comparison to the other methods under study as obvious from the Table 5. It is observed that the proposed algorithm converges to the desired result in 3.7 seconds in comparison to the other edge detectors under study. There is no significant difference in the computation time observed between the other edge detection operators however Canny takes the maximum time to identify the edges.

Table 5. Computation time analysis

Method	Computation Time (in sec)
Canny	5.6
Sobel	4.8
Robertz	4.2
Prewitt	3.9
Laplacian of Gaussian	4.4
Proposed MBFA	3.7

The algorithm is bio-inspired that opens up the gateway for a lot more sophisticated research in edge detection, segmentation and function optimization. The results of the MPFA algorithm are compared with the other conventional edge detectors using Kappa and Entropy measures. The proposed method outperforms the conventional methods and the effect of variation of empirically derived parameters of MBFA on the performance of the algorithm is also discussed. Investigations are still open to find the optimum value of these MBFA parameters that can further enhance the efficiency of edge detection. The proposed MBFA algorithm gives incomplete edges due to its inherent nature of finding the global extremes. The thickness of the edge can be minimized by adding a repellant function to the path already traversed by the bacteria. However, the algorithm is found to be efficient in giving useful information in the form of meaningful edges and opens up the gateway for further research in edge detection.

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