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An image contrast enhancement method based on genetic algorithm

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ABSTRACT

Contrast enhancement plays a fundamental role in image/video processing. Histogram Equalization (HE) is one of the most commonly used methods for image contrast enhancement. However, HE and most other contrast enhancement methods may produce un-natural looking images and the images obtained by these methods are not desirable in applications such as consumer electronic products where brightness preservation is necessary to avoid annoying artifacts. To solve such problems, we proposed an efficient contrast enhancement method based on genetic algorithm in this paper. The proposed method uses a simple and novel chromosome representation together with corresponding operators. Experimental results showed that this method makes natural looking images especially when the dynamic range of input image is high. Also, it has been shown by simulation results that the proposed genetic method had better results than related ones in terms of contrast and detail enhancement and the resulted images were suitable for consumer electronic products.

1. Introduction

Contrast enhancement is a process that is applied on images or videos to increase their dynamic range. Since now, many algorithms have been proposed for such an aim. Histogram Equalization (HE) is one of the most commonly used method for contrast enhancement (Gonzalez and Woods, 2008; Jain, 1989; Zimmerman et al., 1988; Kim, 1997; Kim et al., 1998). It is a simple method and has been used in various fields such as medical image processing and texture analysis (Pei et al., 2004; Wahab et al., 1998; de la Torre et al., 2005; Pizer, 2003). The main objective of this method is to achieve a uniform distributed histogram by using the cumulative density function of the input image (Chen and Ramli, 2003). It has been shown that the mean brightness of the histogram-equalized image is the middle gray level of the input image regardless of its mean (Chen and Ramli, 2003). This is not a suitable property in some applications such as consumer electronic products, where brightness preservation is necessary to avoid annoying artifacts (Chen and Ramli, 2003).

To overcome brightness preservation problem, different methods that were based on Histogram Equalization have been proposed. Mean preserving Bi-Histogram Equalization (BBHE) (Kim, 1997), equal area Dualistic Sub-Image Histogram Equalization (DSIHE) (Wan et al., 1999), Minimum Mean Brightness Error Bi-Histogram Equalization (MMBEBHE) (Chen and Ramli, 2003), and Recursive Mean-Spread Histogram Equalization (RMSHE) (Chen and Ramli, 2003) are HE based methods which tend to preserve the image brightness with a significant contrast enhancement. In BBHE, histogram of the input image is separated into two parts according to the mean of gray levels and each part is equalized independently. DSIHE is similar to BBHE except that it separates the histogram at the median of gray levels instead of the mean. MMBEBHE is an extension of BBHE and provides maximal brightness preservation. In RMSHE, scalable brightness preservation is achieved by partitioning the histogram recursively more than once. This technique is a generation of BBHE. Although these methods preserve the input image brightness on output, they may fail to produce images with natural looks (Menotti et al., 2007).

In order to overcome this drawback, two Multi Histogram Equalization (MHE) methods, i.e. Minimum Middle Level Squared Error MHE (MMLSEMHE) and Minimum Within-Class Variance MHE (MWCVMHE), have been proposed (Menotti et al., 2007). These methods work by dividing the input image into several sub-images and applying the classic HE to each of them. In these methods, number of sub-images is determined by a cost function. The main difference between proposed methods is the way of input image decomposing. Nevertheless, they usually perform a less intensive image contrast enhancement (Menotti et al., 2007). This is the cost that is paid for achieving contrast enhancement, brightness preservation and natural looking images at the same time (Menotti et al., 2007).

The Histogram Equalization based methods is divided into two major categories: global and local methods (Abdullah-Al-Wadud et al., 2007). In Global Histogram Equalization (GHE) (Gonzalez and Woods, 2008), the histogram of the entire image is used for

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contrast enhancement. In this approach, the contrast stretching is limited in gray levels with high frequencies. This causes significant contrast loss for gray levels having lower frequencies (Abdullah-Al-Wadud et al., 2007). To overcome this problem, different Local Histogram Equalization (LHE) methods have been proposed. In Adaptive Histogram Equalization (AHE), at first, the input image is divided into an array of sub-images, and then histogram equalization is applied on each sub image independently. Finally, the sub-images are fused together using bilinear interpolation (Pizer et al., 1987). Block-overlapped Histogram Equalization is another local method (Kim et al., 1998). In this method, a $M * N$ window moves sequentially through each pixel of the input image, then for each block of pixels that are encompassed by this window, Histogram Equalization function is determined and gray level mapping is done for the central pixel. This approach has a high computational cost. In another local method which is called shape preserving histogram modification (Caselles et al., 1999), instead of a rectangular block, connected components and level-sets are used for contrast enhancement. Partially Overlapped Sub Block Histogram Equalization is another local method (POSHE) (Kim et al., 2001). POSHE works same as Block-overlapped Histogram Equalization but the horizontal coordinate of the rectangular sub block increases '*k*' pixels in each step of POSHE instead of one pixel that was used in Block-overlapped Histogram Equalization, where '*k*' depends on amount of sub blocks overlapping. Multi scale contrast enhancement techniques are another local contrast enhancement approach (Jin et al., 2001; Chang and Wu, 1998; Starck et al., 2003). In this approach, multi scale analysis is used for decomposing the image into sub bands and proper enhancement techniques are applied to the sub bands with high-frequency. In these methods, output image is reconstructed through combining the enhanced high-frequency sub bands with low ones.

Some other local methods that do not use histogram have been proposed in literature also. For example Yu et al. proposed a local method based on statistic properties of the image (Yu et al., 2004). This method determines a transformation function for each pixel by considering the local minimum/maximum and local average in a window centered at that pixel. Another local method is based on using 2D Taeger–Kaiser Energy Operator (2DTKEO) to compute the value of local contrast of each pixel (Boudraa et al., 2008). Then the computed value is transformed by a predefined function to emphasizing the pixel's contrast. Finally, a reverse process is performed to obtain the new value of the pixel according to the new value of the contrast.

Dynamic Histogram Equalization is another HE based method which tends to preserve the details of the input image (Abdullah-Al-Wadud et al., 2007). In this method, image histogram is partitioned based on local minima and specific gray level ranges that are assigned to each partition. After partitioning, HE is applied on each partition. Another modified HE approach is presented in (Srinivasan et al., 2006), in this approach the histogram is divided into three regions as dark, mid and bright. Classic HE is performed on each of these regions independently. The final output is a weighted average of the original image and the histogram-equalized output and the weighting factor is calculated for three regions separately according to the variance of each region. In (Eramian et al., 2005), a kind of histogram equalization is described in which the large bins of the original histogram are subdivided to increase the flatness of histogram. Subdivision is accomplished according to local information about pixels and global histogram information. In another technique, which is called Gray-Level Grouping (GLG) (ZhiYu et al., 2006), the histogram components of the input image are categorized into some groups according to a certain criterion, and then these groups are redistributed uniformly over the gray scales. Finally these grouped components are ungrouped. Adaptive GLG (AGLG) (ZhiYu et al., 2006) is an extension of GLG, in which the input image is divided into an array of sub-images and then GLG method is applied to each of these sub-images. Finally, bilinear interpolation is used to reconstruct the final output image from the sub images. Selective GLG (SGLG) (ZhiYu et al., 2006) is another extension of GLG, that histogram components of the input image are grouped and ungrouped selectively to achieve specific results. This method is applicable in cases such as eliminating background noise, enhancing a specific segment of the histogram and so on (ZhiYu et al., 2006).

The approach proposed in (Grundland et al., 2006) is applicable to images with multimodal histograms. In this approach, the probability density function is approximated as a mixture of Gaussians to reduce the impact of the noise. The algorithm locates the valleys of the histogram and then spreads out the modes of the histogram to more evenly occupy the dynamic range. In (Yoon and Song, 2007) transformation function is derived from the generalized local histogram. For obtaining the generalized histogram for a region, fractional count is used instead of integer count 1 for each pixel. The value of the fractional count is determined by a user defined parameter and the spatial activity in the region for which the histogram is calculated.

Histogram specification technique (histogram matching) (Gonzalez and Woods, 2008), is another approach for contrast enhancement. In this method, the shape of the histogram is specified manually then a transformation function is constructed based on this histogram to transform input image gray levels. Dynamic Histogram Specification (DHS) is a method based on histogram specification (ChiaSun and JangRuan, 2005). In this approach, in order to keep original histogram features, the differential information is extracted from the input histogram, and then desired histogram is specified based on this information and some extra parameters such as direct current (DC) and gain value of the input image. In (Jafar and Ying, 2007) a modified version of histogram specification is proposed, in which a block around each pixel is defined and the desired histogram for that block is specified automatically. Histogram specification is done based on an optimization problem, which its main constraint is preserving the mean brightness of the block.

Since now, different genetic approaches have been applied for image contrast enhancement (Munteanu et al., 2000; Saitoh, 1999; Carbonaro and Zingaretti, 1999; Changjiang and Xiaodong, 2006). The proposed method in (Munteanu et al., 2000), is based on a local enhancement technique similar to statistical scaling method (Jain, 1991). In this method, a transformation function is applied to each pixel of the input image. The parameters of the proposed transformation function are adapted using a genetic algorithm according to an objective fitness criterion. In this method, each chromosome is represented as a string of four real genes denoting the four parameters. In another genetic approach, a relation between input and output gray levels are represented by a lookup table (LUT) (Saitoh, 1999).The relation between gray levels in the LUT is determined based on a curve by a genetic algorithm. In this method, an individual is composed of arrayed-bits and represents the form of curve. Evaluation of the chromosomes is done based on sum of intensities of edges in an enhanced image. A general idea for contrast enhancement using genetic algorithm has been proposed in (Carbonaro and Zingaretti, 1999). In this method, at first, the differences of gray level intensities between adjacent edges are calculated. The spatial activity of each neighborhood is determined by the sum of the calculated differences and image pixels are classified by spatial activities. After classification, the contrast value for each pixel in the image is computed using a function that is based on a human visual response. Finally, with regards to the spatial activity of the required image, the parameters of the contrast enhancement function are determined using a genetic algorithm. Proposed method in (Changjiang and Xiaodong,

2006) employs In-complete Beta Transform (IBT), Genetic Algorithm (GA), and Wavelet Neural Network (WNN) to enhance contrast for an image. In this method, a non linear transform curve is obtained using In-complete Beta Transform. IBT in the whole image is approximated using a new kind of WNN. The task of GA is to determine optimal gray levels transform parameters. In this method, original image contrast type is determined using a classification criterion. Parameter space is given based on the contrast type of the image. Local contrast of image is enhanced using discrete stationary wavelet transform (DSWT). The final enhanced image is achieved by adding global and local enhanced image.

In the present paper, we propose a contrast enhancement method based on the genetic algorithm. The main contribution of this method is using a simple chromosome structure and genetic operators to increase the visible details and contrast of low illumination images especially with high dynamic range. The proposed approach maps each gray level of input images to another one such that the result image has more contrast. Simulation results showed that the proposed method worked well and it could produce more natural looking images than some related works. To do comparison with related methods, three different criteria were employed: number of detected edges in enhanced image, PSNR, and visual assessment. In most cases, the proposed method was better than the related ones. Moreover, experiments demonstrated that the enhanced images are suitable for applications such as consumer electronic products.

The rest of paper is organized as follow. The proposed approach is presented with details in Section 2. Section 3 show experimental results and compare them with other previous methods. Finally, we conclude this study in Section 4.

2. Proposed genetic method

In this section, the proposed genetic algorithm for image contrast enhancement is described.

2.1. Chromosome structure

This method uses a simple chromosome structure. An example of the chromosome structure has been shown in Fig. 1. This structure uses a sorted array of random integer numbers. The size of each chromosome is equal to n, where n represents the number of gray levels in the input image. In the proposed structure, the indices indicate the order of gray levels in the image, for example the index 1 indicates the first gray level in the image and so on. In Fig. 1, the first gray level in the image is 0, the second one is 25, the third one is 40, and the last one is 255. In remapping, the first gray level in original image is replaced with the value of first gen of chromosome and so on.

To evaluate each chromosome, based on the mentioned chromosome structure, remapping of the input gray levels is down by the following transformation:

$$T(G(K)) = C_i(K)$$
$$k = 1, 2, \dots, n \tag{1}$$

Where T is the function that used for changing the original image gray levels, G is the array of available gray levels in input image in ascending order, k stands for indexes of G therefore $G(k)$ represents a gray level of the input image which is placed in the kth position of array G. Also, C_i represents the ith chromosome in the population, and $C_i(k)$ represents the value of kth cell and n stands for number of available gray levels in input image. An example of the proposed transformation has been shown in Fig. 2. Fig. 2a shows the histogram of the input image. Fig. 2b is the result of gray level remapping. This remapping has been done based on the chromosome structure, which is shown in Fig. 2c. Fig. 2d represents the array of input gray levels. The remapping of the gray level values in the input image has been done as follows:

0	25	40	65	100	130	194	215	255
1	2	3	4	5	6	7	8	9

Fig. 1. An example of the chromosome structure.

$$T(15) = 0, \quad T(57) = 40, \quad T(73) = 64, \quad T(80) = 119,$$
$$T(240) = 255$$

Initial population, may be generated through a random or user specified process. It plays an important role in search direction. A well selected initial population increases the search procedure convergence speed and results in faster trend to optimum solution. In the proposed method, to generate initial population, at first, the number of input gray levels (n) is calculated. After that, each chromosome is created by using the following steps. These steps should be repeated for population count.

(1) For each chromosome, an array of random integer numbers with length n is generated. To maximize the dynamic range of gray levels: the first element of array is set to 0 and the last one is set to 255
(2) The created array in step (1) is sorted in ascending order. As mentioned earlier, this structure is used for remapping the input gray levels to new ones.

After constructing initial population, the fitness values for all individuals should be calculated. The number of individuals in the population is constant in all generations. Some individuals that have most fitness values are gone forward to next generation. If the crossover rate is called P_c and number of individuals is called P_s; number of individuals that are passed to next generation is equal to $P_s - (P_s * P_c)$. Therefore, the number of new generated individuals in each generation is $P_s * P_c$. These processes are performed while the terminating condition is not satisfied. In the next sub sections, other parts of the proposed genetic algorithm are described.

2.2. Fitness function

In the proposed method, the number of edges and their overall intensity are used as fitness value for each chromosome because a gray image with good visual contrast includes many intensive edges (Saitoh, 1999). This fitness function has been shown in Eq. (2):

$$fitness(x) = \log(\log(E(I(x)))) * n\_edges(I(x)) \tag{2}$$

Where $fitness(X)$ denotes the fitness value of chromosome X and $I(X)$ is the enhanced image. $n\_edges(I(X))$ presents the number of detected edges in the enhanced image which is calculated by a Sobel edge detector (Rosin, 1997). In Eq. (2), sum of the intensity values of the enhanced image, has been shown by $E(I(X))$ which is calculated by the following expression (DaPonte and Fox, 1988):

$$E(I(x)) = \sum_x \sum_y \sqrt{\delta h_1(x,y)^2 + \delta v_1(x,y)^2} \tag{3}$$

where

$$\delta h_1(x,y) = g_1(x+1,y-1) + 2g_1(x+1,y) + g_1(x+1,y+1) - g_1(x-1,y-1) - 2g_1(x-1,y) - g_1(x-1,y+1) \tag{4}$$

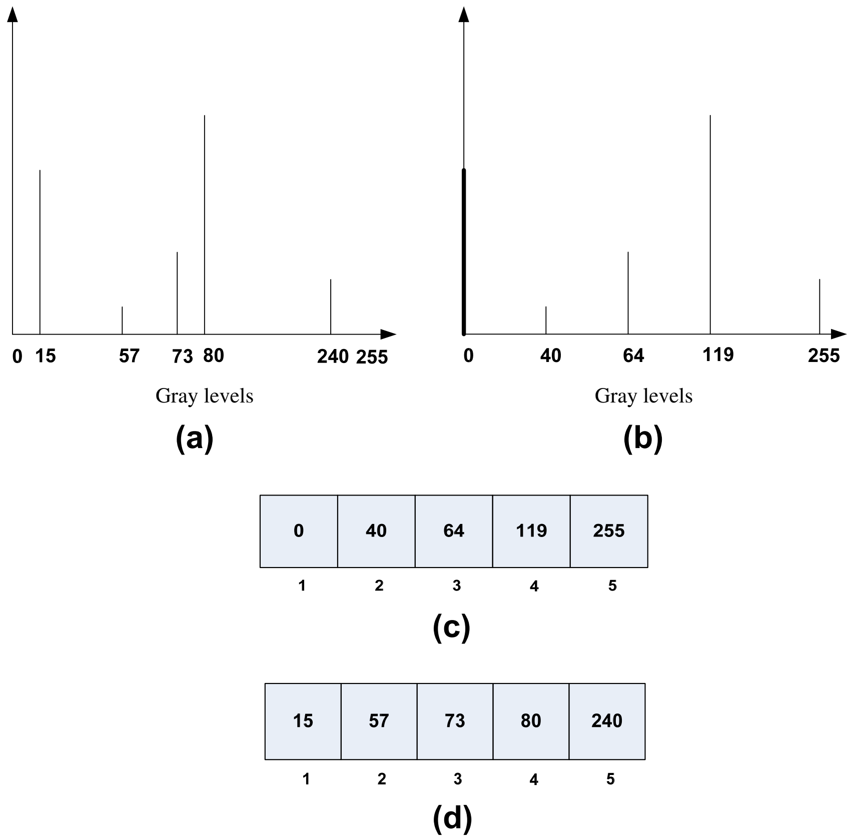

Fig. 2. (a) The histogram of the virtual low-contrast image, (b) the result histogram, (c) chromosome structure and (d) the array of input gray levels.

$$\delta v_1(x,y) = g_1(x-1,y+1) + 2g_1(x,y+1) + g_1(x+1,y+1) - g_1(x-1,y-1) - 2g_1(x,y-1) - g_1(x+1,y-1) \quad (5)$$

In Eq. (2), a log–log measure of the edge intensity is used to prevent producing un-natural images.

2.3. Selection algorithm

Selection of the individuals is done based on the fitness value of the solutions. The probability of selecting an individual is directly or inversely proportional to its fitness value. The roulette wheel selection (Holland, 1975) is used in proposed GA. The main idea of this method is to select genomes stochastically from current generation to create the next generation. In this process, the more appropriate individuals have more probability of survival and go forward to the next generation but the weaker individuals will also have a little probability to select.

In selection process, $P_s * P_c$ individuals are selected to create the same number individuals from them by crossover operator.

2.4. Crossover and mutation operators

Because of constructing individual chromosomes based on a simple structure, complex cross over operators are not necessary. In the proposed method, two point crossover is used. Therefore, $P_s * P_c$ individuals are selected according to our selection process where P_c is crossover rate. As $P_s * P_c$ new individual is needed after doing crossover, two parents are selected and two new child are produced from them. Points in each parent are selected randomly and segments between these two points are substituted to produce new individuals. Finally, each new individual is sorted in ascending order to preserve our individual structure.

For each individual a random number is produced. If it is lower than P_m (mutation constant), mutation will be done for that individual as mentioned follow.

Table 1
Comparison of proposed method and mentioned method in (Saitoh, 1999) based on structural aspects.

	Type of enhancement	Is all problem space searched?	Needed parts for chromosomes	Length of chromosome
Proposed method	Global	Yes	1	Equal to gray levels of the input image (each chromosome is represented by an array of integers)
Saitoh (1999)	Global	Yes	1	Equal to gray levels of the input image (each chromosome is represented by an array of bits)
Carbonaro and Zingaretti (1999)	Local	Yes	3	Fixed and equal to parameters of the transformation function
Munteanu et al. (2000)	Local	Yes	1	Fixed and equal to parameters of the transformation function (equal to 4)
Changjiang and Xiaodong (2006)	Combination of global and local enhancement	Yes	1	Fixed and equal to parameters of the transformation function

Table 2
Applied parameter values in simulating the proposed method and mentioned method in (Saitoh, 1999).

Algorithm	P_c [a]	P_m [b]	Maximum number of iterations	Population size
Proposed method	0.8	0.1	100	10
Proposed method in (Saitoh, 1999)	0.5	0.1	10	100

[a] Crossover probability = P_c.
[b] Mutation probability = P_m.

Table 3
Number of detected edges.

Image	Proposed GA method	HE	GLG	AGLG	Presented method in (Saitoh, 1999)
Galaxia	1964	1347	1350	1256	1819
5236	2500	1887	1989	2324	2233
7741	2887	2309	2473	2869	1430
Crowd	3495	3327	3408	3475	3135
Plane	3320	3260	3320	2995	3271

Table 4
PSNR of enhanced images PSNR = $10 * \log_{10}(L-1)^2/\text{MSE}$.

Image	Proposed GA method	HE	GLG	AGLG	Presented method in (Saitoh, 1999)
Galaxia	14.16	11.52	11.30	11.49	13.9
5236	13.21	12.81	13.05	14.48	12.96
7741	13.75	12.46	12.15	13.71	13.29
Crowd	20.12	12.98	12.81	13.15	20.07
Plane	17.92	13.50	13.57	13.61	17.89

Five percent of the individual chromosome elements are selected randomly for mutation. For each element a random integer number that should be less than or equal to the next element value and more than or equal to the previous element value is generated. This random number is replaced by element.

2.5. Terminating criteria

Terminating criteria is a condition that is used for ending the GA procedure. This condition can be a specific number of generations, timing constraints, etc. In the proposed work, two termination criteria have been considered as:

- When the difference of best fitness in two last consecutive generations is less than ϵ. The value of ϵ has been considered as $0.02 \times$ *best_fitness* (*best_fitness* is the fitness of last generation). OR
- When the attending some max number of generations.

3. Experimental results

In this section, at first the structure of proposed method is compared to some genetic based methods. Table 1 shows this comparison. As it is shown in Table 1, the main difference between proposed method and related ones is in chromosome representation.

To demonstrate the performance of the proposed algorithm, the presented method was implemented by Matlab on PC computer with 1.6 GHZ CPU and 1 GB RAM. Also, some 256 * 256 bench mark images were used to show the performance of the proposed method. The applied parameter values in simulation have been shown in Table 2. Also, some other related methods have been implemented and their results were compared with proposed method. The comparison has been done in terms of ability in contrast and detail enhancement, appropriateness of enhanced images for consumer electronic products and ability of the proposed method to produce natural looking images. Histogram Equalization (Gonzalez

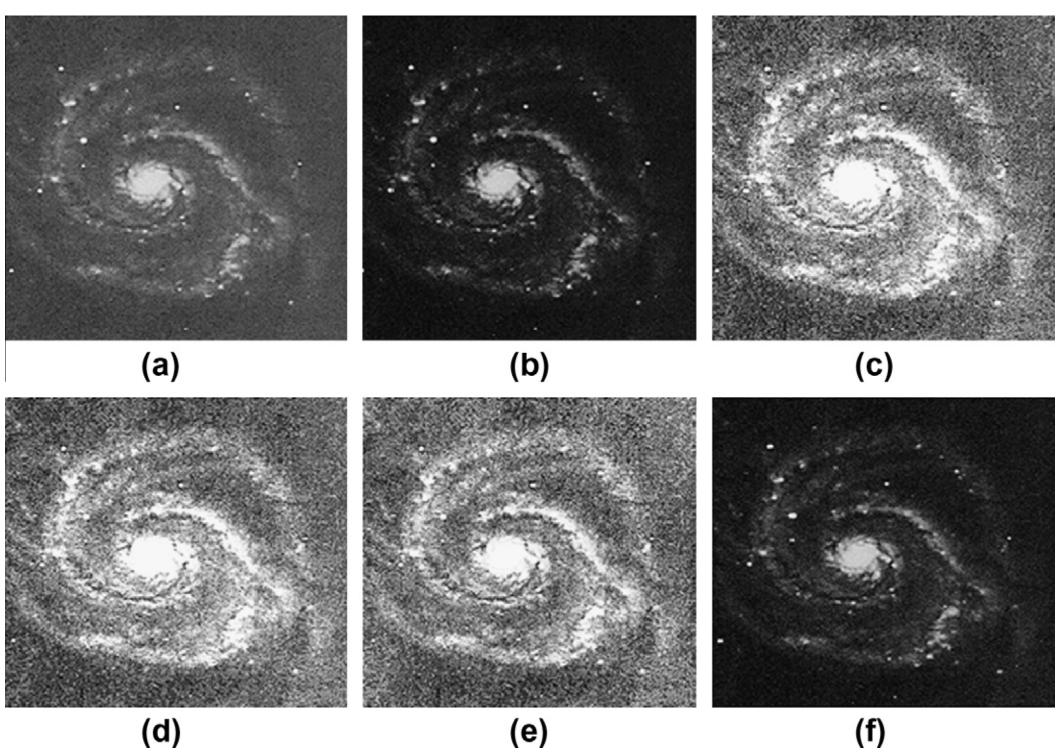

Fig. 3. (a) Enhancement of the 5236 image based on (b) our algorithm (running time: 1.16 s) (c) HE, (d) GLG, (e) AGLG, (f) proposed method in (Saitoh, 1999).

and Woods, 2008), Gray-Level Grouping (GLG) (ZhiYu et al., 2006), Adaptive Gray-Level Grouping (ZhiYu et al., 2006) and the proposed genetic approach in (Saitoh, 1999), are contrast enhancement methods which are used for comparison. The parameters value used in implementing (Saitoh, 1999) method is also shown in Table 2.

In the first step of comparison, the number of detected edges for each of the output images obtained by the mentioned methods was

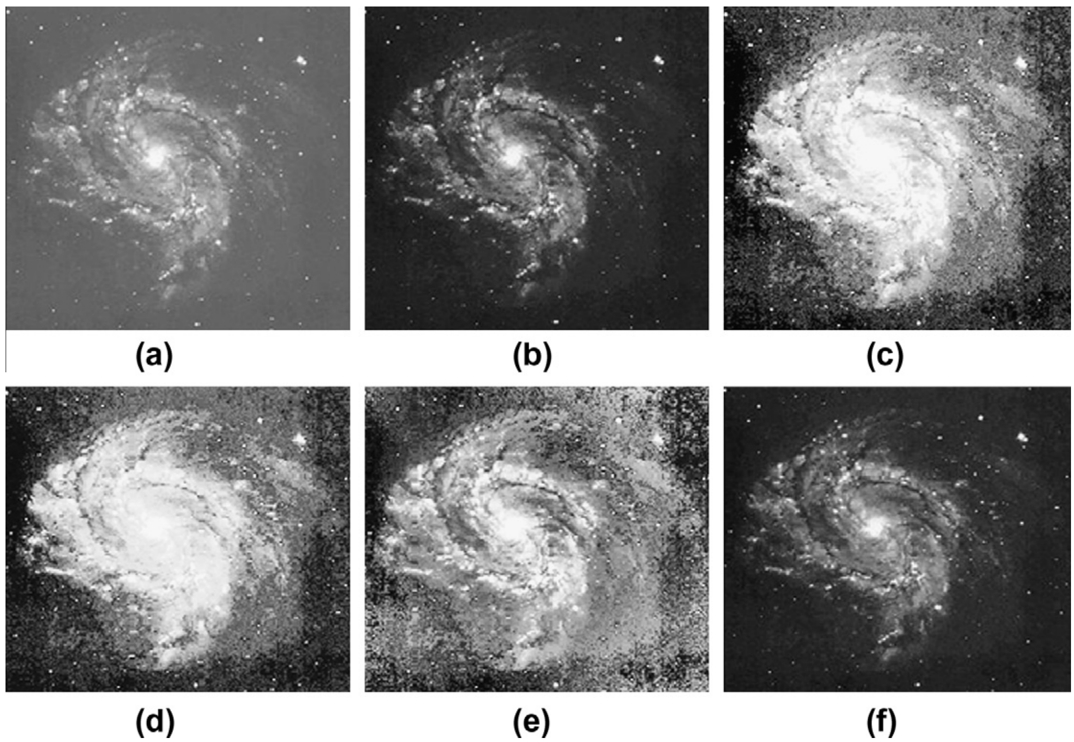

Fig. 4. (a) Enhancement of the 5236 image based on (b) our algorithm (running time: 1.17 s) (c) HE, (d) GLG, (e) AGLG, (f) proposed method in (Saitoh, 1999).

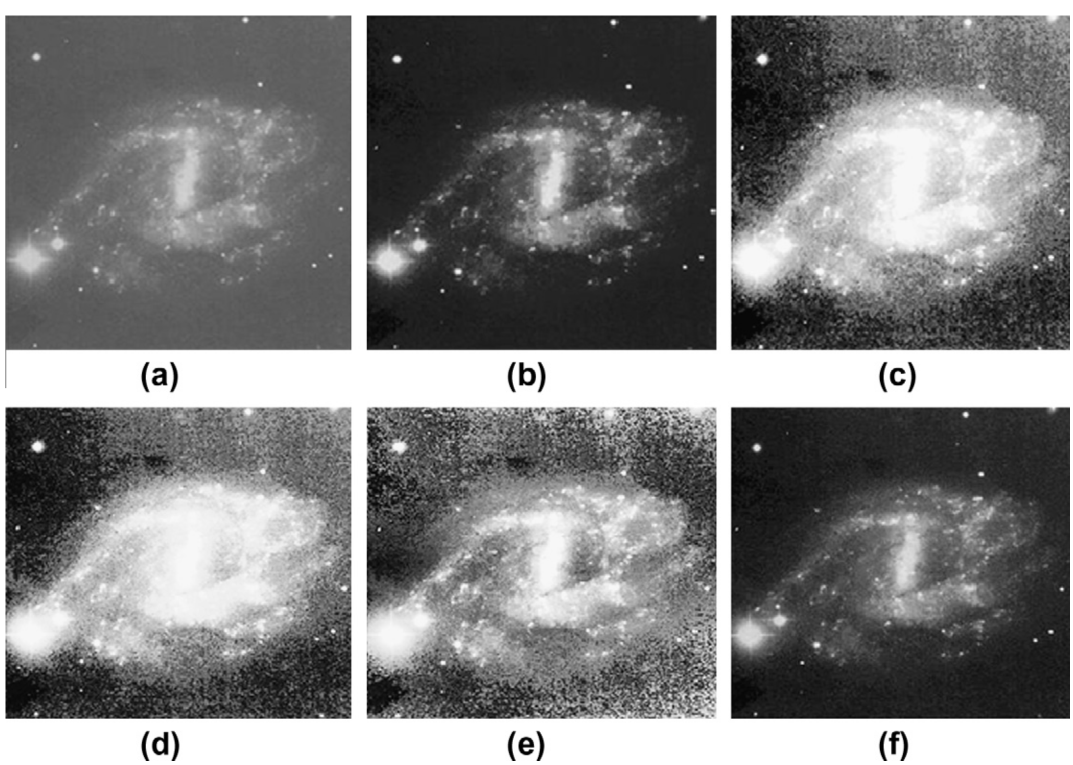

Fig. 5. (a) Enhancement of the 7741 image based on (b) our algorithm (running time: 1.06 s) (c) HE, (d) GLG, (e) AGLG, (f) proposed method in (Saitoh, 1999).

computed. This factor was used to compare the detail content level of the resulted images. The images with the highest number of edges were rated as having high detail contents (Munteanu et al., 2000).

The number of detected edges obtained for each image is presented in Table 3 where a Sobel edge detector was used to detect edges in the enhanced images. In Table 3, the best data value for each image appears in gray. It is clear from this table that proposed GA-based method achieves the best detail content in the proposed images.

Moreover, the PSNR measure (Caselles et al., 1999) was used to assess the appropriateness of the enhanced images for consumer electronic products (Rabbani and Jones, 1991). The data values of PSNR obtained for each image have been shown in Table 4. In this

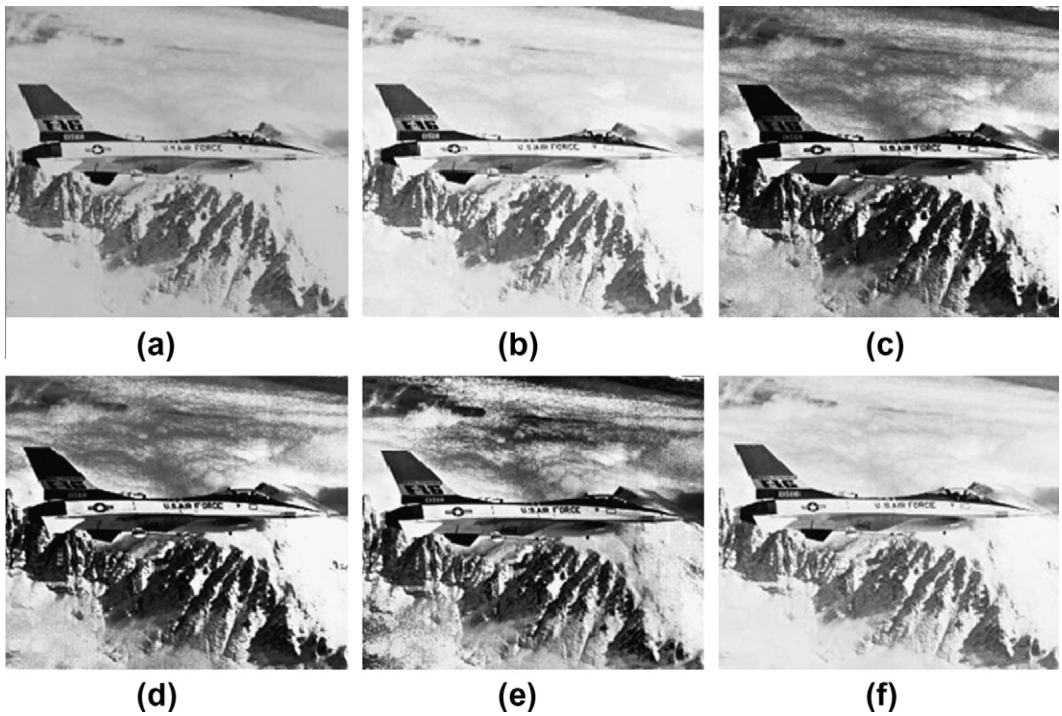

Fig. 6. (a) Enhancement of the plane image based on (b) our algorithm (running time: 1.03 s) (c) HE, (d) GLG, (e) AGLG, (f) proposed method in (Saitoh, 1999).

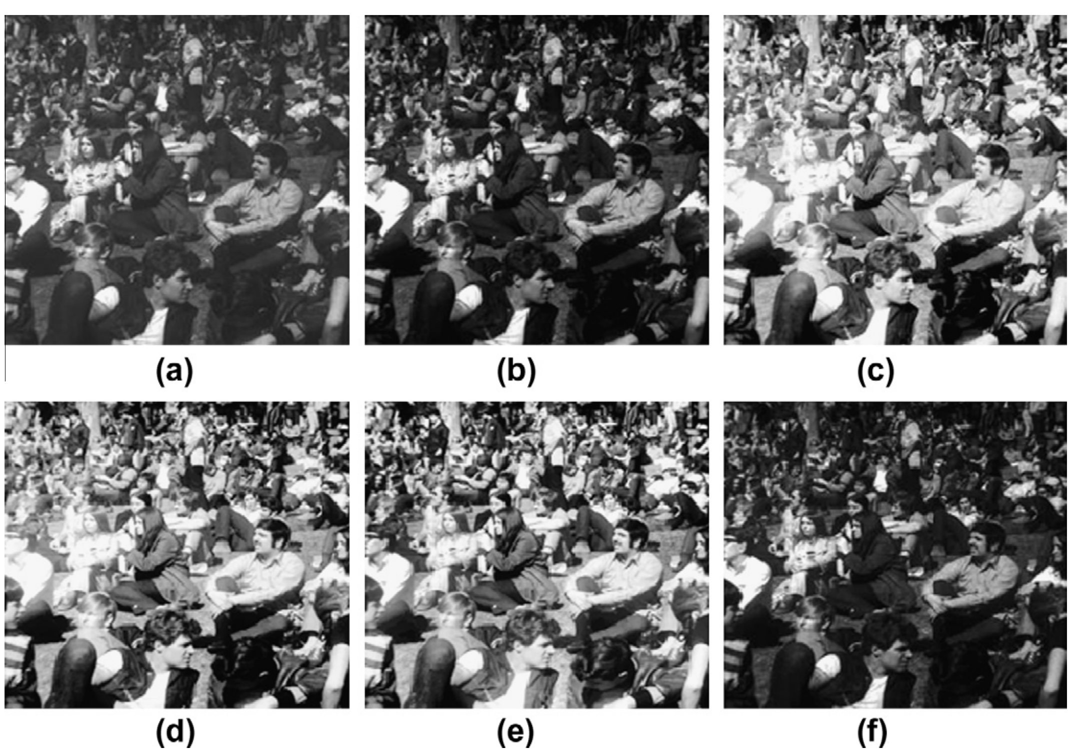

Fig. 7. (a) Enhancement of the crowd image based on (b) our algorithm (running time: 1.15 s) (c) HE, (d) GLG, (e) AGLG, (f) proposed method in (Saitoh, 1999).

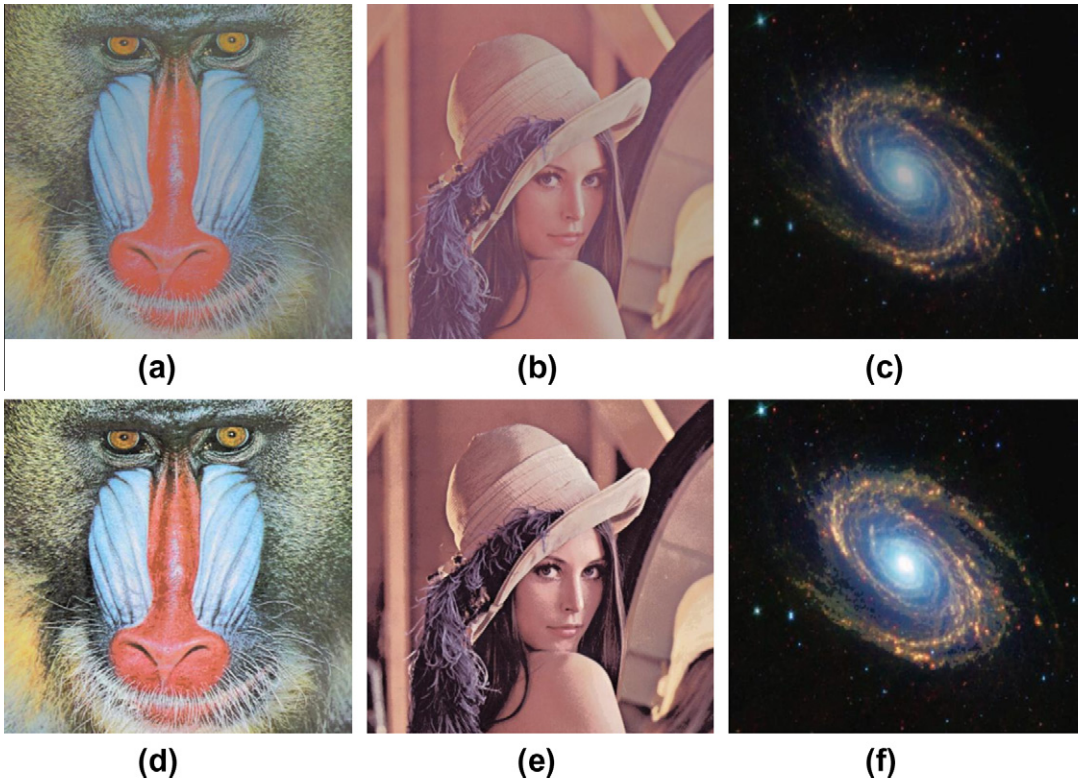

Fig. 8. (a–c) Some input color images, (d–f) result of enhancing (a–c) by proposed method.

Table, the best data value for each image is highlighted in gray. As Table 4 shows the proposed method outperforms other method in most cases.

Finally, we performed an image visual assessment. Simulation results showed the ability of our method in contrast enhancement and producing natural looking images. The enhanced images have been shown in Figs. 3–7. Also, in the caption of each figure the running time of proposed method on the specified simulation platform has been identified. However, to have a real sense of algorithm it should be implemented by C or other programming language (instead of Matlab) and it should be run on a faster Hardware platform.

By visually inspecting the proposed images, it is clear that presented method produced natural looking images with more contrast enhancement. Moreover, Figs. 3–5 show that HE, GLG, AGLG and proposed method in (Saitoh, 1999) enhanced the noise of the input image while the proposed method did not enhance noise.

However, the proposed method has not designed for color images; we applied it on some color ones to watch its affects. Fig. 8 shows the result of applying presented method on three color images. As it is depicted in this figure, by visual assessment, the proposed method worked well in color images also.

In overall, experimental results showed that the proposed method worked well on the low illumination images with high dynamic range and it produced natural looking images. Also, it could provide better results than related methods in all three different criteria and it may be extended for color images.

4. Conclusion

In this paper, we proposed a genetic based method for image contrast enhancement especially when input image has low dynamic range. The proposed method is based on a simple chromosome structure and overcomes the previous methods shortcomings. To confirm the method performance, some standard bench mark images were selected and the proposed method was applied on them. The experimental results were satisfactory. Also, to compare the proposed method with other related ones, three different criteria have been used: number of detected edges, PSNR and visual assessment. The proposed method was better than related ones in most cases. Besides, experiment results demonstrated that the enhanced images are suitable for applications such as consumer electronic products.

In the future, we are going to combine the proposed method with other swarm intelligence methods such as ant colony and electromagnetic to improve results.

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