Chromosome Image Contrast Enhancement Using Adaptive, Iterative Histogram Matching

Seyed Pooya Ehsani, Hojjat Seyed Mousavi, Babak.H. Khalaj
Depatment of Electrical Engineering, Sharif University of Technology, Tehran, Iran
Email: ehsani@ee.sharif.edu, hmousavi@ee.sharif.edu , khalaj@sharif.edu

Abstract*—Vivid banding patterns in medical images of chromosomes are a vital feature for karyotyping and chromosome classification. The chromosome image quality may be degraded by many phenomenon such as staining, sample defectness and imaging conditions. Thus, an image enhancement processing algorithm is needed before classification of chromosomes. In this paper, we propose an adaptive and iterative histogram matching (AIHM) algorithm for chromosome contrast enhancement especially in banding patterns. The reference histogram, with which the initial image needs to be matched, is created based on some processes on the initial image histogram. Usage of raw information in the histogram of initial image will result in more dependency to the input image and acquiring better contrast improvement. Moreover, the iteration procedure leads to a gradual contrast enhancement and getting the best result. The iteration steps may vary depending on the image characteristics and histogram. In order to assess the performance of the proposed algorithm in comparison with existing image enhancement techniques, Constant Gain Transform (CGT) and Local Standard Deviation Adaptive Contrast Enhancement (LSD-ACE), a quantitative measurement, the contrast improvement ratio (CIR), is utilized. The experimental results indicate that the proposed method shows the best results in terms of the CIR measure and, as well as in visual perception.

***keywords*- chromosome karyotyping, contrast enhancement, histogram matching, contrast improvement ratio.**

1. INTRODUCTION

Contrast in chromosome images is of vital importance in many medical applications. Visual examination of medical images especially chromosome images is very essential in diagnosis of many diseases and this is the importance of existence of the contrast in chromosome images. In applications such as karyotyping the contrast is much more important due to banding patterns of chromosomes. These patterns constitute very important features for cytogeneticists to classify different types of chromosomes and generate a karyotype [1]. Clinical diagnostic procedures can be performed using karyotyped images of chromosomes. This procedure can be affected in presence of noise and distortions which may be caused by poor imaging, quantization error and low contrast banding pattern. Therefore, image enhancement is desirable before segmentation and classification of chromosomes.

The main goal of image enhancement is to improve the visibility of details while suppressing noise or not increasing it. Among various techniques for global enhancement, Linear contrast stretching and histogram equalization are two widely used methods [2]–[4].

Linear contrast stretching linearly adjusts the image contrast, and histogram equalization uses a mapping relation obtained from the integral of the image histogram. These algorithms are global algorithms which affect the whole image without any respect of local details. Furthermore, global histogram equalization (GHE) increases noise in the image [5].

As in diagnostic medical images, details is very important, local contrast improvement is very essential. Adaptive contrast enhancement (ACE) [5], [8]–[10], [17] and Adaptive histogram equalization (AHE) [6], [7], [16] are two well-known local enhancement methods.

The ACE algorithms are as follows: an image is separated into two components; the low-frequency components of the image, and the high-frequency component obtained by subtracting the previous component from the original image. In these algorithms the high-frequency component is then amplified and added back to the original image. Here the only parameter is the gain which the high frequency is multiplied by and added to the low frequency component. Two methods are proposed in determining the gain. The first considers the gain as a constant [9] . The other method links the gain to the inverse of the local standard deviation (LSD) of the image [5], [8], [10].

AHE algorithms perform like a mapping function which is obtained from the local histograms of different parts of the image. Although this method improves image contrast, it requires intensive computations which makes the algorithm unhandy [6].

In this paper, we propose an adaptive and iterative histogram matching (AIHM) algorithm for chromosome contrast enhancement especially in banding patterns. The reference histogram, with which the initial image needs to be matched, is created based on some processes on the initial image histogram. Usage of raw information in the histogram of initial image, will result in more dependency to the input image and acquiring better contrast improvement. Moreover, the iteration procedure leads to a gradual contrast enhancement and getting the best result. The iteration steps may vary depending on the image characteristics and histogram.

This paper is organized as follows: Section II describes the model presented for histogram of chromosome images. In section III we present our proposed algorithm for contrast enhancement. A contrast assessment is presented and the results are compared with conventional enhancement algorithms in Section IV. Conclusions are drawn in Section V.

2. HISTOGRAM MODEL

In this section, we present a model for histogram distribution of chromosome images. This model is derived from examining

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a huge set of samples of chromosome images and their relevant histograms, named h:

$$h(j) = \|\{p(x,y)|p(x,y) = j\}\| \tag{1}$$

Where $\|A\|$ is the length of set A.

The presented model is based on decreasing the number of bins of h, which is 256 for 8-bits gray scale images. In other words, the information needed to be analyzed is the coarse changes in the histogram of image sweeping from dark to bright intensities, and fine details depicting changes in adjacent bars of h do not have to be considered for analyzing. Based on the amount of accuracy needed and the limitations which the amount of computations and consumed time create, various numbers of adjacent bins can be integrated into a single bin in reshaped histogram, named $H(j)$ and defined as below:

$$H(j) = \sum_{i=(j-1)\times L}^{j\times L-1} h(i) \qquad 1 \leqslant j \leqslant \frac{256}{L} = J \tag{2}$$

Where L is number of adjacent bins combined into one bin in $H(j)$.

Intensities of image can be categorized as three different levels, mainly based on their visual perceptions, named *black*, *gray*, and *white* regions. $H(j)$ typically has different behavior in each region. Thus, in order to acquire better result in contrast enhancement, it is necessary to process each region individually based on its specific features. In addition, by investigation of various sets of chromosome image histograms, it can be realized that different chromosome histograms depict similar characteristic in each region. This feature makes the presented algorithm suitable for contrast enhancement in most cases. In remaining sections it is assumed the image of chromosome is surrounded by white background.

The main regions of histogram presented above are defined below. All the defined bounds are determined by experimenting a huge set of chromosome samples.

Black region: Based on the sample sets, this region includes the intensities in range of [0,63]. This region consists of most dark pixels, which numbers of pixels fallen in this region is much less in comparison with two other regions.

Gray region: Most image information is fallen in this category, including intensities [64,223]. This region usually constitutes most part of the chromosome surface and its bandings, unless the image is degraded with brighten or darken degradation function critically.

White region: This region includes intensities upper than 223. Except very brighten parts of chromosome, intensities of this category mainly correspond to border of chromosome and its background. Due to some defects in imaging, the border of chromosome consists of a gradual increment in intensity instead of a sharp change. This phenomenon increases the density of pixels in this region.

The corresponding histogram models are shown in Fig. 1. Three mentioned regions are separated by lines. The specified features of each region are visible through the images.

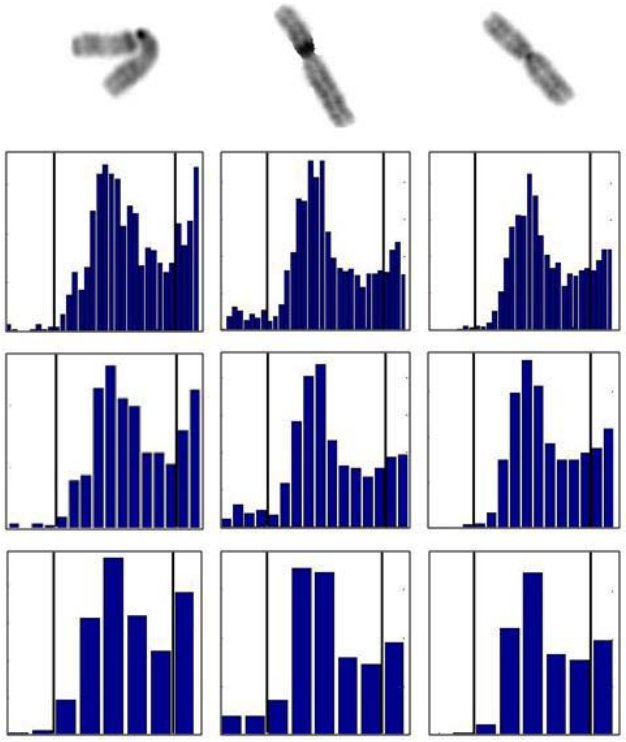

Fig. 1. Reshaped histograms ($H(j)$) of three different chromosome samples. Second, third and forth rows correspond to $L = 8, 16, 32$ respectively.

3. Presented Algorithm

In the preceding section, we described the model of chromosome image histogram. Based on the presented model we introduce a new iterative algorithm for creating suitable histogram used for histogram matching [2], [11] in each iteration. In the remaining of this paper the following variables are defined as:

$h_k(j)$: Histogram of the input image at k^{th} step of iteration. $0 \leqslant j \leqslant 255$

$H_k(j)$: Reshaped histogram of the input image at the k^{th} step of iteration. $1 \leqslant j \leqslant J$

$l_{k+1}(j)$: Histogram used for histogram matching at the k^{th} step of iteration. $0 \leqslant j \leqslant 255$

For convenience we define:

$$l_k^j(i) = l_k(j \times L - \frac{L}{2} + i) \qquad -\frac{L}{2} \leqslant i \leqslant \frac{L}{2} \tag{3}$$

The algorithm creates the histogram with which the initial image needs to be matched ($l_{k+1}(j)$), in each three histogram regions individually. In the k^{th} step of iteration, the output image of previous step is fed to the algorithm as its new input. Based on this input, the algorithm creates a new histogram ($l_{k+1}(j)$) for histogram matching. Finally, the input image is transformed so that the histogram of the output image approximately matches ($l_{k+1}(j)$). The iteration process continues until output contrast reaches to an acceptable level.

For creating the ($l_{k+1}(j)$) in each region of histogram:

Black region: The method gradually increases the density of pixels in dark region of histogram and boosts contrast in areas which were categorized as gray region initially. To do so, the value of each bin in $H_k(j)$ in black region is multiplied by a parameter, named black multiple (BM):

$$l_{k+1}^j(0) = H_k(j) \times BM \qquad j \in BlackRegion \tag{4}$$

Dark pixels remain unchanged by this manner. in addition, the method transforms some pixels in gray region, especially the ones in the border of two regions, to darker intensities.

Gray region: Creation of $l_{k+1}(j)$ in this region is based on difference between adjacent bins in $H_k(j)$. The aggregation of samples in one bin and difference in height of adjacent bins degrade the contrast of the image. The bin which has more number of pixels in comparison with its adjacent bins should have fewer pixels in the next step of iteration and vice versa. Thus, changes in histogram values in order to create $h_{k+1}(j)$ must be in direct proportion with adjacent bins difference. This concept can be more apprehensible through (5) and (6).

$$\begin{cases} \text{diff} = (H_k(j+1) - H_k(j))/\text{NP} \\ l^j_{k+1}(+1) = H_k(j) + \text{diff} \qquad H_k(j) < H_k(j+1) \\ l^{j+1}_{k+1}(-1) = H_k(j) - \text{diff} \end{cases} \tag{5}$$

$$\begin{cases} \text{diff} = (H_k(j) - H_k(j+1))/\text{NP} \\ l^j_{k+1}(+1) = H_k(j) - \text{diff} \qquad H_k(j) \geqslant H_k(j+1) \\ l^{j+1}_{k+1}(-1) = H_k(j) + \text{diff} \end{cases} \tag{6}$$

$$j \in GrayRegion$$

Where Normalization parameter (NP) is used for adjusting the amount of change in each step.

White region: Like black region, total number of bright pixels in this region need to be increased. Hence, the values of bins in white region of $H_k(j)$ are multiplied by another parameter, named white multiple (WM) as in (7)

$$l^j_{k+1}(0) = H_k(j) \times WM \qquad j \in WhiteRegion \tag{7}$$

In addition, the algorithm should solve the issue of smooth changes in border of chromosome in an acceptable manner. To do so, a line with an adjustable slope, named white slope (WS), connects the values of the last bin height in H_k to the value of the brightest intensity in l_{k+1}, obtained from the following equation:

$$l^J_{k+1}(\frac{L}{2} - 1) = WS \times [(J-1) \times L - \frac{L}{2}] + l^{J-1}_{k+1}(0) \tag{8}$$

This operation causes the intensities fallen in this interval, mostly correspond to border of the chromosome, incline to brightest intensity.

Eventually, the piecewise linear histogram ($l_{k+1}(j)$) is created by interpolating lines between determined points described above. Some samples of $l_{k+1}(j)$ and corresponding $H_k(j)$ are shown in Fig. 2. The presented algorithm is depicted by the flowchart in Fig. 3. It is worthy to mention for our sets of samples, we found the typical values for the parameters can be $L = 8, 16, 32$, $BM = 1.5 \ldots 2.5$, $NP = 5 \ldots 10$, $WM = 1 \ldots 1.5$, and $WS = 1 \ldots 2$ experimentally.

4. Results and Comparisons

A. Contrast Enhancement Measurement

Image quality assessment is a difficult procedure due to human eye complicated perception of the image. Here we need a measurement coefficient which shows the contrast enhancement of the processed image with respect to the

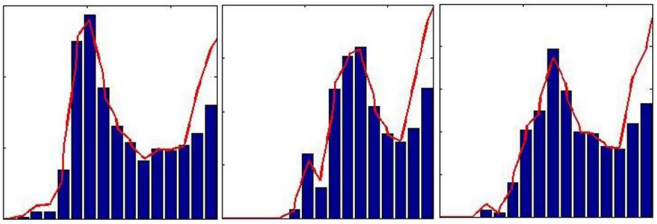

Fig. 2. Matching histogram l_{k+1} (red line) and corresponding reshaped Histogram H_k (blue bars) for three different chromosomes

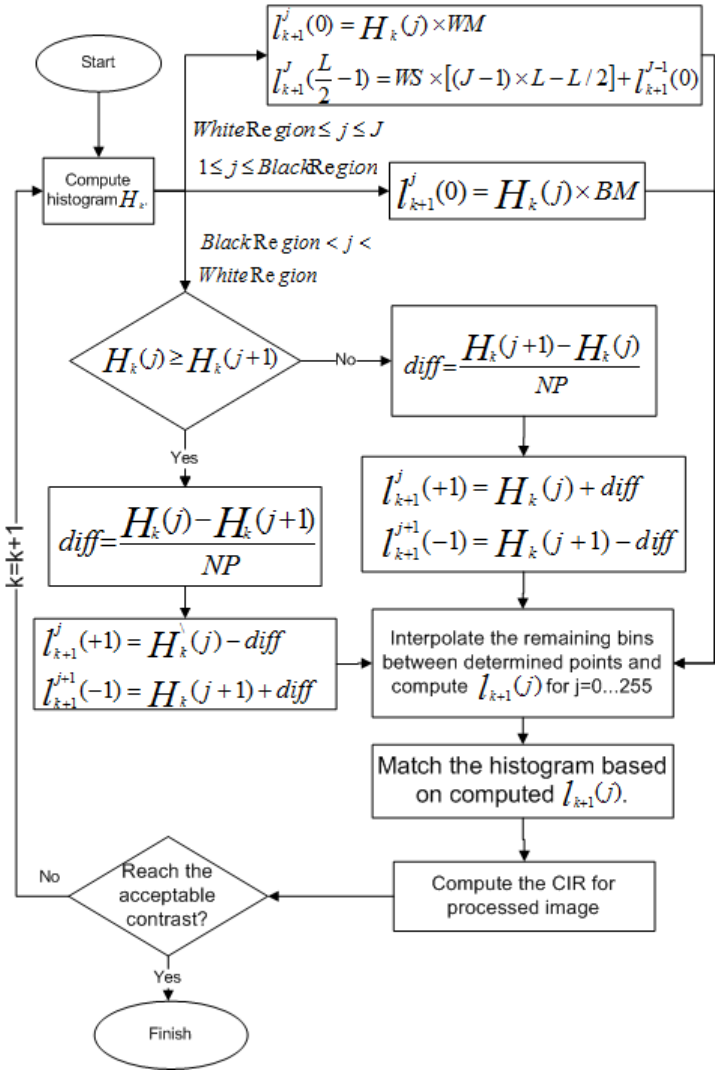

Fig. 3. The itererative flowchart of the presented algorithm proposed in 3.

original image. Quantification of this measurement is generally difficult. In addition, there is no general agreement on contrast enhancement measure for determining the efficiency of enhancement algorithms.

Contrast is defined as the difference in visual properties that makes an object distinguishable from other objects and the background. In grayscale images contrast is determined by the difference in the brightness of the object and its surrounding objects within the same field of view [2]. Among many measures of contrast we utilize the assessment proposed in [12], [13]. In this method, we compute the mean value of luminance in two different concentric rectangular windows centered on each pixel. More Specifically, we can define the local contrast as the following ratio:

$$c(x,y) = \frac{\mid p - a \mid}{\mid p + a \mid} \tag{9}$$

Where p and a are the average values of gray levels in the center window and surrounding window of the pixel location (x, y) respectively. The inner window is a 3×3 and outer is a 7×7 rectangular. Here $c(x, y)$ is the contrast measurement and is in the range of $[0, 1]$. Finally the contrast improvement ratio (CIR) is defined as the following ratio using the enhanced and original image local contrast measurements.

$$CIR = \frac{\sum_{(x,y)\in R} \left(c(x,y) - \hat{c}(x,y)\right)^2}{\sum_{(x,y)\in R} c^2(x,y)} \tag{10}$$

Where R is the region of interest. c and $\hat{c}$ are the local contrast measurements in original and enhanced images respectively. Here, we assume that R is the whole image of the chromosomes. R can also be considered to be just the chromosomes in the image.

In order to evaluate our proposed algorithm, we compare it with two conventional enhancement algorithms. These are CGT and LSD ACE algorithms [8], [10], [14]. The CGT and ACE parameters used in [10] are 5 and 12 for gain constant in CGT and LSD respectively. We also chose 7 for the window size. Our proposed method parameters values are $L = 32$, $BM = 2.2$, $WM = 1.1$, $WS = 1.5$, and $NP = 7$.

B. Compared Results

In the evaluation of the proposed method, a set of human single chromosomes were tested, which consists of 30 chromosomes of different patients. CIRs measured from these images are tabulated in table I. As it can be realized from the results, the proposed method yields the highest CIRs among the tested methods.

Fig. 4 shows five examples of single chromosome image enhancement using different enhancement methods. One can see that our proposed method produces the best visualization effect on banding pattern after enhancing the image. It is worthy to mention that sample images are obtained using *Q-banding*, and inverted for better visualization. The pattern of bands in *Q-banding* is very similar to that seen in *G-banding* [15].

The other algorithms suffer from some weak points. We can mention that they are producing the output image at once and

TABLE I
COMPARISON OF THE CIRS FROM DIFFERENT METHODS FOR ENHANCING SINGLE CHROMOSOME IMAGES

Image	CG	LSD	Proposed method
1	2.675562875	6.333594533	9.732869032
2	1.055708441	6.583052912	21.52955659
3	1.040202647	7.373323675	14.59287442
4	1.002052867	7.25767156	18.32201293
5	4.048655525	5.955722041	14.43489689
6	11.82663866	8.246787183	9.255354951
7	10.27724623	8.013826733	10.09163155
8	6.521509931	6.40763825	12.92893392
9	7.143305475	6.594808857	11.17889268
10	5.172214388	5.366673281	12.56593862
11	2.486648096	5.500632282	10.64514033
12	2.017636874	5.576727734	9.888851743
13	2.534860929	3.210560537	7.586952595
14	2.170376127	2.406010748	6.25855484
15	2.197352221	3.042827151	4.051583786
16	2.775060696	2.830550789	5.208763614
17	1.786466053	2.434934347	4.889593389
18	1.794037715	2.783755193	4.131797078
19	1.688778757	2.439477949	6.417934605
20	1.618208667	2.446527235	6.051675879
21	2.41814173	3.022200719	6.635510457
22	2.720693359	2.62195515	5.529166354
23	0.220677189	0.151650064	1.300281756
24	1.899538099	4.292217031	14.77667609
25	2.617955735	4.688068255	11.85711441
26	3.022888716	4.623733078	9.568797649
27	1.576622526	4.063519187	10.62049706
28	1.082619042	2.667613003	10.86545611
29	1.712789181	3.797279608	11.28449599
30	1.563830555	3.750537674	10.29054638
average	4.144664752	5.857990498	11.53760299

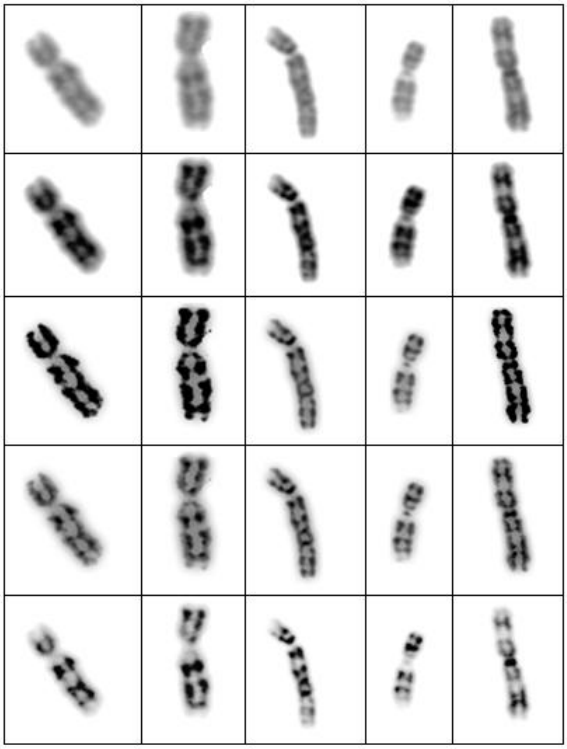

Fig. 4. A comparison of different methods for enhancing single chromosome images. Columns from top to bottom: initial image, histogram equalization, CG transform , LSD transform, proposed method. Samples are obtained by inverting the *Q-banding* images of chromosomes.

no contrast assessment is performed during the process. But in Presented algorithm, the image changes gradually and in each iteration the CIR is computed and the new histogram based on the contrast features of the previous step is created. In addition, the number of iterations in proposed algorithm is variable; it depends on the CIR in each step. The iteration process continues until the CIR reach an acceptable level. Thus, the number of iteration needed for obtaining the best result, may vary from image to image.

Another weak point of the conventional algorithms, especially CG and LSD is that they create some unwanted blurring in edges and borders, which can be seen in the images easily [13]. It is worthy to mention that CG and LSD overemphasize the borders, and as it can be seen in Fig. 4 these algorithms darken the borders of chromosomes. It will corrupt the banding pattern partially.

5. Conclusion

In this paper, we proposed a new iterative algorithm for contrast enhancement of medical images of chromosomes, based on adaptive histogram matching. We first proposed a model for histogram of chromosome images. With assistance of this model a reference histogram created and used for histogram matching in each iteration. There are some parameters in the presented model which could be chosen to meet different requirements and acquire different results. The visual defects of other contrast enhancement algorithms such as not enough clarity in banding patterns differentiaion decreased critically. Eventually, detailed simulations were carried out using various sets of single chromosomes, showing that the proposed method enhances details satisfactorily. Note that we can choose the parameters adaptively based on the input image to produce even better results. Research in this field is in progress.

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