Evolutionary Image Enhancement with User Behavior Modeling

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ABSTRACT
In this paper we present a novel method for image enhancement of gray-scale images based on the simulation of evolution. Our method employs Genetic Algorithms to evolve the shape of the contrast curve in the image, while attempting to partially automate the subjective process of image evaluation (e.g. user behavior) by performing multiple regression on fitness values. Results obtained show the robustness and efficiency of the evolutive method for image enhancement. For several images in the test set our method obtains better results than the classical histogram equalization technique. Extensive statistics performed, shows that multiple regression can be effectively applied to model the user behavior.

1. INTRODUCTION
Genetic Algorithms (GAs) are stochastic search strategies that mimic the evolution of populations of individuals. GAs have been applied in solving difficult optimization tasks pertaining to fields such as pattern recognition, signal processing, image processing, robust control, optimal path planning, digital circuits layout, scheduling, time-tabling [13]. In the field of signal processing they have been applied to digital filter design [22], IIR adaptive filtering, nonlinear model selection, time-delay estimation, active noise control [13], dynamic time warping for speech recognition [13], to name a few of the successful applications. In image processing, GAs proved their efficiency in image compression and coding [10], segmentation [23], figure-ground separation [4], image reconstruction [17], and image enhancement [18], [15].

The problem we address in this paper is the image enhancement of gray-scale images by GAs with real-coded chromosomes, as to increase the robustness and applicability of the method, to ease its application while maintaining high quality output solutions, and to attempt the partial automation of the human subjective image evaluation process. Digital processing and analysis may be carried out to automatically identify targets in images and extract information completely without manual intervention by a human interpreter. However, rarely is digital processing and analysis carried out as a complete replacement for manual interpretation [12]. Often, it is done to supplement and assist the human analyst. One such digital processing of imagery is enhancement. Enhancement is used to make visual interpretation and understanding of imagery easier. By manipulating the range of digital values of pixel intensity or brightness, graphically represented by the histogram of the image, we can apply various enhancements to the data. Most of the enhancement techniques existent to date, are empirical methods, dependent on the particular type of image [7],[11],[19]. More important, these techniques require interactive procedures to obtain satisfactory results, and therefore are not suitable for routine application [7], [18],[19]. In some cases it is desirable to enhance the contrast in only a specific portion of the histogram of the image, in order to enhance specific details in the image. Our GA-based enhancement performs this specific task by evolving the contrast curve to meet the requirements of a human interpreter, and by partially including human image interpretation into the evolution process, in order to attempt the automation of human behavior, as part of the automation of the enhancement technique itself. The initial or given image has a linear contrast curve (equal to the first bisector) that sometimes does not fit the demands for visual imagery interpretation. In this case the GA has to modify this contrast curve in order to extract the best brightness/contrast features.

2. IMAGE ENHANCEMENT USING REAL-CODED GAs
GAs have been previously applied to image enhancement in medical imagery [17] and remote sensing image processing [15]. In [18] the authors approached the problem of enhancement using a Genetic Programming technique that is a variant of GA working on program trees as genetic individuals. Their model was applied to color medical image enhancement, but results reported in [18] demonstrate very low effectiveness when it comes to modeling the user behavior. In [15] the authors have employed a GA with real-coded chromosomes for the evolution of the contrast curve in a gray scale image, with applications to remote sensing.

This paper greatly extends the work done in [15], by considering a more general and efficient representation of the contrast curve at the genetic level, and by modeling the user behavior with a simple but effective multiple regression technique.

In this paper we have employed a real-coded GA, in favor of the classical GA introduced by Holland in [9] that works on chromosomes coded as binary strings of fixed length.

Real-coded GAs use real coded genes in the chromosomes, which means that each free parameter of the optimization problem is represented by one real-valued gene in the chromosome. The value a gene may take is called allele. Real-coded GAs proved quite efficient in solving real-world complex applications [13], due to their suitable coding scheme (one parameter - one gene) and their ability to avoid negative artifacts of mutation operating on binary strings [14]. For the specific task of evolving gray-scale images, we have designed a real-coded GA with the following features.

2.1 Representation of the chromosome

The coding scheme takes into account the features in the images that the GA has to evolve. In gray-scale images the contrast or brightness feature of the image is given by the characteristic or contrast curve that links an array of N_g shades of gray to their respective intensity values. The intensity of a gray shade is a numeric value in the range 0 to 1, where 0 corresponds to minimum intensity (black) and 1 to maximum intensity (white). The contrast curve associated to an image transforms the original image (having a contrast curve equal to the first bisector, by default) into an image with different contrast/brightness features. The contrast curve is coded into the chromosomes using a small number of knots: $n_g < N_g$ corresponding to equally spaced levels of gray and their respective intensity values on the real curve. The chromosome codes only the intensity values for the n_g shades of gray, while the intensity values for the remaining levels of gray are obtained by interpolation through the knots with a cubic spline curve. This scheme allows for having a large number of shades of gray (e.g. N_g = 256) and a contrast curve coded with a short length chromosome $l = n_g$, with l the length of the chromosome (e.g. n_g = 10). Lower length chromosomes implies lower dimension of the search space, and consequently a simpler task for the GA. The contrast curve as a transformation to the image is depicted in Figure 1, while the representation in the chromosome is given in Figure 2.

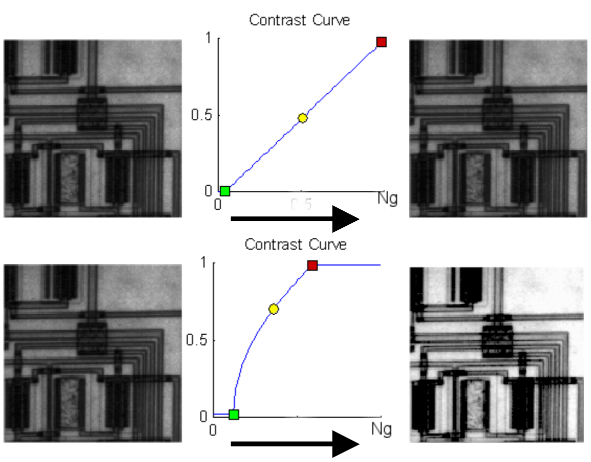

Figure 1. A contrast curve equal to the first bisector (linear): leaves the image unchanged; a contrast curve different from the first bisector changes the image contrast/brightness features.

The initial population is generated randomly, that is we generate N random chromosomes. Following the generation of the initial population, the chromosomes are evaluated by calculating their fitness function, and selection is applied to choose for the better fitted chromosomes. The result of the selection mechanism is a population of N chromosomes that undergoes crossover and mutation yielding the population in the next generation. The process repeats in a cycle until a given stopping criterion is met. In our application the stopping criterion was the maximum number of generations the GA is allowed to run: T_{max}.

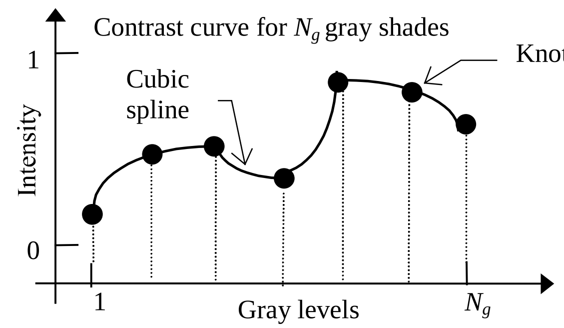

Figure 2. Contrast curve for N_g shades of gray with n_g knots. Only the knots' intensities are coded into the chromosome, the whole curve being generated by cubic spline interpolation.

2.2 Fitness function

The fitness of each chromosome in the population is defined as a subjective fitness score in domain [0, 10]. As we mentioned in the introductive section of this paper, human interpretation of images, and subjective interpretation of the effects of digital image processing, cannot be eliminated from the process of analyzing an image. This is the reason why we have chosen a subjective fitness score that is assigned to each image in the population, for each generation the GA runs, by an expert human interpreter, that decides if the image presented suits his demands regarding contrast, brightness and detail enhancement in several areas of interest in the image. Subjective fitness allocation and subjective selection has been previously applied in color mixing [20] and shape evolution problems [2], in evolving blends of coffee [8], in tracking of a criminal suspect through "face space" [5].

2.3 Selection

The selection mechanism assures that good genetic material in the current generation is perpetuated in the subsequent generations. We have adopted an elitist scheme in which the best chromosome found so far is copied from the current generation into the next generation [3], as we want to avoid loosing the best image as a result of applying the genetic operators (i.e. mutation, crossover, selection). The remaining N-1 chromosomes are selected with a binary tournament selection [6], a mechanism that repeatedly randomly pairs chromosomes in the mating population and picks up the fitter chromosome in the pair.

2.4 Mutation

The mutation operator applied was uniform mutation [14], which randomly selects one gene x_{ij} and sets its value equal to a uniform random number in [0, 1].

2.5 Crossover

The crossover operator has been designed to better mix the genetic material in the parental chromosomes, and to suit our needs regarding contrast and detail enhancement. In [15] a new crossover operator called Gaussian Uniform Crossover (GUX) has been introduced. We have shown that GUX performs a better mixing of genes between parental chromosomes, resulting in better contrast in evolved images, as compared to the classical arithmetical crossover [14], [16]. The GUX operator applies to two randomly selected parents and produces two offspring, as follows:

First, a bit mask of length l is defined:

$$mask = \{mask(i)\}_{i=\overline{1\ldots l}} \text{ with } mask(i) = \begin{cases} 1, \text{ if } r_i \leq 0.5 \\ 0, \text{otherwise} \end{cases}$$

with r_i a sample from a uniform distributed random variable

$$\Re \sim U(0,1). \tag{1}$$

Second, the distance between each corresponding gene in the parents x_1 and x_2 is computed as:

$$d_j = \left| x_{1j} - x_{2j} \right|, \forall j = \overline{1 \ldots l} \tag{2}$$

The offspring genes in x_1^o and x_2^o are calculated from the parental genes in x_1 and x_2, as follows:

$$x^o_{\{1,2\},j} = \begin{cases} x_{\{1,2\},j} + \dfrac{d_j}{3}\chi_j, \text{if } mask(j) = 0 \\ x_{\{2,1\},j} + \dfrac{d_j}{3}\chi_j, \text{if } mask(j) = 1 \end{cases} \tag{3}$$

$\forall j = \overline{1 \ldots l}$ and χ_j a sample from a standard normal distributed variable $X \sim N(0, 1)$. From (3), each gene (indexed j) in the offspring is taken to be a sample from a normally distributed random variable centered on one allele of the two parents, depending on the corresponding mask value, and having a variance $d_j^2/9$. We have chosen a standard deviation of $d_j/3$ because, in this case, the two distributions of the offspring alleles have a small overlap (we assume that samples at 1.5 standard deviations away from the mean are not frequent). A graphical representation of the GUX crossover operator is given in Figure 3. The GUX crossover operator acts much like the uniform crossover for the binary-coded GAs [21], in that it swaps genes between the two parents, based on a stochastic bit swap mask, and allows for genes values around the parental alleles.

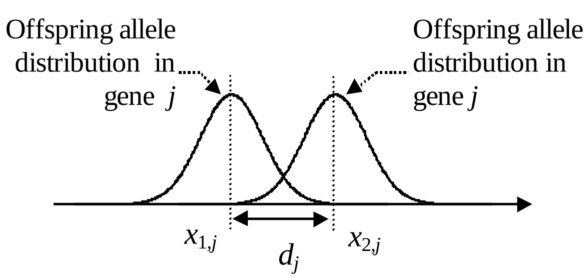

Figure 3. Offspring allele distribution in GUX.

GUX operator allows for generating values *inside* and *outside* the segment connecting the two parental genes $x_{1,j}$ and $x_{2,j}$, thus having a better exploratory effect than other well known crossover operator such as the arithmetical crossover [14] that can only produce genes values *inside* the segment between $x_{1,j}$ and $x_{2,j}$ as it can be seen from the following equation defining the arithmetical crossover:

$$x^o{}_{\{1,2\},j} = a x_{\{1,2\},j} + (1-a) x_{\{2,1\},j} \tag{4}$$

were notations have the same meaning as in (3), and a is a random number taken anew for each gene from a uniform distribution $U([0, 1])$.

Experiments that the authors performed in [15] showed that GUX is capable of yielding better solution contrast curves when compared to the classical arithmetical crossover [14]. This could be explained by considering the following example. Let us say that we have to cross two parents x_1 and x_2 having two corresponding adjacent genes approximately equal in each parent: $x_{1m} \cong x_{1n}$ and $x_{2m} \cong x_{2n}$. For our applications this means that we have two contrast curves for which gray levels m and n are indiscernible in both cases. We would like the crossing over to produce contrast curves for which the gray levels would be different in order to *increase* the contrast. However, from (4), the arithmetic crossover due to its averaging effect will always produce offspring having similar genes of indexes m and n, while GUX (see (3)), can in principle produce different genes in the offspring. In [16] we have shown in the context of a different application that GUX keeps the mean of the parental genes unchanged, while it increases the variance of the parental genes in the offspring. More specifically it can be shown that:

$$\overline{x^o_{\{1,2\}}} = \overline{x_{\{1,2\}}} \tag{5}$$

and

$$\sigma^2_{x^o_{\{1,2\},j}} = \left(1 + \frac{2}{9}\sigma^2_{\chi_j}\right)\sigma^2_{x_{\{1,2\},j}} \tag{6}$$

The notations in (5) and (6) are the same as in (3) with the upper bar in (5) denoting the mean, and σ^2 in (6) denoting the variance. Thus, from (6) it can be noted that the variance of the offspring genes increases by a factor of (1+2/9), where we have used the fact that $\sigma^2_{\chi_j} = 1$ for all j, as it follows from the definition of the random variable χ_j in (3). The variance and implicitly the diversity grows after applying GUX. The parameter that controls the growth of the variance is $\sigma^2_{\chi_j}$ which has been chosen for this application equal to 1.

2.6 Modeling the user behavior

Evolution in GAs is a process that is subject to stochastic errors (genetic drift, premature convergence of the algorithm), that grow in importance as the size of the population (N) diminishes [6]. In our application, the user has to evaluate each individual (image) in the population for a number T of generations. In principle this can be done, but it would be preferable to reduce the user interaction without affecting the control the user has to impose on the process of image evaluation. This argument is further explained in what follows: if the GA is allowed to run for T_{max} generations then the user has to evaluate NT_{max} images. Clearly, if N is big (e.g. N = 100), in order to avoid stochastic errors, and T_{max} is also big (e.g. T_{max} = 100), as to assure that GA yields a good solution (optimal solution), the user will have to evaluate a large number of images (e.g. 10000 images). This is obviously not practical. We propose a method that allows the user to first evaluate a small number of images: Θ, while the rest $N \cdot T_{max}$ - Θ are evaluated as follows: each of the η -th image in the remaining $N \cdot T_{max}$ - Θ, are evaluated by the user who allocates a *subjective* fitness score, as for the first Θ images. The remaining images are allocated an *objective* fitness, obtained by multiple regression (MR) done over the subjective fitness values *previously* allocated. N, T_{max}, Θ and η are fixed parameters of the image enhancement strategy. The procedure of fitness calculation is depicted in Figure 4.

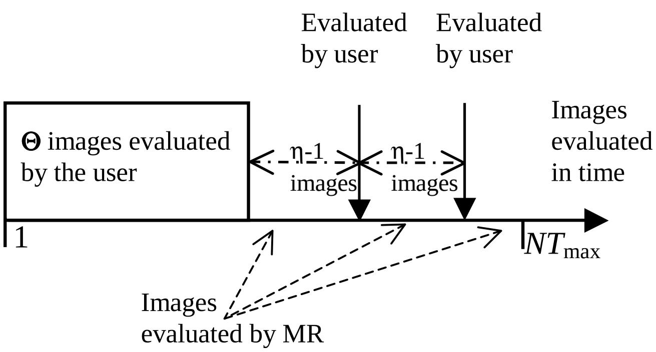

Figure 4. Fitness calculation.

The dependent variable in the MR model is the fitness value (in domain [0, 10]) associated with a contrast curve, while the independent variables are the intensities for the n_g knots in that contrast curve. The MR model automatically produces an objective fitness score based on the subjective fitness scores allocated by the user. If the objective score is bigger than the maximum subjective score previously allocated, then the human interpreter evaluates the respective image. This is done in order to eliminate data extrapolation with the MR model, whenever it might occur. We test the effectiveness of applying MR to produce objective fitness values from the subjective ones, by computing several statistics common to MR methods [1]: a) The *coefficient of determination* or R^2 statistics which gives the percentage of data correctly "explained" by MR (the bigger the R^2, the more suitable is MR for modeling the respective data); b) The *F-test* that tests for the null hypothesis that *all* regression coefficients are zero. The output is the F value and p value ($p < 1$), large values for F, and small values for p indicate that it is likely that not all regression coefficients are zero; c) The *Chi-square test* for the normality of MR residuals (or prediction errors), at the significance level α. Results obtained on a standard image test set are given in the following section.

3. EXPERIMENTAL RESULTS

The test set employed in our experiments comprises six gray-scale images having a default linear contrast curve (equal to the first bisector) that gives a poor contrast to each original image. The task for our GA-based enhancement method is to evolve this default contrast curve in order to find better shapes that give better brightness/contrast quality in the respective images. The images in the test set are: *plane* image, *cape-cod* image, *lena* image, *goldhill* image, *mandrill* image and *boat* image, all having N_g = 256 gray levels. The parameters for our GA-based enhancement method are given in Table 1. The size of the population N, and the maximum number of generations T_{max}, were taken as small as possible to reduce computational overload of the algorithm but still big enough for the GA to find good solutions. The values for the rest of the parameters were taken after experimentation with the algorithm.

From Table 1, it follows that the user has to evaluate about 80 images during the run, instead of evaluating every image that would give $T_{max} \times N = 200$ images. The user doesn't evaluate exactly 80 images because in several runs, images that should be evaluated by the MR model, are evaluated by the user, as to avoid extrapolation. The reduction in the number of images the user evaluates can be estimated at 60% of the total number of images during a run.

The solution images found by the GA are the most typical solutions encountered in 10 independent runs performed for each image by the user. Results for *plane* image are given in Figure 5 and for *Cape-code* image in Figure 6. One may note that the solution obtained by our GA-based enhancement method is better than the original image and it may be argued that it has better contrast than the equalized image, especially when one is interested in a more natural image for the plane and in viewing better relief details in the case of the *cape-cod* image. Results for *lena* image are given in Figure 7 and for *goldhill* image in Figure 8. For the rest of images the results obtained with the GA based method came close to the results obtained with the histogram equalization technique, as it might be observed from Figures 9 and 10.

For all images in the test set, solutions found with the GA-based enhancement method were better than the original images.

Table 1. Parameters in the GA-based enhancement method – population size: N, chromosome length: l, maximum no. of generations the GA is allowed to run: T_{max}, mutation rate: P_m, crossover rate: P_c.

GA				
N	$l = n_g$	T_{max}	P_m	P_c
20	10	10	0.05	0.9

MR	
Θ	η
50	5

By visual inspection of the solution images it can be noted that results obtained with the GA based solution are at least as good as the histogram equalization technique, and in case of the *plane* and *cape-cod* images the GA found better solutions compared to the histogram equalization. As sometimes is quite difficult to rate the images subjectively, we have also employed an objective criteria for evaluating the images, namely the Detail Variance - Background Variance Criterion (DV-BV), [19].

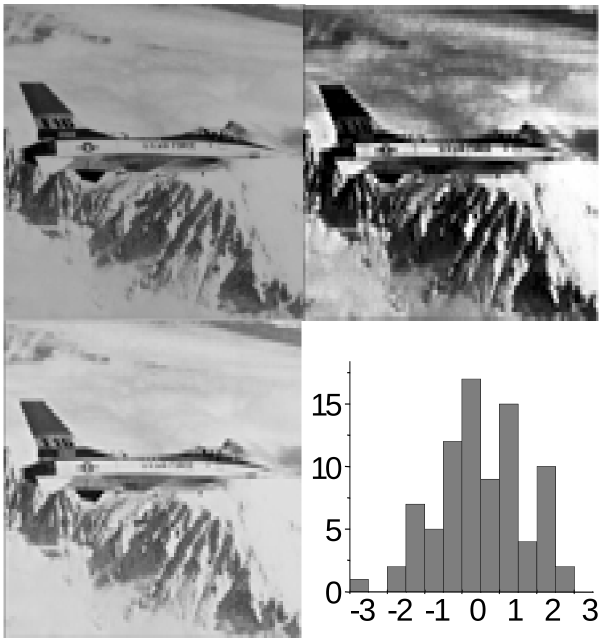

Figure 5. *Plane* image: upper-left: original; upper-right: equalized; lower-left: GA-based solution; lower-right: histogram for MR residuals.

DV and BV values are obtained as follows: firstly, the variance of the gray levels in the neighbouring pixels is calculated at each pixel in the image. Next, the pixel is classified to the foreground when the variance of the gray levels is more than a threshold, and the pixel is classified to the background when the variance of the gray levels is lower than the threshold. The averaged variance of all pixels included in the foreground class is DV, and the averaged variance of all pixels included in the background class is BV.

When the DV value of the resulted image increases and BV is not changed compared to the original gray image, then it is supposed that efficient contrast enhancement has been achieved [19].

In Table 2, we gave the respective DV-BV values together with the relative change of BV (relative to the original image): |ΔBV|. From Table 2 it follows that the GA-based enhancement solutions were better than the original images in all cases except the *boat* image, and they were better than the equalized images in all cases but the *cape-cod* image. One can explain this latter result by looking at Figure 4 and noting that the high DV value in case of the equalized *cape-cod* image comes from the sharp gray-level transition at the coastline, as the land is whitish and the sea is black. However, the GA finds rather a negative image of the Cape Cod, with smoother gray - level transitions between the land (which is gray near the coastline) and the sea (which is white), resulting in a lower DV value. For the *boat* image by inspection of the result image in Figure 10, one can note that visually the result image is better than the original, even if the DV-BV criterion indicates the opposite. This is due to the fact that DV-BV criterion is not a perfect one, and it might yield contradictory results for certain images, like the case of the *boat* image. However, in this paper we made use for comparison the DV-BV criterion because it is the only largely used objective criterion for rating the enhancement results.

Table 2. DV-BV results.

Img.	Original		Equalized			GA-based		
	DV	BV	DV	BV	|ΔBV| [%]	DV	BV	|ΔBV| [%]
plane	19.7	2.9	22.5	3.5	19.3	25.3	3.7	24.4
cape	15.3	0.8	48.5	1.2	44.5	23.5	1.5	84.3
lena	19.4	2.6	22.1	3.2	21.8	27.2	3.1	17.6
gold.	17.9	3.9	21.6	4.4	10	21.7	4.7	17.8
mand.	28.9	6.1	31.5	6.6	6.5	35.3	7.4	17.9
boat	20.1	2.8	26.4	3.4	18.2	15.1	1.94	44.3

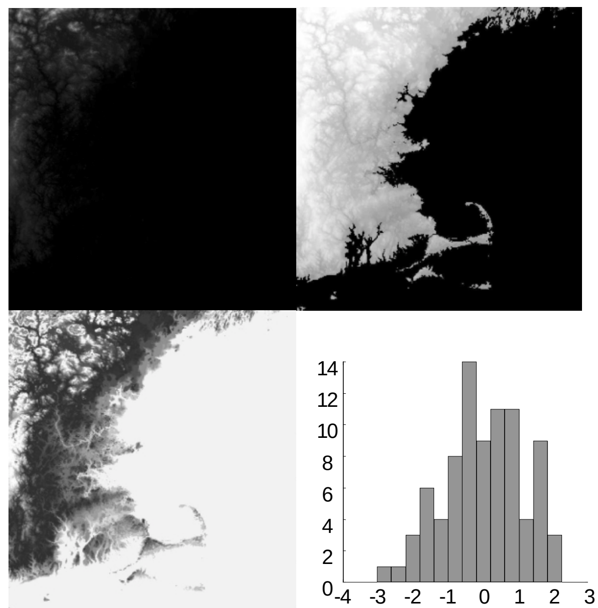

Figure 6. *Cape-cod* image: upper-left: original; upper-right: equalized; lower-left: GA-based solution; lower-right: histogram for MR residuals.

Statistics performed to prove that the MR can model the subjective fitness allocation process are given in Tabel 3. The Chi-square test (χ^2_{81} or χ^2_{84}) was performed for a significance level $\alpha = 0.05$. The number of degrees of freedom (i.e 81, 84) comes form the total number of images the user had to evaluate during the run, that is 80 images evaluated by the user plus 1 and 4, respectively that had to be evaluated as to avoid extrapolation from the MR model. For the Chi-square test we gave the percentage of outliers that can appear when testing for the normal distribution of regression residuals. In Figure 3-6 the histogram of MR residuals was given for a visual assessment of the normality of MR residuals for the GA-based method solutions. Statistics performed for the MR model reveal the effectiveness of applying this model to the task of image evaluation, without violation of any assumptions underlying the model.

Outliers to the normal distribution of the residuals can be observed only in the case of the *goldhill* and *lena* images, which also didn't pass the Chi-square test for normality. However, the percentage of outliers is under 5% for both images.

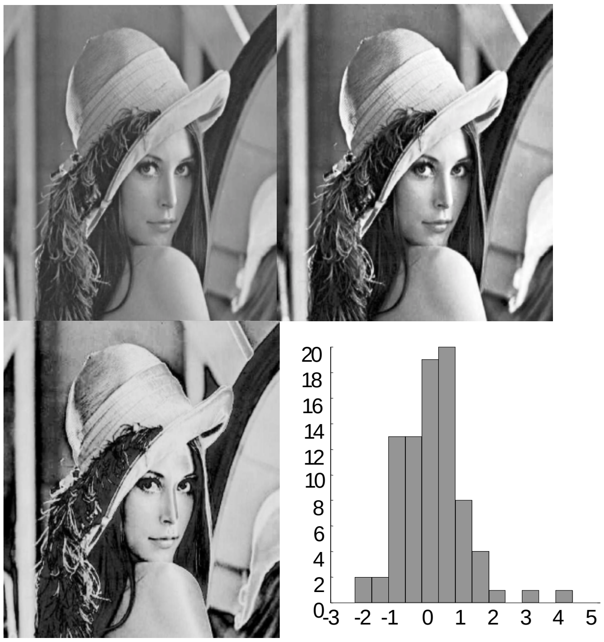

Figure 7. *Lena* image: upper-left: original image; upper-right: equalized; lower-left: GA-based solution; lower-right: histogram for MR residuals.

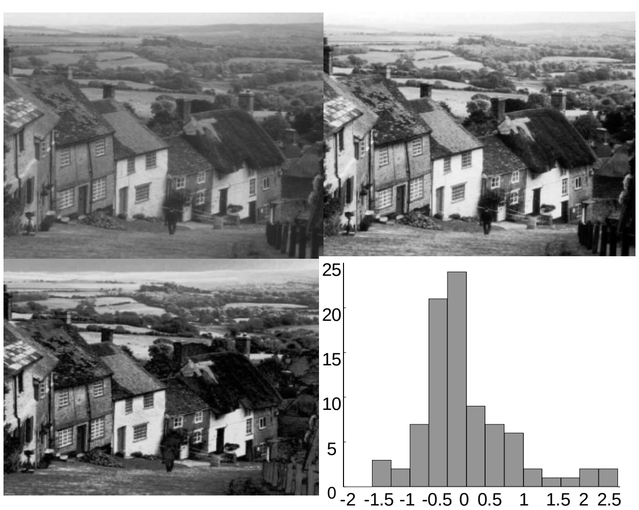

Figure 8. *Goldhill* image: upper-left: original image; upper-right: equalized; lower-left: GA-based solution; lower-right: histogram for MR residuals.

Table 3. Statistics for the MR model.

Image	R^2 **[%]**	F	p	**Chi ^{2}-norm.**	**Outliers [%]**
plane	69.3	17	$<10^{-5}$	Yes	0
cape	71	20	$<10^{-5}$	Yes	0
lena	68.3	16.5	$<10^{-5}$	No	2.38
goldhill	41.3	6	$<10^{-3}$	No	4.6
mandrill	53.3	8.6	$<10^{-3}$	Yes	0
boat	65.7	18.4	$<10^{-5}$	Yes	0

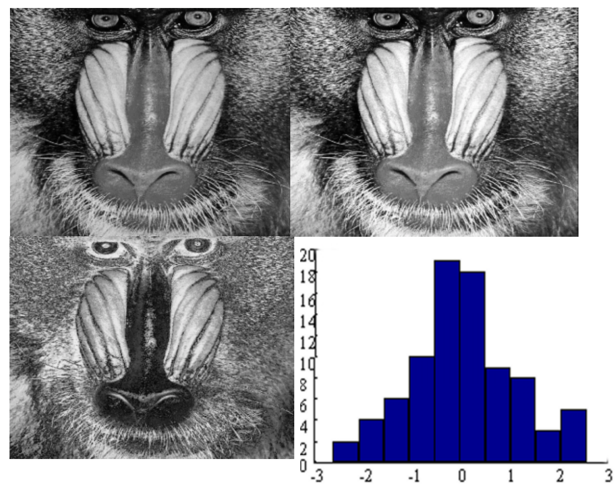

Figure 9. *Mandrill* image: upper-left: original image; upper-right: equalized; lower-left: GA-based solution; lower-right: histogram for MR residuals.

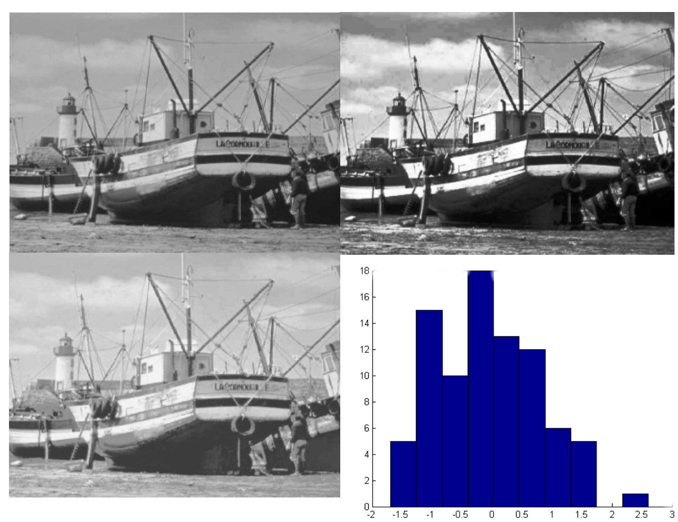

Figure 10. *Boat* image: upper-left: original image; upper-right: equalized; lower-left: GA-based solution; lower-right: histogram for MR residuals.

4. CONCLUSIONS

Results obtained indicate that our evolutionary method for image enhancement with user modeling is a simple, general and robust method. Our method is capable of finding good contrast images that in several cases are better than solutions offered by classical enhancement techniques, such as histogram equalization. The method attempts to partially automate the human interpretation process, yielding high quality solutions with less effort from the human image evaluator. This is the main advantage of the algorithm that is aiming at systematizing and easing the process of human interpretation of images, present in the enhancement method. The enhancement process assumes the evaluation of only a part of the images the algorithm works with, the user performing direct evaluations of the images according to his demands. Therefore, the method can be easily applied by users that are interested in the end-result of the enhancement process and are not familiar with the details of the image processing techniques such as the manual modification of the contrast curve. For future work we will attempt to extend the mechanism of user behavior modeling by including other more complex paradigms such as machine learning models. These models will be expected to further reduce the number of images the user has to evaluate during the run of the GA, while maintaining a high level of control on the enhancement process.

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