Monochrome Multitone Image Approximation on Lowered Dimension Palette with Sub-optimization Method Based on Genetic Algorithm

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Abstract The problem of sub-optimum approximation of monochrome multitone images (MMI) by a palette with reduced amount of tones, called support palette (SP), is solved. The SP palette tones are defined with the images analysis, which arise in related scientific topics as: technical sight, recognition of images, etc. In this work the research objective was to assess the opportunity of using efficiently such analysis, by applying the genetic algorithms (GA) for sub-optimum approximation of MMI, considering the original big size tones palette [1]. The proposed approximation consists in replacing the original MMI pixels with the approximated pixels from a smaller size tone palette. This procedure is of importance in the synthetic vision approach, where image recognition procedures are expected to define the main contours within the image. The developed method reduces the amount of tones used to display an image, whose approximation approach is presented in this paper. In order to solve it, two alternative problems are considered: (1) minimization of losses in such image transformation, and (2) minimization of the SP size (for example, to simplify the image recognition process). The approximated MMI quality is defined as the mean square deviation of pixels brightness (original to approximated). The chromosome in GA is SP, where tones are represented as genes. Such approximations are resulting from the mutational variation of the MMI palette tones, within gene alleles, which are formed by applying the original palette tones. The palette is iteratively changing from

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generation to generation, where the reduction of the stop risks is done on the local extremum. This fact increases the available search opportunities, as provided by the multi-point crossing-over algorithm, whose parameters are able to mutate during such an evolution process. In addition, to demonstrate the result of this work, an appropriate software has been developed, having an easy-to-use user interface, enabling to show the highly efficient processing of the investigated algorithm. The presented solutions are validated with photo examples of several technical objects, on which the sub-optimum method has been applied.

Keywords Monochrome image · Image approximation · Optimization · Genetic algorithm · Gen · Chromosome

1 Introduction

The monochrome multitone image (MMI), called also “grayscale image”, is an array of different brightness pixels of the same tone, which are present in a picture. Quite often, the monochrome images are analyzed for technical sight needs, where the detection of the areas orientation forming the objects is used as support to the recognition process. There is a huge class of MMI’s approximations problems, which have significant difference in their realization and approach direction. For example they are: the image compression algorithms with minimal losses, image filtering or pre-processing for recognition algorithms, image converting to the device format with limited number of supported tones, and others [2–5]. However, many of them use different methods to lower the palette size, and which motivated the authors to research further this transformation, as till today and in their knowledge such approach has not been addressed. It is important to mention that this step in the image processing process has some underlying rules, and which is envisaged to be useful for solving different problems in image analysis. Therefore, the considered problem of MMI’s approximation, as the mapping of the image with a smaller palette, is expected to simplify the pattern recognition tasks, image defects detection and image transformation, for the variety of printing devices.

The proposed approximation consists in replacing the basic palette (BP) pixels of the original MMI (OMMI) with the approximated palette (AP) pixels, which contains less number of tones. This operation can be achieved by different algorithms, which have in common a pixels mapping from an original array $P_{parent} = \left\{p_i | i = \overline{1, n_p}\right\}$ of pixels, where n_p—is the size of BP, to a single pixel $p_{appr} \in \left\{p_j | j = \overline{1, n_a}\right\}$, where n_a—is the size of AP. The mapping rules have to follow some exact criteria, which evaluate the effectiveness of the approximated image. In case of major variations of the imposed criteria, resulting from the selected approximation methods, it is necessary to define the respective conceptual and mathematical models.

2 Image Approximation Model

In a general case, the quality of the approximation is set by a certain criteria. The most common criteria is the “root-mean-square deviation” (RMSD) of pixels brightness between approximated MMI (AMMI) and OMMI or “least square deviation”, defined as follows:

$$\Delta_2 = \frac{1}{\mathrm{n}}\sum_{\mathrm{i}=1}^{\mathrm{n}}\frac{1}{\mathrm{m}}\sum_{\mathrm{j}=1}^{\mathrm{m}}(\mathrm{A}[\mathrm{i},\mathrm{j}] - \mathrm{I}[\mathrm{i},\mathrm{j}])^2 \tag{1}$$

where $\boldsymbol{A}$—is the matrix of AMMI; $\boldsymbol{I}$—is the matrix of OMMI $n \times m = N$—count of all pixels.

The performed research showed that for the considered problem it is more appropriate to use another criteria, which is the “least module of deviation” (LMD):

$$\Delta_m = \frac{1}{n}\sum_{i=1}^{n}\frac{1}{m}\sum_{j=1}^{m}|\boldsymbol{A}[i,j] - \boldsymbol{I}[i,j]| \tag{2}$$

The quality of the MMI approximation depends on the number of AP tones and their values, which are together called the support palette (SP) and the SP tones have to cover the range of OMMI tones (see Fig. 1).

One of the most important factors, which define SP, is to correctly choose the SP tones and their respective values. Often, the size of SP (number of tones) is the user prerogative. It is depends from different application area of approximation, which has different allowable error.

In the previous research [1], the SP covering range is defined by dividing BP in equal parts, where the number of parts, and the number of SP tones, is the same. Such homogeneous distribution was found quite effective for initializing such analysis.

However, the MMI Frequency Diagram of Brightness (FDB) is quite rare to be found equal (see Fig. 2).

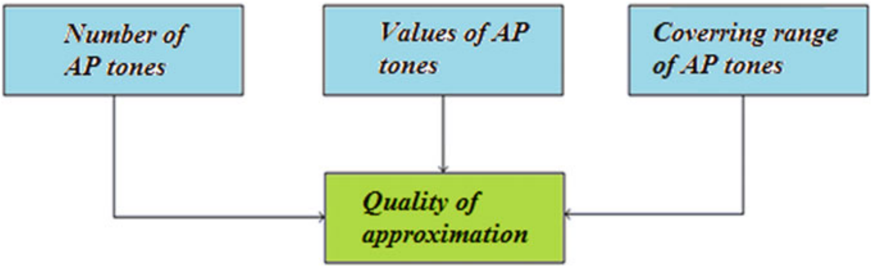

Fig. 1 Approximation parameters influencing the image quality

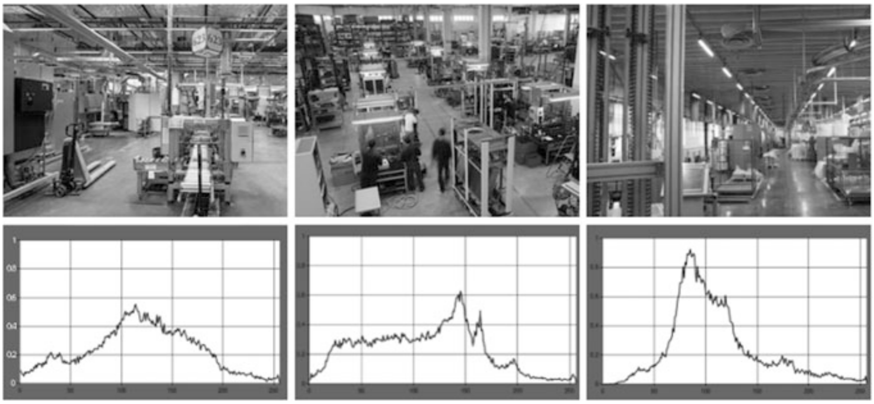

Fig. 2 Three different industrial workplace photos and their respective FDB

Thus, the strategy of maximal measured calculation of pixels number for each range was applied to define the SP covering range for this modified algorithm, which consists of the following steps:

1. determine the count of all tones N,
2. find average count of the pixels N_c according the size of SP,
3. scan DFB by separating ranges, which have the full pixels number N_i of BP, and the minimal deviation from N_c.

Following such approach, the zones, which have smaller number of tones, receive the larger range, because their contribution to the MMI's correctness is less significant. The example of this strategy is present through the integral (accumulated) diagram of brightness, which is the analogue of the integral probability distribution (see Fig. 3).

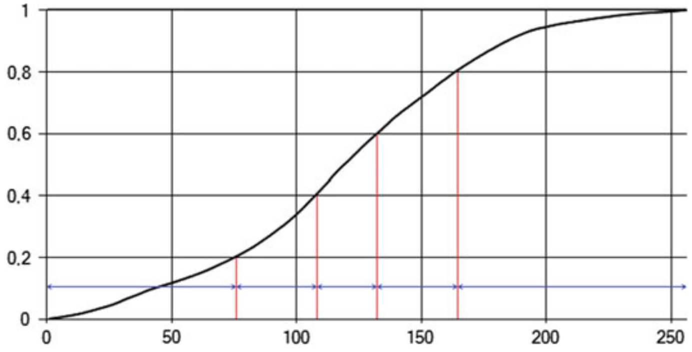

Fig. 3 The integral diagram of the 1st workplace photo

The above diagram shows, in the relative scale, the accumulated number of pixels for increasing brightness, where on Y-axis (number of pixels), shows the decomposition strategy between ranges. However, the follow up research has confirmed a good computational efficiency of this model in defining the covering range.

3 Image Approximation with Genetic Algorithms

The research decision was to use the genetic algorithm (GA) to optimize MMI's approximation, which modifications have been crucial to solve this problem.

The GA's modifications consider the individual to be AMMI and the chromosome to be SP. The genes are represented as separate elements of SP. The BP tones, which enter in a separate gene, are covering the range as gene alleles, which contain the genome of each gene. In the beginning, the chromosome model considers the like bitmap (matrix) of AMMI, but is influenced directly by the genetic operators on this matrix, undergoing a small change. The new created gene-chromosome structure simulates correctly the evolutionarily genetic field, because the chromosome contains the whole genetic information about each individual, so there is no need to push the matrix, which is only used for the chromosome estimation. The algorithm creates the matrix of individuals according to the genetic information contained within each chromosome, and which is evaluated by the optimization criteria. The simplified scheme of gene-chromosome structure is shown in Fig. 4.

The first step of the algorithm creates the initial population, which is based on the random variation of the SP pixels tones, and within the defined ranges limits, which allow creating different chromosomes within the developing population. The individuals of the initial population are estimated according the criteria (1) or (2). The evaluation results are used to perform "roulette" selection of the population. After selecting the evolved population happening under the influence of genetic operators "crossover" and "mutation", the new generation is created. The convergence of the

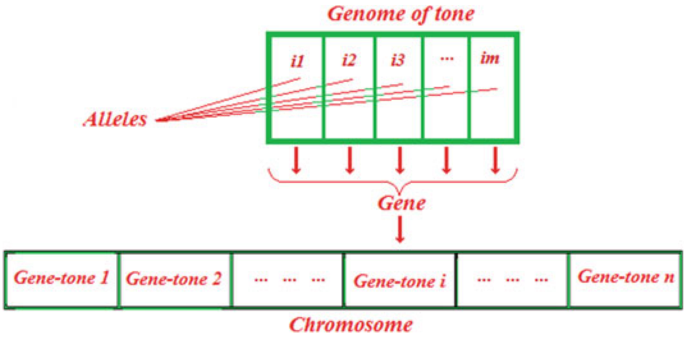

Fig. 4 Scheme of the gene-chromosome structure

algorithm is attainment for the last generation, and found quite simple and sufficient for motivating the current research.

The current research is aimed to understand the influence of the GA's probability factors on the output results. Already stated in the previous work [1], the sub-optimal values of the quantity factors, from the standpoint of result/time has been reported. The algorithm modification, with quite predictable behavior of the quantity factors influence on the chosen values, is estimated to be sufficient, in order to validate the algorithm's performance.

4 Image Approximation Based on Parametrical Sub-optimization of Genetic Algorithm

For the considered problem, the probabilistic component of modified GA consist of the four following parameters:

1. amplitude of initial SP—$\boldsymbol{A_{sp}}$;
2. crossover probability, defining the chromosomes gens recombination with probability $\boldsymbol{p_{cross}}$;
3. mutation probability, where each gene of chromosome changes with probability $\boldsymbol{p_{mut}}$;
4. amplitude of mutation—$\boldsymbol{A_g}$, important in the case of mutation, where a gene changes in range of defined amplitude.

They are necessary to be defined in order to perform the full factorial experiment (FFE) with $n = 4$. The values and their level of variation have been chosen based on the experience acquired in the previous research on heuristic's sphere, and are shown in Table 1.

The performed simulations consist of three experiments, which have different input OMMI for performing the image approximation, based on the industrial workplace pictures, called "Workplace-1", "Workplace-2" and "Workplace-3", having the resolution of 280 × 210 pixels (see Fig. 2).

Each experiment consists of 16 tests, where every test is repeated 30 times. The experiment's structure is presented in Table 2.

Table 1 The factors value and their levels of variation

Factor	x1			x2			x3			x4		
	Variation of initial SP			Crossover probability			Mutation probability			Amplitude of mutation		
Level	max	mid	min	max	mid	min	max	mid	min	max	mid	min
Value	3	2	1	60	40	20	60	40	20	3	2	1
Symbol	+	0	–	+	0	–	+	0	–	+	0	–

Table 2 Matrix and results of optimization experiment of the Workplace-1 photo approximated with 2^4 pallet from 2^8 pallet

№		0	1	2	3	4	5	6	7	8
Factor	X1	0	–	–	–	–	–	–	–	–
	X2	0	–	–	+	+	–	–	+	+
	X3	0	–	+	–	+	–	+	–	+
	X4	0	–	–	–	–	+	+	+	+
Response	У1	0.01528	0.01524	0.01526	0.01524	0.01527	0.01526	0.01539	0.01526	0.01538
	У2	0.01534	0.01525	0.01531	0.01526	0.01531	0.01530	0.01555	0.01530	0.01556
	У3	1.0E−09	3.8E−11	8.1E−10	1.0E−10	4.7E−10	5.2E−10	5.2E−09	4.4E−10	6.0E−09
	У4	3.2E−05	6.2E−06	2.8E−05	1.0E−05	2.1E−05	2.2E−05	7.2E−05	2.1E−05	7.7E−05
№		0	9	10	11	12	13	14	15	16
Factor	X1	0	+	+	+	+	+	+	+	+
	X2	0	–	–	+	+	–	–	+	+
	X3	0	–	+	–	+	–	+	–	+
	X4	0	–	–	–	–	+	+	+	+
Response	У1	0.01528	0.01524	0.01527	0.01524	0.01527	0.01525	0.01538	0.01526	0.01540
	У2	0.01534	0.01525	0.01531	0.01525	0.01532	0.01530	0.01556	0.01529	0.01552
	У3	1.0E−09	8.6E−11	6.0E−10	7.6E−11	5.7E−10	4.4E−10	8.0E−09	4.2E−10	6.2E−09
	У4	3.2E−05	9.2E−06	2.4E−05	8.7E−06	2.4E−05	2.1E−05	8.9E−05	2.0E−05	7.9E−05

In the performed experiments evaluation for the graphic-approximation modification (GAM) of GA, the quality control is made in accordance to the following main parameters:

- y_1—the best individual defined according the criteria (2), based on 30 parallel tests of the FFE line;
- y_2—average value defined from the criteria (2), evaluated among the best individuals of FFE line;
- y_3—dispersion of the best individuals based on the FFE line;
- y_4—RMS of the best individuals based on the FFE line.

The above Table 2 with the performed experiment contains the output results for the Workplace-1 approximation. Under the same scheme the experiments for Workplace-2 and Workplace-3 are performed. The purpose of these experiments is to find out the influence of the FDB form on the GA parameters. The results of all three experiments are obtained in accordance to the main criteria (2), as shown in Table 3.

The FFE analysis, as shown in Tables 2 and 3, put in evidence that the best approximation (absolutely minimal deviation from OMMI), for the three quite different images, was obtained for T9 parameters (see Table 3, row 11). This represents a strong confirmation of the positive influence on the T9 parameters, which almost exclude the probability of the statistical error. For the point T9, the high level has only A_{sp} value. That has been predicted, because this parameter response directly to the genetic variety of the population, which according to the genetic point of view is always considered as one of the key factors indicating the successful population evolution.

Table 3 Results of experiments (minimal deviation from OMMI)

№ Test	y_1*(Workplace-1)*	y_1*(Workplace-2)*	y_1*(Workplace-3)*
T0	*0.015288*	*0.015322*	*0.013876*
T1	*0.015249*	*0.015277*	*0.01382426*
T2	*0.015268*	*0.015302*	*0.013825*
T3	*0.015249*	*0.015277*	*0.013820*
T4	*0.015275*	*0.015317*	*0.013831*
T5	*0.015263*	*0.015278*	*0.013823*
T6	*0.0153930*	*0.0154540*	*0.014112*
T7	*0.0152630*	*0.0152740*	*0.01382452*
T8	*0.015383*	*0.015412*	*0.014370*
T9	*0.0152480*	*0.0152650*	*0.01382406*
T10	*0.0152760*	*0.0152810*	*0.013842*
T11	*0.0152480*	*0.0152750*	*0.013821*
T12	*0.0152730*	*0.0153000*	*0.013826*
T13	*0.0152580*	*0.0152800*	*0.013827*
T14	*0.015386*	*0.015473*	*0.014148*
T15	*0.0152600*	*0.0152800*	*0.013828*
T16	*0.0154030*	*0.0154800*	*0.014522*

The other parameters of T9 are directed to the minimal side. Close to the accuracy of the T9 results, also characterized by the minimal value of the parameters p_{cr}, p_g and A_g. For the performed experiments, when considering the observed vector for these three parameters, it is required to perform an additional experiment, which has the center of plan close to T9. This modification will provide the possibility to find the sub-optimal parameters of the required probabilistic factors.

For all the three different images, the worsts results were obtained exactly in the same points of the experiment (T6, T8, T14 and T16), where the parameters p_{mut} and A_g are having their highest level. Therefore, this fact confirms the requirement that the search of the sub-optimal values of these factors has to be performed in their respective minimal value areas. In addition, this is influencing the stability of the designed algorithm, because these parameters are responsible for this common result in respect to the different images analyzed, and thus avoiding the absolutely random results.

For achieving a more concrete assessment on this influence for the approximation process optimization of the Workplace-1 we have obtained the mathematical model in the form of the regression equation y ($\boldsymbol{x_1}$, $\boldsymbol{x_2}$, $\boldsymbol{x_3}$, $\boldsymbol{x_4}$):

$$\begin{aligned} y_{comp}(x_1,x_2,x_3,x_4) = {} & 0.0152934 + 0.00000056 \cdot x_1 + 0.00000081 \cdot x_2 \\ & + 0.00003869 \cdot x_3 + 0.00003269 \cdot x_4 + 0.00000119 \cdot x_1 \cdot x_2 + 0.00000181 \cdot x_1 \cdot x_3 \\ & + 0.00000006 \cdot x_1 \cdot x_4 + 0.00000056 \cdot x_2 \cdot x_3 + 0.00000031 \cdot x_2 \cdot x_4 \\ & + 0.00002644 \cdot x_3 \cdot x_4 + 0.00000094 \cdot x_1 \cdot x_2 \cdot x_3 + 0.00000244 x_1 \cdot x_2 \cdot x_4 \\ & + 0.00000081 x_1 \cdot x_3 \cdot x_4 + 0.00000006 x_2 \cdot x_3 \cdot x_4 + 0.00000219 x_1 \cdot x_2 \cdot x_3 \cdot x_4 \end{aligned} \tag{3}$$

The above equation is for the experiment based on the OMMI Workplace-1 input. The regression equation of Workplace-2 and Workplace-3 has shown similar results. According to the regression equation, the largest influence was resulting from factors x_3 and x_4, which is the confirmation of the conclusions early made.

Equation (3) is defined from the estimation of the response surface curvature created from the setting space parameters in order to find the minimum RMS area of AMMI from IMMI. This approach allows finding the antigradient direction (shortest path to minimum) from the partial derivatives in (3) according to the setting parameters x_i. The three additional steps, according to the antigradient direction, allow identifying the optimal area of the probabilistic factors, with the best RMS value around 3.05E−06, for all the experiments. For that reason, the decision was taken to perform an additional experiment around this identified area.

In this additional experiment, the influence of $\boldsymbol{A_{sp}}$, parameter will be fixed, by defining FFE with $n = 3$, as shown in Table 4.

This experiment is analogue to the previous one, except that there are 9 tests. As there is close results equality with the previous approximation for all the 3 images, only one experiment with the OMMI Workplace-1 input is performed.

The results analysis of this additional experiment shows that it is impossible to find the best point of the experiment with criteria y_1, because most of them have

Table 4 The factors value and their levels of variation

Factor	x_1			x_2			x_3		
	Crossover probability			Mutation probability			Mutation amplitude		
Level	max	mid	min	max	mid	min	max	mid	min
Value	20	15	10	20	15	10	2	1	1
Symbol	+	0	–	+	0	–	+	0	–

equal accuracy results estimated by the optimization criteria (2) as 0.015248. But according to criteria y_2, y_3 and y_4, the best point of the experiment is T8 (see Table 5, column 10). The analysis made, over all the experiments for OMMI Workplace-1, has shown that there no more accurate results are found. Thus, this one is considered as the extremum candidate, at least for the defined covering range of tones from SP.

By considering the found candidate for the extremum, it is required to add the new criteria for the GA's search quality evaluation, as y_5—the count % of results where $y_1 = 0.015248$. In addition, the new criteria shows that the best point of experiment is T8.

Based on the experiment results, the decision was to calculated the antigradient for the point T8 and perform the 2 steps for factors x_2 and x_3, according to the received vector. The result of the calculation is the step with −1 for factor x_2 and 0 for x_3.

The first step, according to y_5 has repeated the result of T8, but the second step has improved the percentage of extremum to 19% (see Table 6, column 6).

As mentioned before, every experiment is repeated 30 times. The analysis of the results from the implemented "steep descent" algorithm has shown that this algorithm is appropriate for finding the optimal (or possibly sub-optimal) solution of the OMMI approximation problem. Now, we can calculate the minimal number of parallel GA's runs based on the found optimal parameters, which guarantee at least one optimal results with an acceptable probability (for example, three sigma).

The calculation of the required number of algorithm runs (every of them is independent) is defined according to the following formula:

$$N = \frac{\ln(1 - p_d)}{\ln(1 - p_o)} = \frac{\ln(1 - 0.9973)}{\ln(1 - 0.76)} \approx 4.1 \tag{4}$$

where p_d—is desired probability to find the extremum, p_o—probability to find extremum in the single run.

The number of parallel runs should be rounded up to a greater value, for example in our case $N = 5$, providing the high probability $P = 0.999204$.

For the validation of this algorithm 50 experiments have been conducted, where each of them was repeated 5 times. As expected, at least one optimum was found in all 50 of them. Overall, the number of repetitions (250) was negative 0.336%,

Table 5 Output results of additional experiment

№		0	1	2	3	4	5	6	7	8
Factor	X1	0	+	–	+	–	+	–	+	–
	X2	0	+	+	–	–	+	+	–	–
	X3	0	+	+	+	+	–	–	–	–
Response	У1	0.01524	0.01525	0.01524	0.015248	0.015248	0.01524	0.015248	0.01524	0.01524
	У2	0.01525	0.01527	0.01527	0.015253	0.015252	0.01525	0.015256	0.01525	0.01525
	У3	3.0E−11	2.7E−10	6.3E−10	2.77E−11	2.56E−11	7.05E−11	5.16E−11	1.01E−11	4.51E−12
	У4	5.5E−06	1.6E−05	2.5E−05	5.26E−06	5.06E−06	8.39E−06	7.18E−06	3.18E−06	2.12E−06
	У5	0.20	0.00	0.00	0.13	0.27	0.03	0.03	0.50	0.57

Table 6 Results of the additional steps

№ Step	y_1	y_2	y_3	y_4	y_5
S1	0.015248	0.0152507	1.57E-11	3.96E-06	0.57
S2	0.015248	0.0152494	9.08E-12	3.01E-06	0.76

indicating that the actual probability of obtaining a positive result after 5 repetitions for this experiment was 0.9957.

5 Conclusion

The proposed conceptual and mathematical model of the modified GA's has proven to be an extremely effective tool (when ranges are fixed) for the optimization of the MMI approximation process.

It is suggested to modify the model by including the number of variable settings in order to better cover the ranges of each separate gene.

There is an idea that such modification of GA will enable to have a solution when performing the "absolute" optimization process of AMMI, i.e. fulfilling the minimal deviation from OMMI.

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