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Color recipe prediction by Genetic Algorithm

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Abstract

In this paper, a new method for color recipe prediction is proposed by applying Genetic Algorithm. This method is able to do both spectrophotometric and colorimetric color matching based on its fitness function. It is shown that the problem of the limitation of colorant numbers in colorimetric color matching can be solved. In addition, this algorithm is capable of decreasing the color difference under second illuminant and reduces metamerism problem by applying a fitness function based on the color differences under two illuminants.

Keywords: Color recipe prediction; Genetic Algorithm; Colorimetric matching; Spectrophotometric matching

1. Introduction

One of the most important processes in textile dyeing is the recipe match prediction. It needs a combinatorial solution of colorants to produce color recipes for a target color sample. There are two basic steps in a recipe prediction:

(i) Selection of colorants for a specific color match
(ii) Determination of the magnitude of each colorant concentration to match the reference color.

Spectrophotometric and colorimetric color matching are two separate methods that are conventionally used. Colorimetric algorithms try to minimize the differences of the tristimulus values between a target and a color sample. So colorimetric matching accounts also for both observers and light source characteristics. On the other hand, this method directly tries to produce small color differences under a specific illuminant. Spectrophotometric color matching tries to achieve a sample with spectrophotometric curve similar to target reflectance curve. Therefore, this method indirectly produces small color differences. Whereas it tries to match the target reflectance curve approximately, it is not able to decrease the color differences under a particular illuminant as the colorimetric matching.

The most difficulty in these methods is to find a completely satisfactory digital method for calculation of colorant formula based on the goal of matching (spectrophotometric or colorimetric). The prediction of colorant concentrations is a nonlinear process and to find a solution, some approximation assumptions are needed.

The most common computational method for colorimetric matching was purposed by Allen [1] that is based on Park and Stearns' method [2]. This method was constructed using the case of single-constant Kubelka–Mank theory [3]. One of the problems in colorimetric matching is the limitation of colorant number to three. Allen suggested a way to increase the number of colorants to four using Kubelka–Mank two-constant theory [4]. Another disadvantage of colorimetric matching is metamerism. Since in this method the differences of the tristimulus values between a target and a sample color are minimized under a particular illuminant it is possible to meet an incredible difference for another illuminant.

For the spectrophotometric matching, least square technique that was purposed by McGinnis [5] is a common method. In this method the number of equations (usually 16

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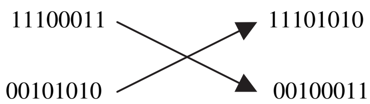

Fig. 1. Single-point cross over.

Fig. 2. Chromosome mutation in its third position.

wavelengths in the visible spectrum) is almost more than the number of unknown quantities (number of colorants), so it is impossible to satisfy exactly all equations. The accuracy of this method depends on the condition number of the coefficient matrix that consists of the Kubelka–Mank K/S function of each initial colorant in various wavelengths. It is clear that if it is an ill-conditioned matrix the results are in doubt.

In this paper, we introduce Genetic Algorithm as a technique for color recipe prediction. We show that how GA can help to solve some of the computational problems of color matching. The proposed algorithm is able to do both the steps in color matching, selection of colorants and determination of each colorant concentration.

2. Genetic Algorithm [6–8]

Genetic Algorithm developed by Holland is a stochastic global search method that mimics the metaphor of natural biological evaluation. GAs work with a population of individuals, each representing a possible solution to a given problem. All individuals of one generation are evaluated by a given fitness function. The highly fit individuals are given opportunities to reproduce new offspring by cross breeding with other individuals in the population. After a number of iterations, the population consists of individuals that are well adapted in terms of the fitness function.

The simplest form of Genetic Algorithm involves three types of operators: selection or reproduction, crossover and mutation.

Selection: this operator selects chromosomes in the population for reproduction according to their fitness function values. The fitter the chromosomes, the more times it is likely to be selected to reproduce. This operator may be implemented in several ways such as roulette wheel and rank based selection.

Crossover: this basic operator takes two individuals and cuts their chromosome strings at some randomly chosen position to produce two "head" segments and two "tail" segments. The tail segments are then swapped over to produce two full length chromosomes. The two offsprings each inherit some genes from each parent. The simplest form of it is that of single-point crossover. Fig. 1 indicates an example that two chromosomes are crossed over after fourth locus in each to produce the two new offsprings.

Mutation: this operator is a random process where some of the bits in a chromosome are replaced by another (0 → 1 and 1 → 0) to produce a new genetic structure. Fig. 2 shows the third bit of the chromosome being mutated. The rate of mutation is often seen as providing a guarantee that the probability of searching any given string will never be zero.

The basic steps of a standard Genetic Algorithm are as follows:

1. Generate a random population of L bit chromosomes of specific size (n). It should be consider that the population size affects the efficiency and performance of GA.
2. Calculate the fitness of each chromosome in the population.
3. Select a pair of chromosomes from the current population for mating by a random selection method.
4. Based on probability of crossover, apply this operator on the selected pair that have been chosen for crossover and

Table 1
The reflectance values of colorants and wool substrate

	Green	Blue1	Bordo	Yellow1	Violet	Blue2	Red2	Yellow2	Substrate
400	0.0844	0.1947	0.0608	0.0539	0.1617	0.0902	0.1030	0.0510	0.2542
420	0.0835	0.2611	0.0665	0.0457	0.2593	0.0958	0.0951	0.0432	0.3071
440	0.1012	0.3369	0.0618	0.0428	0.2959	0.1364	0.0748	0.0447	0.3572
460	0.1423	0.3082	0.0507	0.0440	0.2199	0.2305	0.0560	0.0584	0.4002
480	0.1817	0.2271	0.0425	0.0562	0.1392	0.2683	0.0449	0.1196	0.4402
500	0.1878	0.1513	0.0372	0.1007	0.0873	0.2067	0.0394	0.2889	0.4809
520	0.1525	0.0969	0.0345	0.1951	0.0539	0.1333	0.0377	0.5428	0.5146
540	0.1108	0.0636	0.0343	0.3029	0.0431	0.0874	0.0402	0.7250	0.5436
560	0.0779	0.0487	0.0354	0.4129	0.0352	0.0559	0.0519	0.8122	0.5703
580	0.0615	0.0413	0.0451	0.4920	0.0372	0.0446	0.1347	0.8351	0.5941
600	0.0514	0.0411	0.0955	0.5463	0.0388	0.0368	0.3337	0.8482	0.6151
620	0.0493	0.0413	0.2060	0.5725	0.0542	0.0360	0.4942	0.8541	0.6332
640	0.0499	0.0422	0.3318	0.5885	0.1383	0.0358	0.5738	0.8642	0.6494
660	0.0538	0.0761	0.4110	0.6025	0.3141	0.0363	0.6080	0.8723	0.6644
680	0.0682	0.1964	0.4496	0.6225	0.4792	0.0512	0.6339	0.8841	0.6772
700	0.1012	0.3718	0.4706	0.6476	0.5497	0.0955	0.6579	0.8943	0.6875

Table 2
The color characteristics of 20 used color samples

	L^*	a^*	b^*
1	27.2981	14.3636	−9.7904
2	15.0287	14.5151	−2.1418
3	16.4500	4.4729	−14.2535
4	17.6713	2.4209	−2.1054
5	14.4173	3.2702	−4.0093
6	25.2296	−17.6389	6.8865
7	15.8149	14.1610	−6.1109
8	15.9338	1.0377	−14.2969
9	19.8819	−10.4849	−8.1853
10	15.6864	10.4986	−6.4840
11	17.5120	2.8265	−10.5357
12	18.7475	2.5467	−1.8430
13	18.4165	2.5896	−2.2636
14	24.4288	11.9262	−15.8359
15	27.9181	−15.4468	−11.6744
16	26.1359	−14.7700	−10.6505
17	25.9173	−11.6492	−2.9572
18	25.7545	−9.5442	−2.7712
19	16.7240	13.6058	−5.0100
20	28.1095	−16.8636	−13.8191

also mutate the correspondent bit that is selected for mutation based on the probability of bit mutation.

5. Repeat steps 2–4 until the production of next generation exceeds the size of the previous generation.
6. Go through steps 2–6 until the termination criteria met.

If the GA has been correctly implemented, convergence is met. When the population converges, the average fitness will approach that of the best chromosome.

Many strategies have been suggested in the literatures to improve GA's operators and algorithm. We use some of them in our algorithm that are mentioned in the next section.

3. Experimental

In this section, we explain the proposed method for color recipe prediction via Genetic Algorithm. The main concerns in this method are as follows:

The parameters (genes) in GA model are colorant concentrations. Each of them is represented by a 14 bit binary number, so the chromosomes consist of the number of colorants multiplied by 14 binary digits. The population size is set to be 100.

Two types of fitness function based on the goal of matching, spectrophotometric or colorimetric have been used. In each iteration after estimating colorant concentrations, a reflectance curve for the sample is calculated by Eqs. (1) and (2) based on single-constant Kubelka–Mank theory:

$$K/S = (K/S)_{\text{sub}} + \sum_{i=1}^{n} C_i (K/S)_i \tag{1}$$

$$R = 1 + K/S - \left((K/S)^2 + 2K/S\right)^{0.5} \tag{2}$$

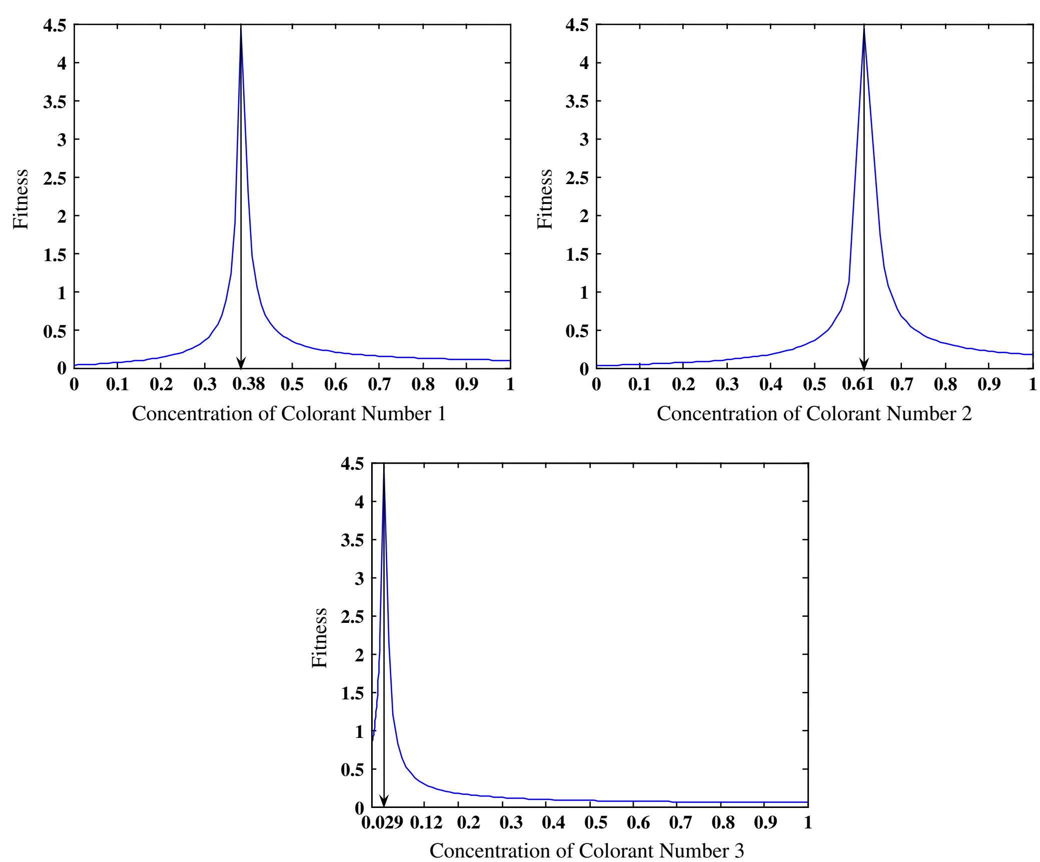

Fig. 3. Illustration of GA performance for sample 1 by a fitness function based on ΔE as an example.

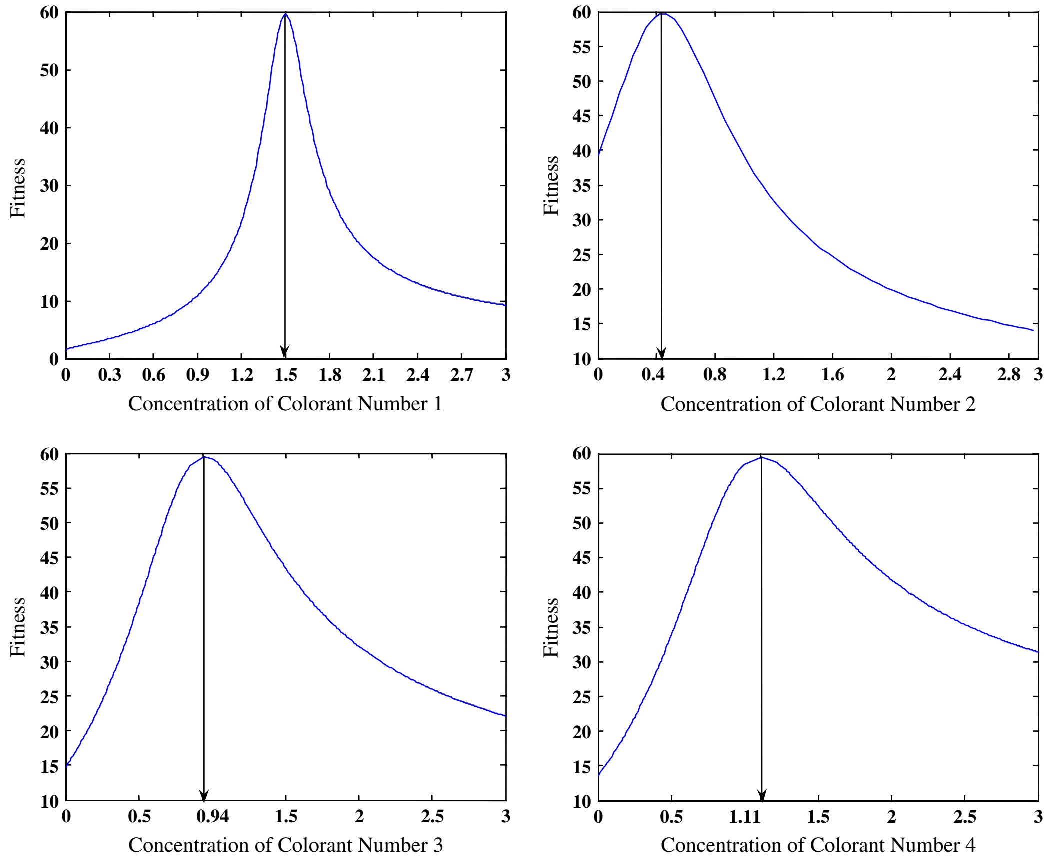

Fig. 4. Illustration of GA performance for sample 4 by a fitness function based on ΔR as an example.

In case of spectrophotometric match, the fitness function will be as in Eq. (3):

$$\mathrm{Fitness} = 1/(\Delta R + \varepsilon) \tag{3}$$

where $\Delta R = \sqrt{\sum_i (R_{\mathrm{std}}(\lambda_i) - R_{\mathrm{mix}}(\lambda_i))^2}$.

In addition, for colorimetric match as in Eq. (4):

$$\mathrm{Fitness} = 1/(\Delta E + \varepsilon) \tag{4}$$

In Eqs. (3) and (4) ε is an insignificant value to avoid division by zero. Moreover, in Eq. (4) ΔE is the color difference between the target and achieved sample color. It can be evaluated by any acceptable color difference formula under a desirable illuminant such as D_{65}.

We used fitness remapping and it improved the GA performance. There are several suggestions for applying fitness remapping and we used one of the commonly employed methods as fitness scaling [9]. To apply fitness scaling or fitness shifting the value of ($2 \times$ average-maximum) is subtracted from the raw fitness score and then divided by the average of the adjusted fitness value. Care must be taken to prevent negative value. If there is any negative value, it will be set to zero.

For crossover operator, a multiple crossover technique is used. The disruptive nature of multipoint crossover appears to encourage the exploration of the search space, rather than favoring convergence to highly fit individuals early in the search, thus making the search more robust [6].

The number of crossover points, have been determined randomly between one and the number of colorants.

The other parameters and steps for the algorithm are as for standard GA that is explained in the previous section.

4. Using the proposed GA for color recipe prediction

For each recipe prediction, the proposed algorithm is used twice, first for colorant selection and then for estimation of each colorant concentration.

(1) At first the algorithm is applied in the presence of all colorants. After the GA is converged and the best recipes are found, a middle step is used to choose the colorants. In this step, the best chromosome is examined to show the variation of fitness value with respect to elimination of each colorant. For example if there are eight colorants, eight new fitness values are calculated in the absence of each colorant. Then the colorant with the least negative effect on the fitness whose effect is smaller than a limited value is eliminated. Then this process is repeated by seven colorants and so on, until no colorant gets the chance of omission. It is clear that in this step it is possible to get a specific number of colorants by changing the restrictions.

Table 3
The results of color recipe prediction by the proposed GA

No.	Selected colorants	Concentrations	ΔR	ΔE^{a}
1	2 3 4	0.3836 0.6141 0.0286	0.053	0.2253
	2 3 4	0.3993 0.6143 0.0571	0.0119	0.9361
2	3 4 5 6 7	1.6383 0.3071 0.4607 0.4147 0.6143	0.2223	0.0795
	2 3 4 5 7	0.6705 1.6383 0.8192 0.4904 0.5116	0.0115	1.8587
3	1 3 5 6 8	0.7947 0.4074 1.5301 0.2103 0.2024	0.2213	0.378
	2 3 4 5	1.6383 0.4096 0.3825 1.6031	0.0162	1.4498
4	1 2 4 7	1.1457 0.6600 0.5629 1.0220	0.3187	0.3398
	2 5 7 8	1.4968 0.4095 0.9435 1.1133	0.0168	1.901
5	1 2 3 4 5	1.5045 0.1926 1.2287 0.5119 0.4988	0.2453	0.1132
	2 3 7 8	1.6383 1.6383 0.0148 0.8192	0.0126	1.9614
6	1 5 6 7 8	0.7582 0.0489 0.7914 0.1621 1.4350	0.0557	0.3698
	1 5 6 7 8	1.4695 0.000 0.3072 0.2048 1.2288	0.0143	1.7392
7	3 4 5 6 7	1.2833 0.2723 1.0308 0.2449 0.2370	0.1512	0.0003
	1 2 5 7 8	0.1280 0.4095 1.1648 1.4144 0.6144	0.0144	2.0269
8	1 2 3 7 8	1.0965 1.6383 0.5220 0.2048 0.000	0.0367	0.5022
	1 3 5 6 7	1.4336 0.2086 1.2285 0.3070 0.3131	0.0122	0.9598
9	1 3 6 7 8	1.1264 0.2295 1.4335 0.1303 0.2048	0.1309	0.0936
	1 2 4	0.8192 1.6383 0.6912	0.0099	1.4115
10	1 2 3 7 8	0.3776 0.7679 1.6047 0.1667 0.0512	0.1389	0.0127
	1 3 5 6 7	0.2564 0.2241 0.6339 0.6143 1.6379	0.0137	0.7607
11	1 4 5 6 7	0.5619 0.2046 0.7821 0.7224 0.7135	0.0592	0.0009
	1 3 5 6 7	0.5215 0.2048 0.2374 1.1263 0.8049	0.0086	0.3359
12	1 4 5 6	0.2411 1.3324 1.5877 0.1327	0.2503	0.2127
	1 6 7 8	0.4096 0.8191 1.2287 0.6400	0.0145	1.42
13	1 3 4 5 6	0.3988 0.6099 0.8160 0.6711 0.3961	0.1228	0.0009
	1 3 6 7 8	0.4739 0.4096 0.8191 0.8584 0.4095	0.011	1.0115
14	1 3 5 7	0.3487 0.2216 0.6656 0.2296	0.098	0.1477
	3 5 6 7	0.2305 0.5375 0.3200 0.3071	0.0141	0.3381
15	5 6 8	0.3360 1.0751 0.3372	0.0765	0.0911
	1 5 6 7 8	1.0436 0.2048 0.4095 0.0512 0.0568	0.0188	2.295
16	1 5 6 7 8	0.000 0.1535 1.4272 0.1056 0.3072	0.0374	0.1193
	1 5 6 7	1.2077 0.0650 0.6304 0.1152	0.016	1.3712
17	1 2 3 7 8	1.2416 0.3103 0.1472 0.0505 0.3712	0.0695	0.0189
	3 5 6 7 8	0.3071 0.0001 1.0239 0.0255 0.4095	0.0184	2.4699
18	1 3 5 6 8	0.8171 0.2067 0.2135 0.2956 0.4630	0.0738	0.0049
	1 3 6 7 8	0.2047 0.2687 0.8191 0.1024 0.4095	0.0184	1.8083
19	3 4 5 6 7	1.2180 0.2432 0.6689 0.3344 0.3399	0.1137	0.0068
	1 3 5 6 7	0.1399 1.0259 0.4095 0.3583 0.8121	0.018	0.6175
20	1 5 6 7 8	0.4991 0.0248 1.1775 0.0592 0.0512	0.0266	0.0595
	1 3 4 5 6	0.6528 0.0384 0.0247 0.1024 0.9782	0.0087	1.3111

For each sample, the first row is the result of a colorimetric color matching (the fitness function is based on ΔE) and the second row is the result of a spectrophotometric color matching (the fitness function is based on ΔR).

[a] ΔE is the CIELAB color difference under D_{65} and 1964 standard observer.

(2) After selecting the suitable colorants, the GA is applied with the selected colorants. When the GA is converged, the chromosome with the best fitness consists of the final colorant concentrations.

In order to evaluate the performance of this method, some color samples that are reported in another research [10] is used. These samples were prepared on wool fabric using a combination of the eight colorants and their reflectance values are presented in Table 1.

5. Results

To show the performance of the proposed method, 20 arbitrary color samples from the mentioned reference were

Table 4
The color differences between the target and matched sample by GA by a fitness function based on ΔE (D_{65}) for two illuminants

ΔE	No.									
	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
Under D_{65}	0.2253	0.0795	0.3780	0.3398	0.1132	0.3698	0.0003	0.5022	0.0936	0.0127
Under A	0.2735	0.5960	0.9891	1.4960	0.4339	1.2374	0.6955	0.7118	0.6953	1.7524
ΔE	No.									
	11	**12**	**13**	**14**	**15**	**16**	**17**	**18**	**19**	**20**
Under D_{65}	0.0009	0.2127	0.0009	0.1477	0.0911	0.1193	0.0189	0.0049	0.0068	0.0595
Under A	1.3215	3.0559	2.0569	1.4498	1.5290	0.9505	0.3426	1.4482	1.7998	0.5172

used. The color characteristics of these samples in CIELAB color space consist of L^*, a^* and b^* and are presented in Table 2.

The proposed GA with both the fitness functions based on ΔE and ΔR are used to select colorants between eight existing colorants and then to estimate the recipe for each sample. It takes between about several seconds (20–30 s) and maximum a few minutes (3–4 min) for the algorithm to be converged. Fig. 3 indicates the behavior of the fitness function based on ΔE for one of the samples (number 1) as instance. In addition, Fig. 4 shows the similar result with a fitness based on ΔR for another sample (number 4). It illustrates that the concentration of each colorant that estimated by GA has the highest fitness value so the GA is approach to the best answer.

Table 3 shows the results of applying the proposed GA to predict the recipes for the 20 color samples. The results demonstrate that the proposed GA is able to do both the common color matching (colorimetric and spectrophotometric) by an acceptable precision. However, it seems that the GA is more powerful in convergence and final results for colorimetric matching (fitness function based on ΔE). The problem of the limitation of colorant numbers in colorimetric color matching is solved completely by this method.

As mentioned before in colorimetric matching the differences of the tristimulus values between a target and a sample color are minimized under a particular illuminant so it is possible to meet an incredible difference for another illuminant and to achieve a metameric pair for target. Table 4 shows the color difference for the 20 experimental samples under illuminants D_{65} and A. It can be observed by applying the proposed GA with a fitness function based on ΔE under illuminant D_{65}, usually the color difference under illuminant A is also acceptable. However, for some samples there is a noticeable color difference under A. To face this problem we introduced another fitness function as in Eq. (5). Illuminant A is used as a second illuminant because it is a common illuminant that is different enough from D_{65}.

$$\text{Fitness} = 1/(\Delta E_{D_{65}} + \Delta E_{A} + \varepsilon) \tag{5}$$

For the samples whose color difference under illuminant A is almost noticeable, the method is repeated by a fitness function based on Eq. (5). Experimental results show that the proposed GA can be converged by the fitness function based on Eq. (5). Table 5 illustrates that by applying a fitness function based on two illuminants it is also possible to decrease the color difference under second illuminant. However, the color difference under D_{65} increases slightly in comparison with previous condition but it remains acceptable. Since this GA is more efficient by a fitness function based on the color difference under one illuminant (Eq. (4)) and also that the color difference under illuminant A is usually acceptable, it is suggested that the GA is run by a fitness function as in Eq. (4). However, if the color difference under second illuminant is incredible and it is necessary to decrease, the GA can be repeated by a fitness function as in Eq. (5).

6. Conclusion

Genetic Algorithm is introduced as a technique for color recipe prediction. It is able to do both spectrophotometric and colorimetric color matching. If a spectrophotometric match is considered the fitness function increases by reducing the difference between the spectrophotometric curves of the target and the match sample. If a colorimetric match is the

Table 5
The results of color recipe prediction by the proposed GA with a fitness function based on color differences under two illuminants (Eq. (5))

No.	Selected colorants	Concentrations	ΔR	ΔE (D65)	ΔE (A)
10	3 4 5 6 7	0.3840 0.2688 0.7937 0.6526 1.2019	0.0475	0.1466	0.9976
12	1 2 3 4	0.7387 0.6268 0.8007 0.6521	0.0986	0.5367	0.28
13	1 3 4 6	0.5188 1.0044 0.4727 0.6700	0.0438	0.2557	0.5975
15	1 6 7 8	0.8960 0.8036 0.0961 0.0128	0.0465	0.0362	0.305
19	4 5 6 7	0.2917 0.8120 0.4414 1.6367	0.0283	0.4303	0.4392

goal, it can be defined as a function to decrease the color difference between a target and a color sample under a particular illuminant. The experimental results show that the proposed GA can be converged with both of these fitness functions by an acceptable precision for final results. However, the GA is more powerful in convergence and results for colorimetric matching. By applying this method, the problem of the limitation of colorant numbers in colorimetric color matching is solved. In colorimetric matching if an incredible color difference under second illuminant is met, the fitness function can be changed to decrease the color differences under two illuminants. Results illustrate that the GA can be converged by this fitness function but it is more efficient with a fitness function based on the color difference under only one illuminant.

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