Estimation of Color Matching Functions for Tiled LCDs based on Genetic Algorithm

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Abstract

This paper presents an estimation method of the color matching functions (CMFs) for the seamless color reproduction in a tiled liquid crystal display (LCD) system. Based on results of visual experiments, the color matching functions are determined using the genetic algorithm. Experimental results indicate that the estimated CMF by the proposed method yields smaller color differences than the existing CMFs.

1. Introduction

Need of a large sized display system is increasing for the public information display, advertisement, or media façade applications. Multi-screen or tiled display system made of multiple flat displays with narrow bezel is widely utilized for these applications because of its cost effectiveness. However, individual flat display panel should be carefully calibrated to minimize differences in the luminance and color, especially on the border [1].

This paper focuses on the seamless color reproduction for the tiled LCDs with the light emitting diode (LED) backlights. Even though two LCD panels are calibrated based on the CIE 1931 CMFs [2-5] to yield the same CIE XYZ coordinates on their borders, observers may still perceive color differences on the border of neighboring panels. This phenomenon is quite noticeable when the LED backlights have slightly different spectrums [6]. This may be due to the fact that the CIE 1931 CMFs are not accurately reflect the characteristics of the human color perception [7-11]. Nevertheless, most of the commercial color measuring devices utilize the CIE 1931 CMFs to calculate the CIE XYZ coordinates. In addition, the variations in the color perception between the observers with the normal color vision are reported in [12]. This indicates that it is difficult to define the ideal CMFs that overcome the inter-observer variability in the color perception.

In this paper, the CMFs are estimated using the genetic algorithm for the seamless color reproduction in the tiled LCDs with the LED backlights having different spectrums. In [13], the estimation of the CMFs using the genetic algorithm is proposed. However, there is no attempt made to resolve the variations in the color perception between the observers. Furthermore, The Y and Z CMFs are represented by a single Gaussian distribution whereas X CMF is denoted by a mixture of two Gaussian distributions. In the proposed method, the training samples for the genetic algorithm are determined by a two-step procedure to reflect the inter-observer variability in the color perception. In the first step, participants in the color matching experiments are asked to obtain the color matched pairs of the constant patches. In the second step, the rank ordering experiments are performed using the color matched pairs from the first step. The resulting pairs are utilized as training samples for the genetic algorithm. In addition, the XYZ CMFs are represented by the linear combinations of a set of the Gaussian distributions.

In Section 2, the human visual experiments to obtain the training sample for the genetic algorithm are described. The proposed estimation method is outlined. In Section 3, experimental results are discussed. Finally, Section 4 concludes this paper.

2. Proposed Method to Estimate The CMFs

Figure 1 illustrates a flowchart of the proposed method. In the proposed method, human visual experiments are performed to obtain the training samples of the color matched pairs. The XYZ CMFs that minimize the color differences of the color matched pairs are estimated by the genetic algorithm. Each of the procedures in Figure 1 is described next.

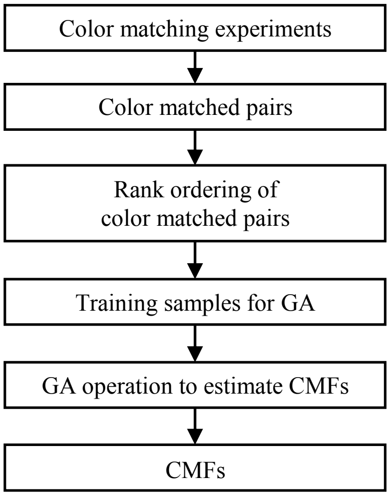


Figure 1. Flowchart of the proposed method

2.1 Visual Experiments to Obtain Training Samples

In the proposed method, two different human visual experiments are performed to reflect the inter-observer variability in the color perception. In the first step, a constant patch is displayed on the reference display. Participants in the visual experiments are asked to adjust the RGB values of the testing display so that there is no perceived color difference in the constant patches displayed on the reference and testing displays. This procedure is repeated for each of the constant patches. After these experiments, a set of the color matching pairs are obtained. The number of the color matching pairs becomes the number of participants.

In the second visual experiments, the color matched pairs obtained from the first experiments are displayed on the reference and testing displays. Participants are asked to rank the perceived similarity using the criterion listed in Table 1 [14]. The scores given by the participants are summed and the color matched pair yielding the minimum value is selected as the training sample for the genetic algorithm. The spectrums of the selected color pairs are measured using a spectroradiometer. This procedure is repeated for each of the constant patches.

Table 1. Criterion of the second visual evaluation

	Definitely different	A little different	Similar	Almost same	Exactly same
Score	4	3	2	1	0

2.2 The Estimation of The CMFs by GA

Gene Structure

The XYZ CMFs to be estimated by the genetic algorithm is represented as a gene. The Y and Z CMFs are represented by a mixture of ten Gaussian distributions. The bimodal X CMF is represented by a mixture of twenty Gaussian distributions. Each Gaussian distribution is denoted by three parameters, as depicted in Figure 2. Consequently, a gene representing the XYZ CMFs has 120 parameters. Each parameter is coded as a 15 bit binary numbers. Table 2 lists the ranges of the values of three parameters.

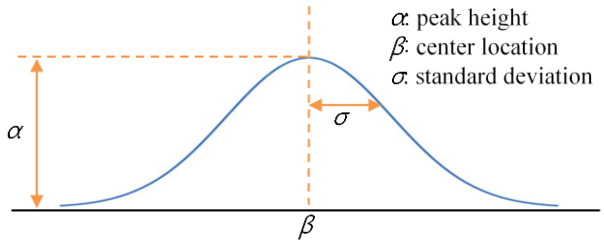


Figure 2. Description of a Gaussian distribution with three parameters

Table 2. Ranges of parameters of Gaussian distribution

CMFs	α		β		σ	
	Min	Max	Min	Max	Min	Max
X_L	-0.3	0.5	45	85	10	30
X_R	-0.5	1.5	180	250	10	40
Y	-0.3	1.5	130	180	20	60
Z	-1.0	2.0	40	90	10	40

Genetic Operations

The objective of the genetic algorithm is to estimate the CMFs that minimize the color differences between the color matched pairs. In order to calculate the probability of the reproduction of a gene, the XYZ color coordinates are calculated for the color matched pairs using the CMFs specified by the gene. The XYZ color coordinates are then converted to the $L^*a^*b^*$ coordinates to calculate the color difference between the color matched pairs. The fitness value for the ith gene is calculated by the following equation.

$$F(i) = \sum_{k=1}^{N} \sqrt{(L_{R,k,i} - L_{T,k,i})^2 + ({a^*}_{R,k,i} - {a^*}_{T,k,i})^2 + ({b^*}_{R,k,i} - {b^*}_{T,k,i})^2} \quad (1)$$

where $(L_{R,k,i}, a_{R,k,i}, b_{R,k,i})$ and $(L_{T,k,i}, a_{T,k,i}, b_{T,k,i})$ represent the $L^*a^*b^*$ coordinates of the kth patch on the reference and testing displays, respectively. They are calculated using the ith CMFs and the spectrums measured from the selected color pairs. In Equation (1), N is the number of the color matched pairs. The reproduction probability for the ith gene is determined by the following equation.

$$Prob(i) = \frac{2}{M} - \frac{F(i)}{\sum_{j=1}^{M} F(j)} \quad (2)$$

where M denotes the number of genes utilized in the genetic algorithm. The CMFs or genes yielding smaller color differences between the color matched pairs have higher reproduction probabilities.

For the crossover operation, 50% of the gene population is randomly selected. Suppose that the ith and jth genes are the pair of the genes selected for the crossover operation. The locations of the bit exchange between the ith and jth genes are randomly selected and their bits are exchanged. The number of the exchanged bits is 50% of the total number of bits assigned to a given gene. For the mutation operation, 20% of the gene population is randomly selected. From the selected gene, 1% of the bit locations within the gene are randomly selected and their binary values are swapped. These genetic operations are repeated until the pre-determined stopping criterion is satisfied.

3. Experimental Results

3.1 Visual Experiments to Obtain Training Samples

Figure 3 illustrates twenty one constant color patches utilized in the two-step visual experiments to determine the training samples for the genetic algorithm. The two LCD displays with the LED backlights were utilized for the experiments. The spectrums of the two displays were measured using a spectroradiometer. Figure 4 (a) and (b) illustrates the spectrums of the reference and testing displays, respectively. The differences in the measured spectrums can be noticed in Figure 4.

Twenty five university students with normal corrected vision participated in the visual experiments. In the first step, participants were asked to obtain the color matched pairs for each of the twenty one constant patches in Figure 3. Consequently, the twenty five color matched pairs were determined for each of the twenty one constant patches. In the second step, participants were asked to rank the perceived similarity between the twenty five color matched pairs using the criterion listed in Table 1. The color matched pair yielding the lowest sum of the scores were selected as the training sample for the genetic algorithm. Figure 5 illustrates an example of a histogram of the averaged scores from the second visual experiments. In Figure 5, the vertical axis represents the averaged scores from the second visual experiments and the horizontal axis denotes the number of the color pairs that are sorted in ascending order.

3.2 Estimation of the CMFs by Genetic Algorithm

The XYZ CMFs to be estimated were represented as genes. The Y and Z CMFs were represented by a mixture of ten Gaussian distributions whereas the bimodal X CMF was represented by a mixture of twenty Gaussian distributions. Each Gaussian distribution was denoted by three parameters specified in Figure 2. Consequently, a gene representing the XYZ CMFs had 120 parameters. Each parameter was coded as a 15 bit binary numbers. Thus, each gene had 1,800 bits (=120 parameters * 15 bits). The initial population for the genetic algorithm consisted of 3,000 genes. Three genetic operations, the reproduction, crossover and mutation, were applied through 1,000 generations. Figure 6 presents a graph of the sum of the fitness values during 1,000 generations. In Figure 6, the vertical axis represents the sum of the fitness values specified in Equation (1) and the horizontal axis denotes the number of iterations. Because the fitness value represents the color difference, it should be minimized. It can be noticed from Figure 5 that the sum of the fitness values are saturated after 600 iterations.

Figure 7 (a) and (b) illustrates the CIE 1931 CMFs and the CMFs estimated by the proposed method, respectively. The wavelength yielding the maximum value of the XYZ CMFs are listed in Table 3.

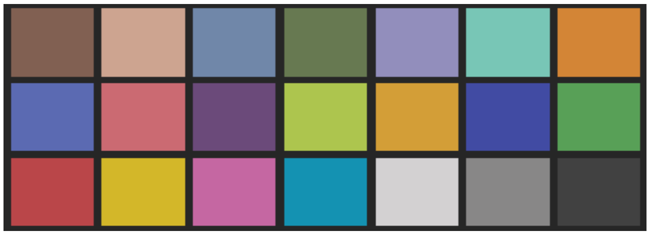
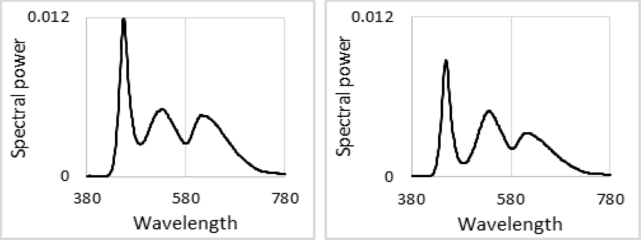


Figure 3. Color patches used to determine the training set



(a) Spectrum of reference display (b) Spectrum of testing display

Figure 4. Spectrums of the reference and testing displays

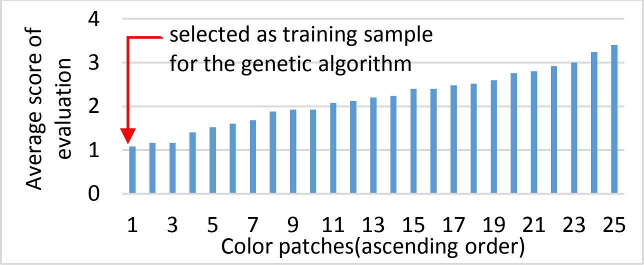


Figure 5. An example of the second visual experiments to determine the training samples for the genetic algorithm

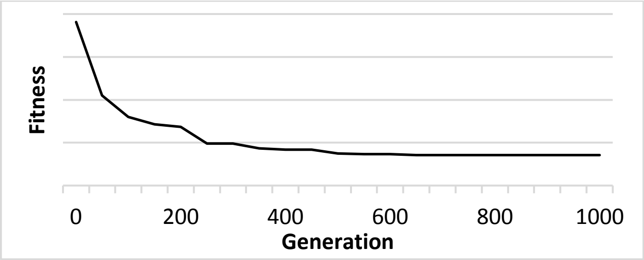
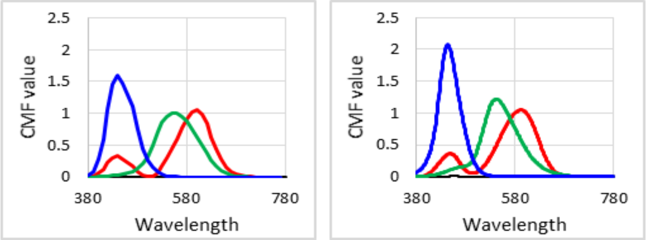


Figure 6. Change of fitness values during GA iterations



(a) CIE 1931 XYZ CMFs (b) Estimated CMFs by GA

Figure 7. CMFs of the CIE 1931(a) and CMFs by the proposed method

Table 3. The wavelengths that yield the maximum values of the XYZ CMFs

	X CMF	Y CMF	Z CMF
CIE 1931	600 nm	550 nm	440 nm
Proposed	591 nm	542 nm	443 nm

3.3 Performance Evaluation with Training Samples

The effectiveness of the proposed CMFs was compared with that of the CIE 1931 CMFs, CIE 2006 CMFs [15] and the CMF proposed in [13]. The XYZ coordinates of the selected color pairs were calculated using the aforementioned four different CMFs and the spectrums measured from the selected color pairs using a spectroradiometer. The resulting XYZ coordinates are then converted to the $L^*a^*b^*$ coordinates to calculate the color difference between the color matched pairs. Table 4 lists the values of ΔE that are averaged over the twenty one training samples. The proposed CMFs yields the smallest value of 2.5 among the four different CMFs tested in this experiment.

3.4 Performance Evaluation with Testing Samples

The performance of the proposed CMFs was evaluated using the testing samples that were not utilized in the estimation of the CMFs by the genetic algorithm. The twenty testing samples were randomly selected in the (R,G,B) color space. Unlike the previous experiment with the training sample, the color matched pairs for the testing samples were determined using the device characterization procedure [1].

Figure 8 illustrates a flowchart of the color matching using the four different CMFs utilized in this experiment. In order to perform the device characterization for the testing display, the patches of grays and RGB primaries were displayed on the testing display. The spectrums of the grays and RGB primaries were measured by a spectroradiometer. In addition, the XYZ coordinates of the grays and RGB primaries were calculated using the measured spectrums and the CMFs selected for this experiment. Consequently, four sets of the XYZ coordinates were determined for each of twenty testing samples. Finally, the XYZ-to-RGB conversion matrices were determined for the testing display.

Each of the testing samples was displayed on the reference display. The spectrum of the testing sample on the reference was measured by a spectroradiometer. In addition, the XYZ coordinates of the testing sample were calculated using the measured spectrums and the CMFs selected for this experiment. The color matched pair on the testing display is then calculated using the XYZ-to-RGB conversion matrices determined for the testing display.

The color matched pairs for the testing samples were displayed on the reference and testing displays. It should be mentioned that non-uniformity of the luminance between the reference and testing displays was compensated in advance. The human visual experiments were performed. Participants are asked to rank the perceived similarity using the criterion listed in Table 1 [14]. The scores given by the participants are averaged and listed in Table 5. The proposed CMFs yields the smallest score of 0.88. This value is in-between 'almost the same' (=1) and 'exactly same' (=0) in Table 1.

Table 4. Color difference of the training samples

	CIE 1931	CIE 2006	Ozaki et al.[13]	Proposed
Average ΔE	3.86	3.15	4.04	2.50

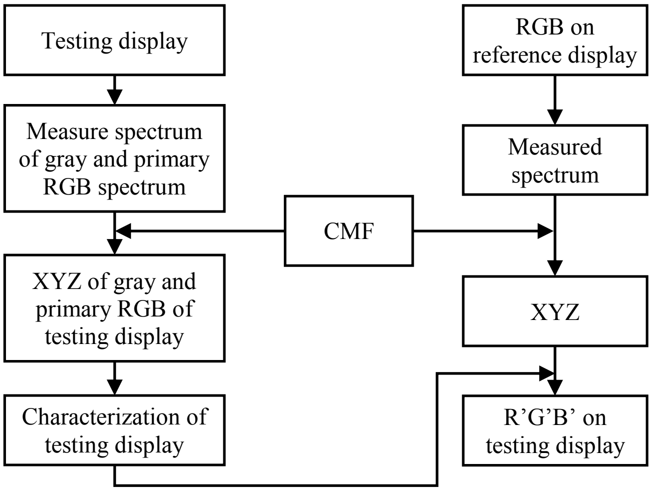


Figure 8. Flowchart of the color matching procedure for testing samples for evaluating CMFs

Table 5. Result of subjective evaluation with testing samples

	CIE 1931	CIE 2006	Ozaki et al.[13]	Proposed
Average score	1.69	1.39	1.93	0.88

4. Conclusion

In this paper, the CMFs are estimated using the genetic algorithm for the seamless color reproduction in the tiled LCDs with the LED backlights having different spectrums. In the proposed method, the training samples for the genetic algorithm are determined by a two-step procedure to reflect the inter-observer variability in the color perception. In the first step, participants in the color matching experiments are asked to obtain the color matched pairs of the constant patches. In the second step, the rank ordering experiments are performed using the color matched pairs from the first step. The resulting pairs are utilized as training samples for the genetic algorithm. In addition, the XYZ CMFs are represented by the linear combinations of a set of the Gaussian distributions. Experimental results indicate that the proposed CMFs yields the smallest color differences for the training and testing samples among four different CMFs utilized in the experiments.

Acknowledgement

This work was supported by the research grant from Samsung Electronics.

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