

# Metameric Observers: A Monte Carlo Approach

Mark D. Fairchild & Rodney L. Heckaman, Rochester Institute of Technology, Rochester, New York 14623

## Abstract

*No two observers perceive color the same. To one observer, the colors of two objects might match perfectly; yet to another, those same two objects might not match depending on the spectral characteristics of the colors of the two objects, their illuminant, and each of the observer's spectral eye response. Here we create a large, representative group of such observers – said to be metameric - from data that characterizes the variability in these characteristics over the human population. Further, we show that the degree of mismatch between any metameric pair of objects might be large enough that the color naming of each object can be different for certain observers.*

## Background

No two observers perceive color the same. To one observer, the colors of two objects might match perfectly; yet to another, those same two objects might not match depending on the spectral characteristics of the two objects, their illuminant, and each of the observer's eye response. Minimizing this, the effect of observer metamerism, is an important yet difficult problem for those in the field of making and using colorants – dyes and dyers, paint and painters, and color displays and projectors – particularly as observer metamerism has been difficult to quantify. To this end, CIE publication 801<sup>1</sup> describes a procedure based on replacing a standard colorimetric observer with what they term as the standard normal deviate observer. However, this procedure is rarely used in practice simply because it cannot possibly be representative of the entire population of human observers<sup>2,3</sup>. And yet, the differences in the factors that affect the spectral response of the human eye have been made available only in the last few years so that observer metamerism can be

realistically quantified over a representative population of human observers.

## Computational Model of Color Matching Functions

The color matching experiment used to derive maximum-saturation estimates of color matching functions with monochromatic primaries can be characterized as a system of three linear equations (Equation 1) with three unknowns at each wavelength. Given that a unit of energy of wavelength,  $\lambda$ , is matched by RGB amounts of three monochromatic primaries of unit energy at wavelengths  $\lambda_R, \lambda_G, \lambda_B, T_l$  and  $T_m$ , are the spectral transmittances of the lens and macula respectively,  $L, M$ , and  $S$ , are the cone spectral responsivity functions, and  $R, G$ , and  $B$ , are the spectral tristimulus values. Solving Equation 1 for  $R, G$ , and  $B$ , at each wavelength results in the determination of a set of color-matching functions for the  $\lambda_R, \lambda_G$ , and  $\lambda_B$ , monochromatic primaries. Normalization of the color matching functions after they are obtained might be desired for some applications, but is not required.

## Monte Carlo Simulation of Individual Observer Color Matching Functions

Equation 1 can be used to derive simulated individual color matching functions by choosing appropriate values for the  $T_b, T_m, L, M$ , and  $S$  for a particular individual. Populations of simulated color matching functions can be derived by randomly selecting the  $T_b, T_m, L, M$ , and  $S$  values from the distributions in their values observed in the human

population. Such a collection of simulated color matching functions can then be used to

$$\begin{vmatrix} T_l(\lambda)T_m(\lambda)L(\lambda) \\ T_l(\lambda)T_m(\lambda)M(\lambda) \\ T_l(\lambda)T_m(\lambda)S(\lambda) \end{vmatrix} = \begin{vmatrix} R(\lambda)T_l(\lambda_R)T_m(\lambda_R)L(\lambda_R) + G(\lambda)T_l(\lambda_G)T_m(\lambda_G)L(\lambda_G) + B(\lambda)T_l(\lambda_B)T_m(\lambda_B)L(\lambda_B) \\ R(\lambda)T_l(\lambda_R)T_m(\lambda_R)M(\lambda_R) + G(\lambda)T_l(\lambda_G)T_m(\lambda_G)M(\lambda_G) + B(\lambda)T_l(\lambda_B)T_m(\lambda_B)M(\lambda_B) \\ R(\lambda)T_l(\lambda_R)T_m(\lambda_R)S(\lambda_R) + G(\lambda)T_l(\lambda_G)T_m(\lambda_G)S(\lambda_G) + B(\lambda)T_l(\lambda_B)T_m(\lambda_B)S(\lambda_B) \end{vmatrix} \quad (1)$$

computationally estimate mean color matching functions along with their spectral variance and covariance functions. Such an estimate can then be considered a candidate for a standard colorimetric observer system, complete with covariance functions as originally proposed by Nimeroff<sup>4</sup> and Nimeroff et al.<sup>5</sup> Such a system was previously derived by Monte Carlo simulation by Fairchild<sup>6</sup> using a model of color matching functions similar to the CIE 2006 model<sup>3</sup>. The key step, and novel contribution of this work relative to previous instantiations, is an accurate simulation of a population of color matching functions is accurate estimation of the baseline spectral  $T_b$ ,  $T_m$ ,  $L$ ,  $M$ , and  $S$  functions along with estimates of the magnitude and statistical distribution of their variability in the human population. This significantly increases the accuracy of the created populations of color matching functions. Derivation of these spectral functions is described in the following sections.

### Lens Spectral Transmittance

The lens spectral transmittance function in the color matching function simulation is derived from the two-component model of Pokorny and Smith<sup>7</sup> [see also Pokorny *et al.*<sup>8</sup>, Xu et al.<sup>9</sup>]. According to the two-component model, the lens spectral transmittance is made up of one component,  $TL_2$ , that remains stable after age 20 and a second component,  $TL_1$ , the portion affected by aging. Data for  $TL_1$  and  $TL_2$  are presented in Pokorny and Smith as shown in Figure 2. Average lens transmittance functions are then computed as a function of observer age,  $A$ , using Equation 2 for observers between the ages of 20 and 60 years and Equation 3 for observers older than 60 years.

$$T_l = T_{L1}[1 + 0.02(A - 32)] + T_{L2} \quad (2)$$

$$T_l = T_{L1}[1.56 + 0.0667(A - 60)] + T_{L2} \quad (3)$$

To represent a population of observers for the Monte Carlo simulation of color matching functions, the observer age,  $A$ , was randomly selected according to the probability density function defined by the histogram of

ages in the population of the United States during the 2000 census<sup>10</sup> as shown in Fig. 1.

Additionally, the lens transmittance has random variation between observers of identical age. Pokorny and Smith characterized this variability in terms of variation in the age predicted by the model for observers of a given age. This variability, expressed in terms of age,  $A$ , in the two-component model, was found to have a standard deviation of 20% of the actual age. This added variability is represented in the Monte Carlo color matching function model by first selecting an observer age randomly from the census-data distribution, and then randomly perturbing that age using a normal distribution with a standard deviation equal to 20% of the initially selected age according to Equation 4.

$$A = A_{census} + \delta \quad (4)$$

$A$  is the age ultimately used for a random individual observer in the simulation,  $A_{census}$  is the age initially selected from the census-data distribution (limited to the range from 20-75 years), and  $\delta$  is a normally-distributed random variable with a mean of 0.0 and standard deviation of  $0.20A_{census}$ . The result is essentially to low-pass filter the census-data histogram. This added variability is only likely to be important in the Monte Carlo model if small population sizes were simulated.

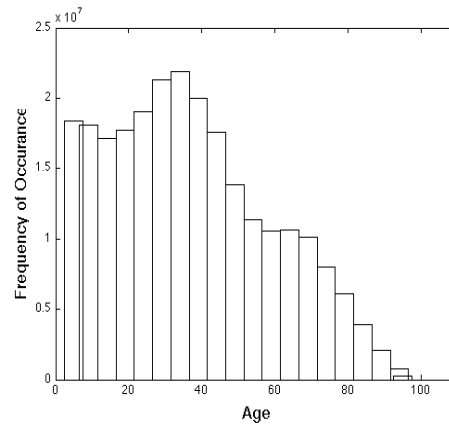


Figure 1: Age distribution from the 2000 US census

## Macula Spectral Transmittance

The baseline macular pigment spectral density (converted to transmittance for the simulation of color matching functions) function used is that of Bone *et al.*<sup>11</sup> and available online<sup>12</sup>. These data are similar to others that have been published and described [Porkorny and Smith, Berendschot and van Norren<sup>13</sup>, and the CIE<sup>3</sup>].

Berendschot and van Norren estimate that the standard deviation of peak macular density is 0.13. This value, along with a normal distribution, were used in the Monte Carlo simulation. It was assumed that the variability across observers is multiplicative in density to preserve zero density values for all observers at the wavelengths where the macular pigment does not absorb light and simulate the reported standard deviation at the peak density. The Bone *et al.* data have a peak macular density of 0.352. Thus, Equation 5 was used to scale the baseline macular function randomly to represent various individual observers.

$$D_m(\lambda) = D_{m,Bone}(\lambda) \left[ \frac{0.352 + \delta}{0.352} \right] \quad (5)$$

$D_m$  is the individual macular density function (converted to transmittance for the color matching function simulation),  $D_{m,Bone}$  is the average function of Bone *et al.* (1992) illustrated in Figure 2, and  $\delta$  is a normally-distributed random variable with a mean of 0.0 and standard deviation of 0.13.

## Cone Responsivity Functions

The baseline cone spectral responsivity functions (sometimes called cone fundamentals) are those derived by Stockman and Sharpe<sup>14</sup> and available online<sup>15</sup> and plotted in Figure 2. The variability in cone spectral responsivity functions across observers has been studied recently through both genetic and psychophysical techniques. Sharpe *et al.*<sup>16</sup> provide a summary of the distributions of L- and M-cone responsivity functions in a population of observers. Their data were used to derive a statistical representation of these distributions for the Monte Carlo simulation of color matching functions. The

S-cone responsivity function is taken to have no variability between observers since it has been less well studied and any variability will be small compared to the variability in color matching functions caused by the lens and macula transmittance functions.

Neitz and Neitz<sup>16</sup> in their description of the molecular genetics of normal color vision describe the complexity of the L- and M-cone responses as having peak sensitivities mediated by the spectral wavelength tuning of their respective genes. This tuning gives rise to discrete spectral variants encoded into the X chromosome gene array – particularly in those of the L photo-pigment. However, the Sharpe *et al.*<sup>17</sup> results show that both L- and M-cone peak wavelengths are not discretely related to genotype, but have a rather continuous range of variation. They attribute this to differences in ocular media transmittance, cone shape, and pigment density. Thus, their data are summarized as a statistical normal distribution of peak wavelengths with the L-cones having a standard deviation of 1.6 nm in peak wavelength and the M-cones a standard deviation of 2.5 nm.

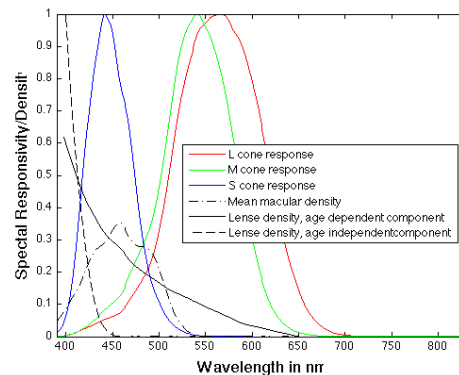


Figure 2: Baseline L, M, and S cone spectral responsivities according to Stockman and Sharpe<sup>15</sup>, Baseline macula spectral density  $D_{m,Bone}(\lambda)$  according to Bone *et al.*<sup>11</sup>, and the age dependent and independent lens density according to Pokorny and Smith<sup>7,8,9</sup>

The L- and M-cone spectral responsivity functions were randomly selected from a population with means corresponding to the Stockman and Sharpe<sup>15</sup> functions and peak wavelengths distributed as follows. The mean cone responsivity functions are first transformed from wavelength (nm) to wave-

number (cm-1) where the functions are shifted additively to represent various individual functions. The wavenumber representation is used to be consistent with the work of Dartnall<sup>18</sup> and Wyszecki and Stiles<sup>19</sup> illustrating that absorption curves typically retain their shape across changes in peak wavelength when represented on a wavenumber scale.

The wave number offsets were randomly selected from normal distributions with mean wave number offset of 0 cm<sup>-1</sup> and standard deviations of 51 cm<sup>-1</sup> for L cones and 89 cm<sup>-1</sup> for M cones. Once shifted in peak wavenumber, the functions were then converted back to the wavelength scale to compute simulated color matching functions.

### Results and Discussion

Figure 3 illustrates the S-, M-, and L-cone spectral responses shown as blue, green and red respectively and computed via Equation 1 for 1,000 simulated individuals randomly sampled from the statistics of cone responsiveness, macula density, and lens aging as detailed in the above. The variability in S-cone response arises exclusively from variability in macula density and lens aging which, in turn, combine to give a double peak in response not only in the S-cones, but in the M-cones to a lesser extent as effects of macula and lens density vary contrary to each other thereby modulating cone response.

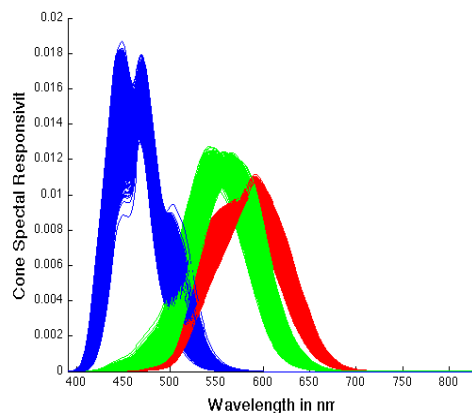


Figure 3: Cone spectral responses for 1000 simulated individual observers randomly sampled from the  $T_s$ ,  $T_m$ ,  $L$ ,  $M$ , and  $S$  values of Equation 1

Figure 4 illustrates variation in perception of each of the 24 X-Rite Color Checker patches across the 1,000 simulated observers in CIE 1976 L\*a\*b\*. As shown, the distributions expand considerably in the higher chroma colors as the spectra of these colors narrow with increased sensitivity to variations in observer response. Conversely, the distributions contract as the neutral axis is approached and their respective spectra broaden with less sensitivity to observer variation.

The extent of each of these patch's variability across the 1,000 simulated observers compare at least within an order of magnitude with those reported by Alvin and Fairchild<sup>20</sup> and Sarkar *et al.*<sup>21</sup> based in Stiles and Burch<sup>22</sup> and the CIE 2006 model. Further, a category sort of the variation for each of the patches and over the 1,000 observers found no reliable categories as in the eight (8) categories found by Sarkar *et al.*

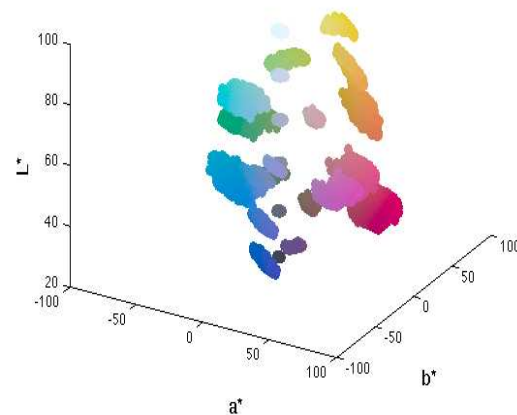


Figure 4: Variations in perceived color of the 24 X-Rite Color Checker patches for each of the 1,000 simulated observers in CIE 1971 L\*a\*b\*

In order to illustrate the degree of observer metamerism occurring across the simulated observers, two sets of Gaussian colorants shown in Figure 5 were chosen with peak wavelength at the points of maximum variance in the cone spectral responses for these simulated observers. The concentrations of these two sets of colorants were computed for each patch in the X-Rite Color Checker so that the resulting metameric pairs shown spectrally in Figure 6 match for the CIE 1931 2° Observer. The widths of the Gaussian shaped colorants were adjusted to 75 nm where a minimum of negative going concen-

trations occur. As shown, only patch 15, red, exhibited any negative concentration of significance.

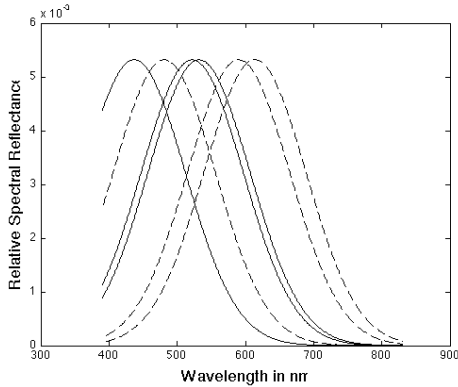


Figure 5: The relative spectral reflectances of two sets of Gaussian-shaped colorants of width 75 nm and with peak wavelength chosen at points of maximum variability for the 1,000 simulated observer cone spectral responses.

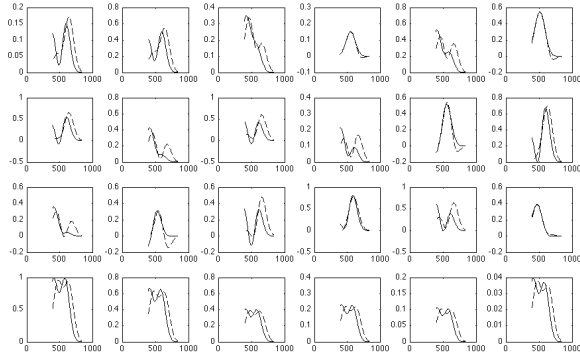


Figure 6: Spectral reflectances of the metameric pairs for each of the 24 X-Rite Color Checker patches that match for the CIE 1931 2° Observer

Finally, the degree of mismatch was computed in CIE DE94 (Selected over DE2000 for computational efficiency and accuracy) for each pair and for each of the 1,000 simulated observers. Figure 7 illustrates on the left of each patch the match for the standard observer and, on the right, the degree of mismatch for the 95<sup>th</sup> percentile simulated observer in CIE DE94 where this observer's CIE DE94 is given in Table 1. Clearly and in lieu of patch 15, the color naming of many of the 24 metameric pairs would be different for the 95<sup>th</sup> percentile simulated observer - even in the neutrals. Further research is being completed with color name boundaries and psychophysical confirmation to establish this point unequivocally.

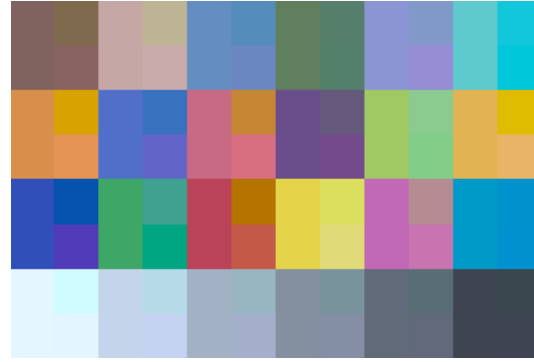


Figure 7: The metameric pairs for each of the 24 X-Rite Color Checker patches as seen by the standard observer on the left and the 95<sup>th</sup> percentile simulated observer on the right.

Table 1: CIE DE94 between the metameric pairs for each of the 24 X-Rite Color Patches and the 95<sup>th</sup> percentile simulated observer.

10.5	13.1	8.4	0.4	8.6	1.1
20.0	8.9	22.9	4.0	1.1	8.6
8.6	2.9	33.0	2.8	15.0	1.6
13.6	12.5	10.7	9.0	7.0	5.3

## Conclusions

A model of observer metamerism was demonstrated using Monte Carlo techniques from newly available data on the physiological variations in color vision that can be said to be representative of the human population. The model was applied to the creation of a 1,000 simulated observers representative of the human population. Metameric pairs of each of the 24 patches of the X-Rite Color Checker demonstrated that the degree of mismatch between these pairs can, in some observers, have different color names.

Currently, the set of simulated observers are being analyzed using the techniques of the analysis of variance as suggested by Nimroff *et al.*<sup>5</sup> to further authenticate the model as representative of the human population by a more direct comparison with previous work.

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