Corresponding-pair procedure: a new approach to simulation of dichromatic color perception

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The dichromatic color appearance of a chromatic stimulus **T** can be described if a stimulus **S** is found that verifies that a normal observer experiences the same sensation viewing **S** as a dichromat viewing **T**. If dichromatic and normal versions of the same color vision model are available, **S** can be computed by applying the inverse of the normal model to the descriptors of **T** obtained with the dichromatic model. We give analytical form to this algorithm, which we call the corresponding-pair procedure. The analytical form highlights the requisites that a color vision model must verify for this procedure to be used. To show the capabilities of the method, we apply the algorithm to different color vision models that verify such requisites. This algorithm avoids the need to introduce empirical information alien to the color model used, as was the case with previous methods. The relative simplicity of the procedure and its generality makes the prediction of dichromatic color appearance an additional test of the validity of color vision models. © 2004 Optical Society of America

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1. INTRODUCTION

We describe what a dichromat really perceives when shown a given chromatic stimulus **T** (test), in terms that a subject with normal color vision can understand. The problem, often approached in the literature,[1–5] would be solved if we found a stimulus **S** (simulation) that verifies that the sensation experienced by the dichromat seeing **T** is the same as that of a normal subject seeing **S** under certain reference conditions.

Brettel and co-workers[4,5] have proposed the most recent solution to this problem. Their idea is that since different colors (Gamut I) can be perceived by a dichromat as equal to **T**, if one of the colors had the additional property of having the same appearance for normals and for the dichromat, this would be the simulation **S** that we are looking for. Therefore **S** belongs to the intersection of Gamut I and the set of colored stimuli whose appearance is the same for normals as for that dichromat (Gamut II). The rationale of their algorithm, then, is the computation of the intersection of Gamuts I and II in a particular color space, namely, a linear cone-excitation space with the Stockman *et al.* fundamentals.[6]

As we discuss in Section 2, both the color space used in this algorithm and the way Gamut II is derived may be improved. In fact, the rationale of the algorithm can be generalized for use with more advanced color vision models. The eventual benefits of this generalization include the possibility of a more accurate description of the experimental behavior of dichromats. However, this generalization presents several drawbacks:

1. With some models, Gamut I must be computed numerically (Section 3).
2. Experimental information on Gamut II (the colors perceived as equal by normals and dichromats) was introduced *ad hoc*; i.e., in the formulation of Brettel and co-workers[4,5] the algorithm requires information that is not contained in the particular color space they operate with. This requirement could be avoided by use of more general models. However, when one is dealing with such models, the computation of Gamut II poses several problems: (a) Not all models can predict the set of colors perceived as equal by normals and dichromats (see Section 4). (b) Even when they do, the existence and uniqueness of the intersection with Gamut I is not guaranteed (see Section 4). (c) In any case (assuming Gamut II can be computed and assuming that the intersection exists and is unique), Gamut II is obtained at high computational cost (see Section 3).

In this paper we propose an alternative algorithm, the corresponding-pair procedure that does not involve the computation of Gamuts I and II. Our procedure can be applied only to color models that fulfill certain conditions, but, as we will show, these conditions are also required by the generalized Brettel *et al.*[5] algorithm. In this way, the corresponding-pair procedure solves the problems described above, without introducing additional constraints on the color vision model.

2. DISCUSSION OF THE BRETTEL *et al.* ALGORITHM

As we said above, the algorithm by Brettel and co-workers[4,5] requires the computation of two color sets, Gamut I and II. In the linear LMS space, the Gamut I is a line containing **T** and parallel to the long (L), the middle (M), or the short (S)-wavelength-sensitive axis for protanopes, deuteranopes, and tritanopes, respectively.

The difficulty with this algorithm is determining Gamut II. If we consider subjects with a normal and a dichromatic eye (a unilateral dichromat), we will find two spectral stimuli λ_1 and λ_2, verifying that each of them elicits the same sensation in both eyes of the subject, with the possible exception of brightness.[7–17] The values of λ_1 and λ_2 are characteristic of each type of dichromacy.

Brettel and co-workers[4,5] assume that λ_1, λ_2, the equal-energy white, and all mixtures of λ_1 and λ_2 with white are perceived as equal by a normal and a dichromatic eye, brightness included. Therefore these stimuli constitute Gamut II. In the linear LMS space these mixtures lie on two hemiplanes intersecting in the axis defined by the white stimulus. The simulation **S** is the intersection of the confusion line containing **T** and one of these two hemiplanes.

Let us discuss some relevant aspects of the construction of Gamut II. Although it is assumed that any stimulus in Gamut II shown to the normal and the dichromatic eyes of a unilateral dichromat has the same appearance, in fact the relative luminances of the stimuli presented to each eye must be adjusted to reach a perfect match.[11–13] A clear exception is Alpern's unilateral tritanope,[10] who perceived these stimuli as equal with the same luminance. In most studies in this field, however, luminance is not one of the free parameters of the experiment. Brettel and co-workers also simplify the problem by assuming that luminance must not be adjusted.

As Brettel and co-workers themselves point out, the choice of λ_1 and λ_2 is not a simple task, as can be seen from an analysis of the literature on unilateral color vision defects.[7–17] It is commonly accepted that dichromats perceive only two hues and discriminate along what a normal subject would call a saturation axis, with zero saturation for the neutral point. These hues are a blue and a yellow for protanopes and deuteranopes, and a green and a red or purplish-red for a tritanope, but, owing to the large dispersion of the experimental results, the agreement among researchers ends here. For instance, for deuteranopic observers, values as far apart as 450 nm,[13] 451–453 nm,[11] 470 nm,[14,15] and 473–476 nm[16] have been found for the blue stimulus; and 560–570 nm,[14,15] 584 nm,[11] 580–595 nm,[13] and even 610 nm[16] have been reported for the yellow one.

This disparity is due largely to the problem of correctly diagnosing the subjects. Not all the subjects reported as unilateral dichromats had a normal and a dichromatic eye. In some cases, the experimental evidence suggests that unilateral dichromats are really anomalous subjects with different degrees of anomaly in each eye.[7,8,11,12,14–17] Even worse, the diagnosis is dubious in many cases. However, the important point is that in the matching experiments with unilateral dichromats, the subject is allowed to change the wavelength and the luminance, but not the colorometric purity, of the stimulus viewed by the normal eye to match the appearance of the stimulus seen by the dichromatic eye. Alpern's[10] study of a tritanope subject is the exception. Therefore, strictly speaking, we cannot affirm that there are spectral stimuli perceived as equal by normals and dichromats. Finally, Alpern's paper demonstrated that the psychophysical matching method used (haploscopic matching versus hue naming) influences the results. In fact, the 660-nm stimulus used in the model by Brettel and co-workers is perceived as equal by both eyes of a unilateral tritanope only in a hue-naming experiment.

The colors used by Brettel and co-workers to obtain Gamut II are 475 and 575 nm for protanopes and deuteranopes and 485 and 660 nm for tritanopes. In spite of what we have discussed up to this point, this choice is certainly not arbitrary. It may be reasonably assumed that for a normal observer, 475, 575, and 485 nm are free of the Abney effect.[18] Thus a change in colorimetric purity would, at least, not produce a hue change either for a normal observer or, from the definition of Gamut II, for a dichromatic observer. This property, however, is not verified in the neighborhood of 660 nm.[18]

3. CORRESPONDING-PAIR PROCEDURE

If dichromatic and normal versions of the same color vision model are available, the tristimulus values of **S** can be obtained by applying the inverse of the normal model to the color descriptors of **T** computed with the dichromatic model (Fig. 1). That is,

$$\mathbf{S} = m^{-1}(m(\mathbf{T}, \mathbf{p}'), \mathbf{p}), \tag{1}$$

where m is a mathematical operator comprising all the transformations of the model from the tristimulus values to the perceptual stage and $\mathbf{p}'$ and $\mathbf{p}$ are, respectively, the set of parameters defining the dichromat and the normal observers (see Appendix A for an example). Equation (1) is formally identical to the corresponding-pair equation in the literature on chromatic adaptation, where $\mathbf{p}'$ and $\mathbf{p}$ would represent two different adaptation conditions. Therefore we will call this strategy the corresponding-pair procedure and will refer to **T** and **S** as a corresponding pair.

Equation (1) is valid only if model m verifies certain conditions. In the first place, to avoid having an infinite number of solutions, the number of descriptors of normal and dichromatic color appearance must be the same. Second, the normal model must be invertible, either analytically or numerically. Finally, for **S** to be real, the values of the dichromatic perceptual descriptors for each stimulus must lie within the range of those of the normal observer.

The general form of Eq. (1) may be simplified if the algorithms of the dichromatic and the normal model coincide beyond a given stage, since it would suffice to compute the inverse of the output of the last stage in which the two models differ (again, see Appendix A). Note that with some models we might be forced to invert from the perceptual stage. This is the case, for instance, for ATD95,[19,20] if we admit that the dichromatic subjects lack

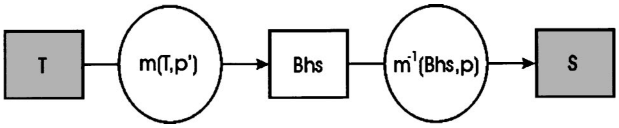


Fig. 1. Corresponding-pair procedure. The stimulus **S** that produces the same sensation in a normal observer as stimulus **T** in a dichromat is the corresponding pair of **T** for the normal observer. **S** is obtained by inverting the dichromatic perceptual descriptors of **T**, **BhS** (brightness, hue, and saturation, or whatever color descriptors are given by the model), with the normal model. If the perceptual descriptors are computed from the output of more than one stage of the model, as happens with ATD95, we must invert the model from the perceptual stage. If the perceptual descriptors of the model are computed from its last opponent stage, it suffices to invert the model from that stage. This is the case for linear ATD models, for instance.

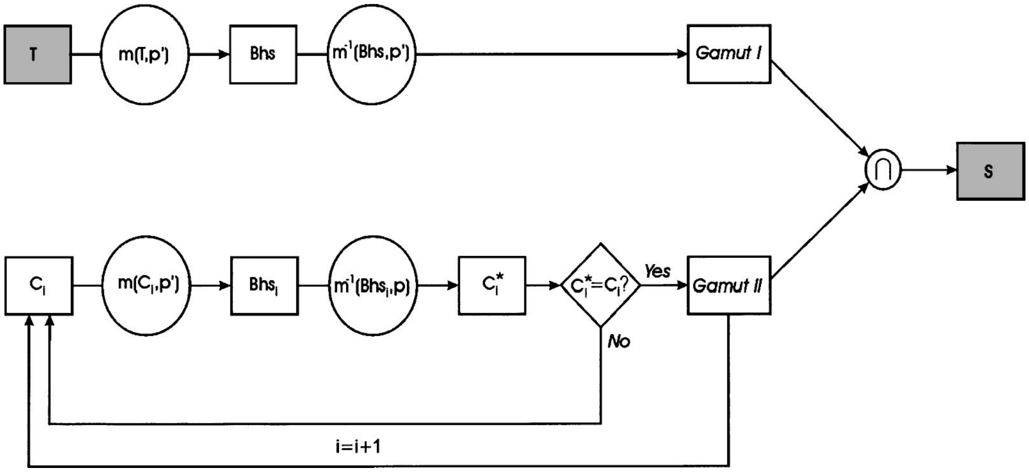


Fig. 2. Algorithm of Brettel *et al.*[5] The stimulus **S** that produces the same sensation in a normal observer as stimulus **T** in a dichromat is the intersection of Gamut I and Gamut II. Gamut I changes with **T** and contains those colors that have the same perceptual descriptors as **T**, computed with the dichromatic model. Gamut II (which is independent of **T**) is the set of colors perceived equally by normals and dichromats. When these gamuts cannot be described analytically, an iterative algorithm may be used to obtain them. For example, for Gamut II the algorithm starts from a random vector $\mathbf{C}_i$. This vector belongs to Gamut II if the vector that produces the same sensation in a normal, $\mathbf{C}_i^*$, is also $\mathbf{C}_i$. If samples $\mathbf{C}_i$ are taken from a dense enough grid, a good estimate of Gamut II can be obtained.

certain opponent mechanisms in both opponent stages. The reason is that hue and saturation depend on the second-opponent-stage descriptors, whereas brightness is computed from the first-opponent-stage responses. With inversion from the second stage only, **T** and **S** would have different brightness.

Using the same notation as in Eq. (1), we describe in Fig. 2 the strategy used by Brettel *et al.*[5] If this generalized algorithm is to be applied to a given model, it must verify the same properties as the corresponding-pair algorithm. But the algorithm of Brettel *et al.* additionally requires the inverse of the dichromatic model. This inverse is not unique, and when its analytical form is not available, it must be computed with an iterative process. With the inverse of the normal model, we must compute those colors that have the same descriptors for normals and dichromats. In the worst case, even if the analytical form of this inverse is available, to obtain Gamut II we must resort again to an iterative algorithm (see Fig. 2 for an example). If the analytical forms of Gamut I and II are known, either because they can be computed with the model or because additional information is used, as was done by Brettel and co-workers, the strategy can be notably simplified. Nonetheless, for any model m that verifies the requisites of Eq. (1), the computational cost of this strategy is, in general, significantly greater than that of the corresponding-pair procedure. The advantage of the corresponding-pair procedure is that the same solution is reached with a simpler algorithm.

4. SIMULATION OF DICHROMATIC COLOR APPEARANCE WITH DIFFERENT MODELS

The main difficulty of the corresponding-pair procedure lies in finding an appropriate color vision model. This is also the case when we try to apply the generalized Brettel *et al.*[5] algorithm. In what follows, we show examples of one-opponent-stage linear models (Ingling and Tsou,[21] Guth *et al.*,[22] Boynton[23]), two-opponent-stage linear models (De Valois and De Valois in their 1993 version[24]; nothing changes significantly if the 1997 version[25] is used) and two-opponent-stage nonlinear models (Guth's ATD95[19,20] and Seim and Valberg's SVF formula[26]). Our aim is not to determine which model is best but to show how using the corresponding-pair procedure with different models is simpler than using the generalized Brettel *et al.* algorithm. We proceed with each model in the same way: Different hypotheses are introduced to obtain dichromatic versions of each model that meet the requisites of Eq. (1); these dichromatic versions are then used to compute the corresponding pairs of a set of test colors.

Dichromatic versions of the color vision models were obtained with two hypotheses:

1. Substitution hypothesis. Dichromacy arises from the substitution of one photopigment by another (M by L for protanopes, L by M for deuteranopes, and L or M by S for tritanopes), but the subsequent neural circuitry is normal.[27]
2. Nulling hypothesis. Photopigments are changed as in the substitution hypothesis, and one of the opponent chromatic mechanisms (red–green for protanopes and deuteranopes, blue–yellow for tritanopes) is nulled in some or all of the opponent stages of the model.[28–30]

A. Example 1: Dichromatic Appearance of Equiluminant Colors

To predict the dichromatic color appearance of equiluminant colors with our algorithm, we generated a 100 × 100 grid that covers the chromaticity diagram, from which we selected only the chromaticities corresponding to real colors. The luminance level does not change the results when the linear models are used. With the nonlinear models, we considered two luminance levels: 10 and 100 cd/m^2, although only the results for 10 cd/m^2 are shown.

The corresponding pairs of these colors were computed by particularizing Eq. (1) for each model (see Appendix A for an example with linear models) and were plotted in a chromaticity diagram. The resulting color sets constitute the loci of colors that describe dichromatic appearance. Figure 3 shows the loci derived from the substitution hypothesis. Figures 4 and 5 display the results obtained with the nulling hypothesis.

Before describing these figures in detail, it is worth noting that not all colors posses a corresponding pair. This can be seen in Fig. 3, where we have plotted all the loci, and in Fig. 6, where we show that the corresponding pair is lacking in some colors also with Brettel *et al.*'s algorithm. Usually the purplish-blue corner of the color diagram is the most affected, although in some models wide regions of purples or bluish-greens also lack a real corresponding pair.

Figure 3 shows the predictions obtained with the substitution hypothesis. In this case, it is the cone fundamentals used that affect the result. This is why different models with similar cone fundamentals (including scaling) lead to similar predictions. The loci of colors describing protanopic and deuteranopic appearance coincide in all cases, although the corresponding pair of a given color is not the same for the two dichromats, in agreement with experimental evidence. Neither the equal-energy white nor the achromatic stimulus of the model considered belongs to the dichromatic color-appearance loci, and the range of perceived hues predicted for dichromats with the substitution hypothesis disagrees with experimental data. The closest we get to the experimental results with this hypothesis is with ATD95 for protanopes and deuteranopes, whereas tritanopic behavior is best matched with the models that use the Smith–Pokorny[31] fundamentals scaled to unity, assuming that S cones contain the M pigment. Note that for protanopes and deuteranopes, the predictions of all models differing only in cone scaling intersect at the copunctual point of tritanopes. For tritanopes, they intersect in the protanopic copunctual cone for S = M and in the deuteranopic for S = L. This result can be easily explained, as shown in Appendix B.

With the nulling hypothesis (Figs. 4 and 5), the linear models predict that dichromatic appearance is matched by mixtures of the model's achromatic point and one of two spectral colors (blue and yellow for protanopic and deuteranopic subjects and reddish purple and bluish-green for tritanopic subjects). This is not true for the two nonlinear models (Fig. 5): The loci of dichromatic color appearance are not straight lines passing through the achromatic points but curves intersecting the spectral locus. This intersection changes slightly with luminance.

As with the substitution hypothesis, the loci of the stimuli that describe protanopic and deuteranopic appearance coincide. The loci describing tritanopic color appearance are the same regardless of which cone (L or M) has replaced the S cones.

Assuming that the dichromatic color appearance loci of Brettel *et al.*[5] are qualitatively correct, the two nonlinear models show the best agreement with these results for red–green defectives. Nevertheless, with the SVF formula, protanopic and deuteranopic subjects have identi-

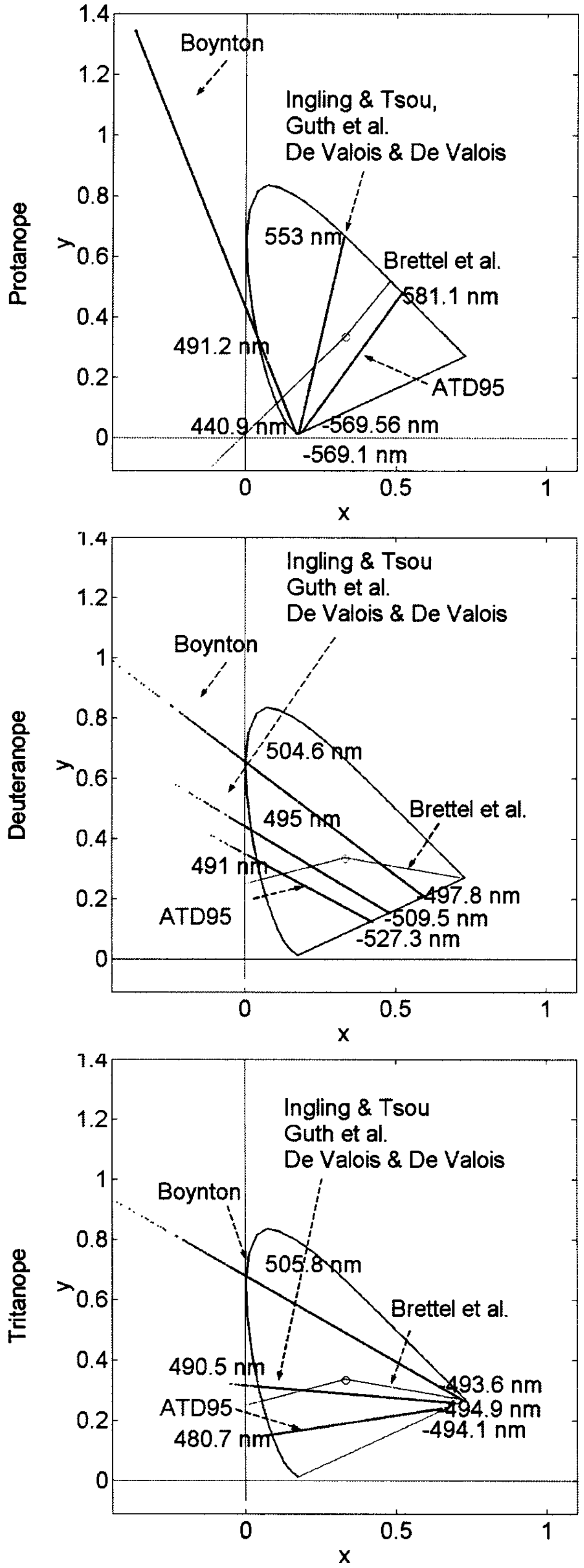


Fig. 3. Loci of colors that describe protanopic, deuteranopic, and tritanopic color appearance. The substitution hypothesis and the corresponding-pair algorithm were used with different cone-excitation spaces and with linear and nonlinear opponent-color models. The lines do not contain the achromatic point of the corresponding model. The loci obtained with the Brettel *et al.*[5] algorithm are plotted as thin curves. Note that not all the colors are real.

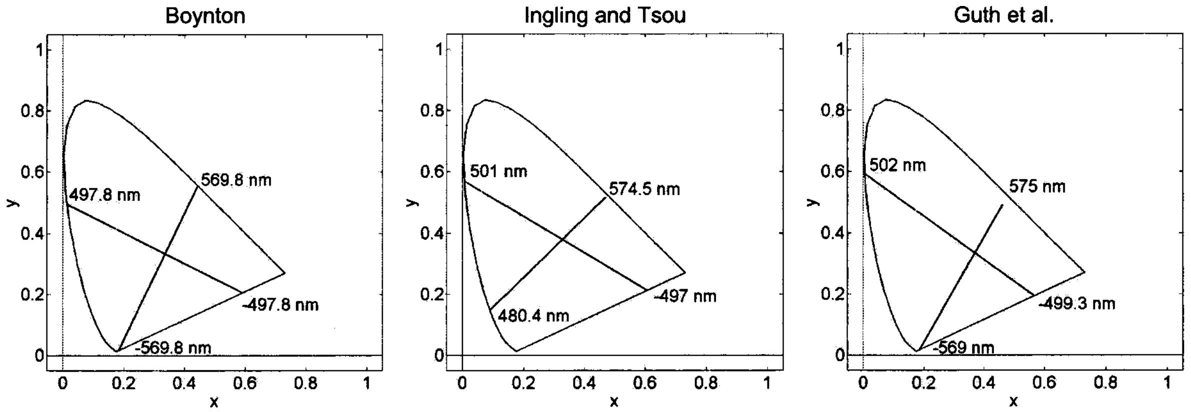


Fig. 4. Loci of colors that describe protanopic, deuteranopic, and tritanopic color appearance with the nulling hypothesis and the corresponding-pair algorithm, with one-opponent-stage models. From left to right, results from Boynton,[23] Ingling and Tsou,[21] and Guth *et al.*[22] Only real corresponding pairs are plotted.

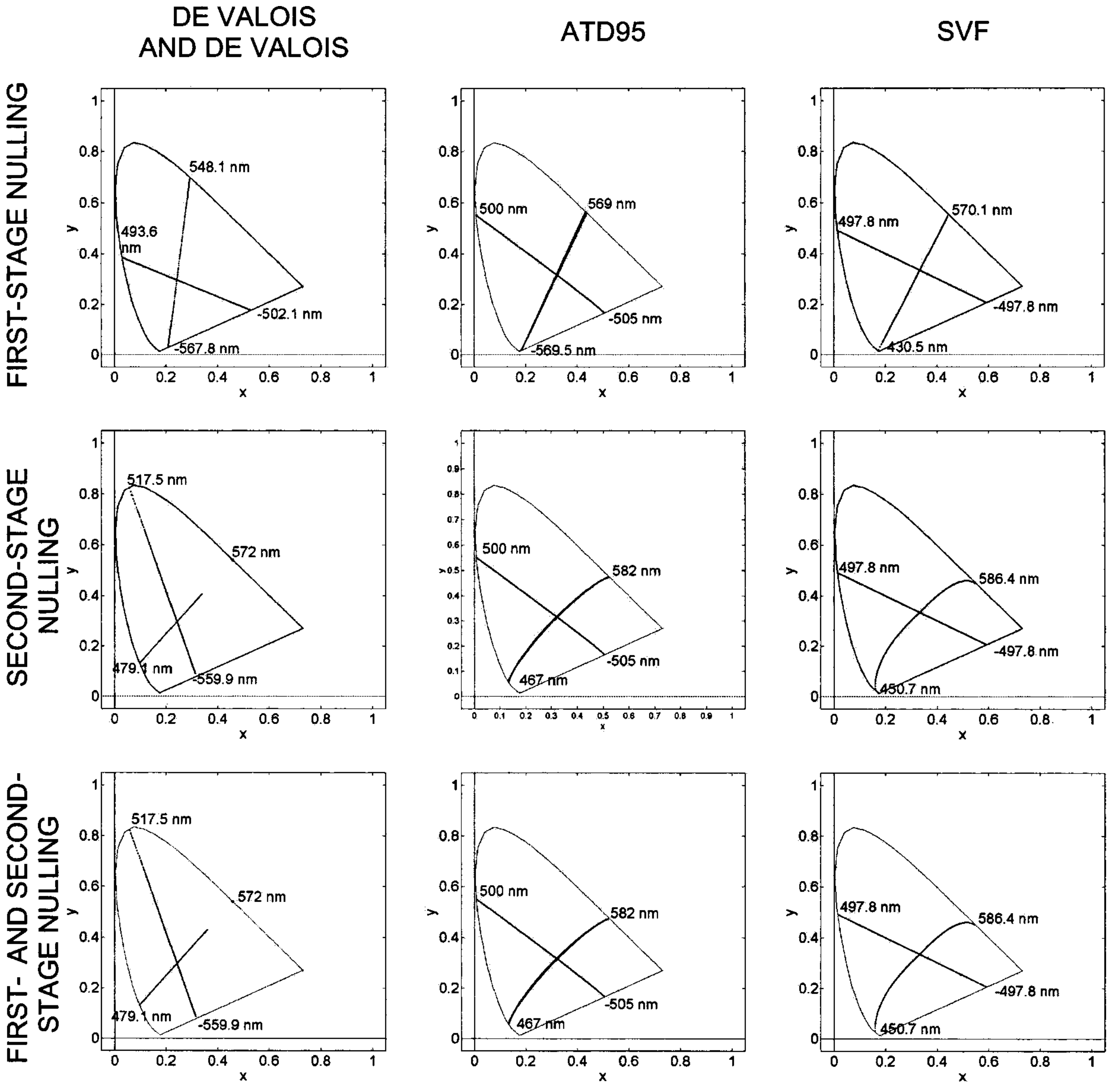
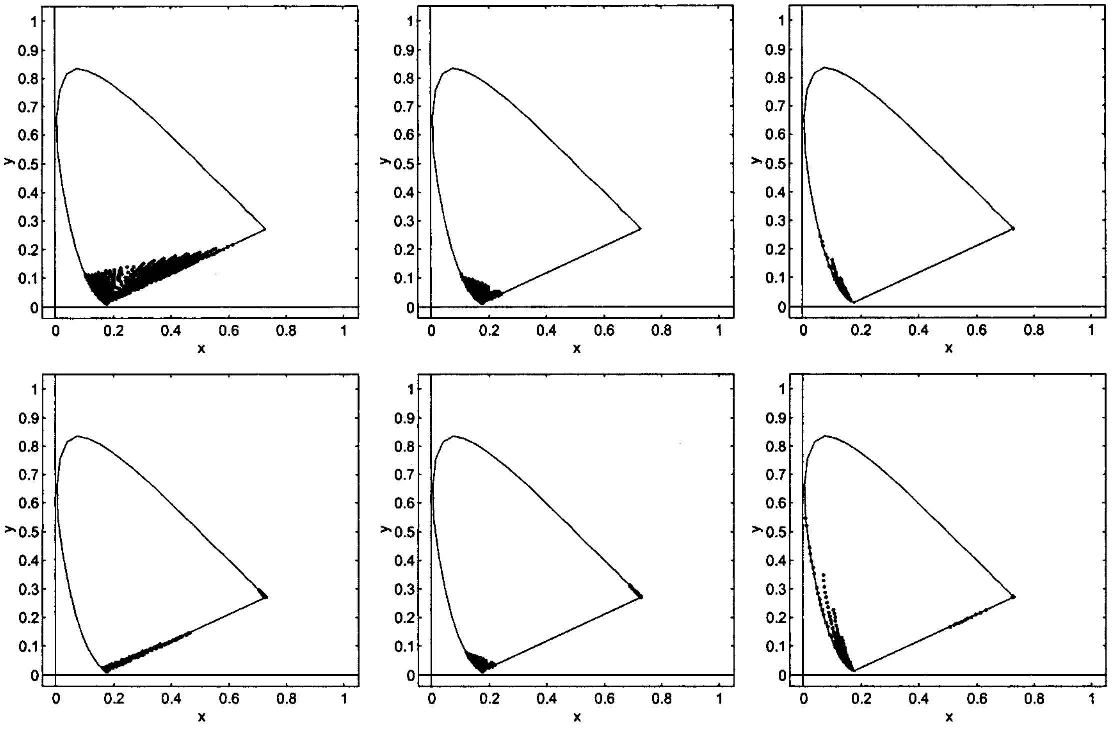


Fig. 5. Loci of colors that describe protanopic, deuteranopic, and tritanopic color appearance with the nulling hypothesis and the corresponding-pair algorithm, with two-opponent-stage models. Only real corresponding pairs are plotted.



(a) (b) (c)

Fig. 6. 10-cd/m^2 stimuli whose appearance for (a) a protanope, (b) a deuteranope, and (c) a tritanope cannot be simulated by Brettel *et al.*'s[5] algorithm (top panels) and ATD95 with the corresponding-pair procedure (bottom panels).

cal behavior, because the M cones are not used to compute the opponent responses.[26] Surprisingly, none of the models considered predicts the behavior of the tritanope correctly.

B. Example 2: Pictorial Simulation

In Fig. 7 we show the corresponding pairs of a photograph of Picasso's "Dora Maar" with use of a one-opponent-stage model (Boynton[23]), a linear two-opponent stage model (De Valois and De Valois[24]) and a nonlinear two-opponent stage model (ATD95). With each model we used the hypothesis that, according to the analysis carried out in Subsection 3.A, yields the best results. The colorimetric purity of the colors is low enough to ensure that each color's corresponding pair always exists. The results obtained with Brettel *et al.*'s algorithm have been included for comparison.

It can be seen that all models agree about which colors are transformed into blues and which into yellows for the red–green defectives, although the actual yellow can be more or less reddish and the actual blue more or less purplish. The situation is similar for the tritanope.

5. APPLICABILITY OF THE ALGORITHM BY BRETTEL *et al.* TO OTHER MODELS, ON GAMUT II

We now address the question, Can we apply the algorithm developed by Brettel and co-workers[4,5] to the same models that we have been using with the corresponding-pair procedure? As we say in Section 1, this means calculating the confusion colors of stimulus **T**, which is easy, and the colors that have the same appearance for normals as for dichromats (Gamut II), which is not, as we shall see.

With the notation of Eq. (1), colors in Gamut II verify that

$$\mathbf{C} = m^{-1}(m(\mathbf{C}, \mathbf{p}'), \mathbf{p}). \tag{2}$$

As an example, let us consider a linear one-opponent-stage model (see Appendix A). Equation (2) then becomes

$$M_{LMS\to ATD}(I - M_{LMS\to ATD}^{-1} M_O M_{LMS\to ATD} M_C) \times M_{XYZ\to LMS}\begin{pmatrix} X_T \\ Y_T \\ Z_T \end{pmatrix} = \begin{pmatrix} 0 \\ 0 \\ 0 \end{pmatrix}. \tag{3}$$

The zero-luminance stimulus (the trivial solution) always verifies Eq. (3). But it can be easily shown that

$$\det(I - M_{LMS\to ATD}^{-1} M_O M_{LMS\to ATD} M_C) = 0. \tag{4}$$

Therefore there is always a nontrivial solution. The problem lies in the fact that in many cases this solution is (a) a single stimulus (except for luminance), usually with low colorimetric purity or (b) not a real stimulus. For instance, in the model of De Valois and De Valois,[24] only the zero-luminance stimulus has the same appearance for normals as for dichromats.

The problem cannot be solved even if a more lax definition of Gamut II is used, for instance,

$$\mathbf{C} = m^{-1}(m(\mathbf{C}, \mathbf{p}') + \delta, \mathbf{p}), \tag{5}$$

where δ represents a threshold change in the color descriptors of **C**. In such cases, the intersection between

Fig. 7. Picasso's "Dora Maar" as seen by protanopes, deuteranopes, and tritanopes, according to the predictions of Brettel *et al.*,[5] Boynton[23] (nulling hypothesis, with S = M for the tritanope), De Valois and De Valois[24] (first- and second-stage nulling for red–green defectives and substitution, with S = M, for the tritanope), and ATD95 (second-stage nulling for red–green defectives and first-stage nulling for tritanopes).

Gamut I and II would not be unique. A procedure must be implemented to select a single stimulus among all those that are at threshold distance from **C**, this increasing the computational cost. Even then, as shown in Fig. 8, we do not ensure that the intersection between Gamut I and Gamut II exists for all colors.

6. CLOSING REMARKS

We have demonstrated that the color perceived by a dichromat may be simulated by the corresponding-pair procedure without making any assumptions about the spectral colors perceived as equal by normals and dichromats or about how to obtain Gamut II. We have also shown that the strategy used by Brettel *et al.*,[5] as described in Fig. 2, cannot be implemented in many color vision models with a strict definition of Gamut II.

The procedure that we propose is applicable to any color vision model that verifies that (a) the number of perceptual descriptors of normal and dichromatic color appearance is the same, (b) the inverse of the normal model is either analytically or numerically calculable, and (c) the dichromatic perceptual descriptors for each stimulus

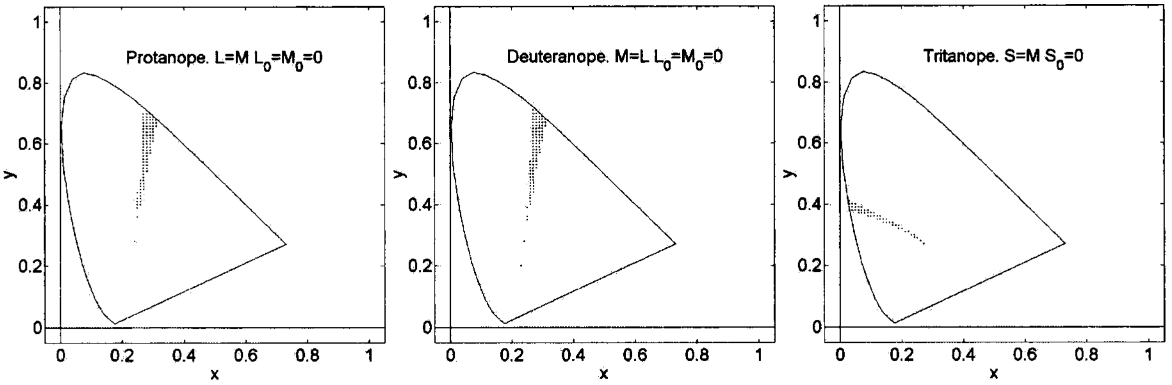


Fig. 8. Example of Gamut II computed with the De Valois and De Valois[24] model and the first-opponent-stage nulling hypothesis. Since the analytical solution is a color with tristimulus values [0 0 0], we have considered thresholds in the color descriptors, assuming that if the differences among dominant wavelength, colorimetric purity, and luminance of color **C** and its corresponding pair **C**′ are less than 3 nm, 5%, and 1%, respectively, **C** belongs to Gamut II. Even with this lax definition, the algorithm of Brettel *et al.* cannot be used, since the intersection of Gamut II and Gamut I does not exist for all colors.

are within the range of possible values for a normal observer.

With linear models, the colors describing dichromatic appearance are mixtures of two spectral stimuli and the achromatic stimulus of the model. With nonlinear models, the colors describing dichromatic appearance differ not only in colorimetric purity but also in dominant wavelength, and both parameters change with luminance. Not all stimuli may be simulated, because some colors do not have real corresponding pairs. We have shown the lack of corresponding pairs also with the algorithm of Brettel *et al.*, basically in the same regions of the chromaticity diagram. This is not a difficulty when one is trying to simulate dichromatic color appearance in a CRT monitor, because the stimuli that can be generated generally have lower purities than the stimuli that cannot be simulated. It is possible that with a more advanced color vision model this problem could be solved.

APPENDIX A: WORKING EXAMPLE: THE CORRESPONDING-PAIR PROCEDURE IN LINEAR MODELS

Linear one-opponent-stage models for normal color vision have the following general form:

$$\begin{pmatrix} A \\ T \\ D \end{pmatrix} = M_{LMS\rightarrow ATD}\begin{pmatrix} L \\ M \\ S \end{pmatrix} = M_{LMS\rightarrow ATD}M_{XYZ\rightarrow LMS}\begin{pmatrix} X \\ Y \\ Z \end{pmatrix}, \tag{A1}$$

where $M_{XYZ\rightarrow LMS}$ is a matrix that transforms XYZ into cone responses and $M_{LMS\rightarrow ATD}$ is the matrix that transforms cone responses into opponent responses. Perceptual descriptors, B (brightness), h (hue) and S (saturation) can be computed from the ATD outputs. For the purposes of the corresponding-pair algorithm, however, we may consider that the model ends at the ATD stage, because BhS is computed from the last stage of the model with equations that are the same for normals as for dichromats.

If we admit that either the substitution hypothesis or the nulling hypothesis accounts for dichromatic behavior, the dichromatic version of the model may be written as follows:

$$\begin{pmatrix} A_d \\ T_d \\ D_d \end{pmatrix} = M_{d,LMS\rightarrow ATD}\begin{pmatrix} L \\ M \\ S \end{pmatrix} = M_{d,LMS\rightarrow ATD} \times M_{d,XYZ\rightarrow LMS}\begin{pmatrix} X \\ Y \\ Z \end{pmatrix}, \tag{A2}$$

where $M_{d,XYZ\rightarrow LMS} = M_C M_{XYZ\rightarrow LMS}$ and $M_{d,LMS\rightarrow ATD} = M_O M_{LMS\rightarrow ATD}$. The matrix M_C that modifies the normal cone responses takes the following form for red–green defectives:

$$M_{C_{\text{protan}}} = \begin{bmatrix} 0 & 1 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix}, \qquad M_{C_{\text{deutan}}} = \begin{bmatrix} 1 & 0 & 0 \\ 1 & 0 & 0 \\ 0 & 0 & 1 \end{bmatrix}. \tag{A3}$$

For tritanopes, the S cones might contain either the L or the M photopigment, and therefore

$$M_{C_{\text{tritan}}} = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 1 & 0 & 0 \end{bmatrix} \text{ or } \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 1 & 0 \end{bmatrix}. \tag{A4}$$

The matrix that modifies the opponent responses is the identity in the substitution hypothesis. In the nulling hypothesis,

$$M_{O_{\text{protan/deutan}}} = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 1 \end{bmatrix}, \qquad M_{O_{\text{tritan}}} = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 0 \end{bmatrix}. \tag{A5}$$

The normal model is a particular case of Eq. (A2), with M_O and M_C equal to the identity. With the notation of Eq. (1), the model is defined by operator $m(\mathbf{C}, M_O, M_C)$:

$$m(\mathbf{C}, M_C, M_O) = M_O M_{LMS\rightarrow ATD} M_C \times M_{XYZ\rightarrow LMS}\begin{pmatrix} X_C \\ Y_C \\ Z_C \end{pmatrix}, \tag{A6}$$

where **C** is a color. The normal version of the model is just $m(\mathbf{C}, I, I)$, I being the three-by-three identity matrix.

If we apply the corresponding-pair procedure with operator $m(\mathbf{C}, M_O, M_C)$, the tristimulus values of the simulation are given by

$$\begin{pmatrix} X_S \\ Y_S \\ Z_S \end{pmatrix} = m^{-1}(m(\mathbf{T}, M_C, M_O), I, I) = M_{XYZ\rightarrow LMS}^{-1} M_{LMS\rightarrow ATD}^{-1} M_O M_{LMS\rightarrow ATD} \times M_C M_{XYZ\rightarrow LMS}\begin{pmatrix} X_T \\ Y_T \\ Z_T \end{pmatrix}. \tag{A7}$$

With two-opponent-stage linear models,

$$\begin{pmatrix} A_2 \\ T_2 \\ D_2 \end{pmatrix} = M_{ATD_1\rightarrow ATD_2}\begin{pmatrix} A_1 \\ T_1 \\ D_1 \end{pmatrix} = M_{ATD_1\rightarrow ATD_2} M_{LMS\rightarrow ATD}\begin{pmatrix} L \\ M \\ S \end{pmatrix} = M_{ATD_1\rightarrow ATD_2} M_{LMS\rightarrow ATD} M_{XYZ\rightarrow LMS}\begin{pmatrix} X \\ Y \\ Z \end{pmatrix}. \tag{A8}$$

Using the notation of Eq. (1), we may write

$$m(\mathbf{C}, M_C, M_{O1}, M_{O2}) = M_{O2} M_{ATD_1\rightarrow ATD_2} M_{O1} M_{LMS\rightarrow ATD} M_C \times M_{XYZ\rightarrow LMS}\begin{pmatrix} X_C \\ Y_C \\ Z_C \end{pmatrix}. \tag{A9}$$

Again, the normal version of the model is just $m(\mathbf{C}, I, I, I)$. The corresponding-pair procedure now yields the following solution:

$$\begin{pmatrix} X_S \\ Y_S \\ Z_S \end{pmatrix} = m^{-1}(m(\mathbf{T}, M_C, M_{O1}, M_{O2}), I, I, I) = M_{XYZ\rightarrow LMS}^{-1} M_{LMS\rightarrow ATD_1}^{-1} M_{ATD_1\rightarrow ATD_2}^{-1} M_{O2} \times M_{ATD_1\rightarrow ATD_2} M_{O1} M_{LMS\rightarrow ATD} M_C \times M_{XYZ\rightarrow LMS}\begin{pmatrix} X_T \\ Y_T \\ Z_T \end{pmatrix}. \tag{A10}$$

APPENDIX B: SUBSTITUTION HYPOTHESIS

In this appendix, we study the effect of the cone scaling in linear models when the corresponding-pair procedure is used with the substitution hypothesis.

With this hypothesis, M_O is the identity I in Eq. (A7) and $M_{O1} = M_{O2} = I$ in Eq. (A10). Thus it would be enough to invert the cone stage. The results obtained depend not only on the cone primaries used but also on the scaling conditions. If the simulation obtained with a given color vision model is

$$\begin{pmatrix} X_S \\ Y_S \\ Z_S \end{pmatrix} = M_{XYZ\rightarrow LMS}^{-1} M_C M_{XYZ\rightarrow LMS}\begin{pmatrix} X_T \\ Y_T \\ Z_T \end{pmatrix} \tag{B1}$$

with use of another model differing only in the cone scaling conditions, the corresponding pair is

$$\begin{pmatrix} X_{S'} \\ Y_{S'} \\ Z_{S'} \end{pmatrix} = M_{XYZ\rightarrow LMS}^{-1} k^{-1} M_C k M_{XYZ\rightarrow LMS}\begin{pmatrix} X_T \\ Y_T \\ Z_T \end{pmatrix}, \tag{B2}$$

where k is a diagonal matrix with the scaling constants

$$k = \begin{bmatrix} k_L & 0 & 0 \\ 0 & k_M & 0 \\ 0 & 0 & k_S \end{bmatrix}. \tag{B3}$$

The predictions of the two models are identical for all colors only if

$$k^{-1} M_C k = M_C, \tag{B4}$$

that is, if the product of matrices k and M_C is commutative:

$$M_C k = k M_C. \tag{B5}$$

It is easy to prove that this equation is verified simultaneously for the three types of dichromats only if k is a global scaling factor (that is, $k_L = k_M = k_S$). Otherwise, when we subtract Eq. (B1) from Eq. (B2), the predictions are the same only for colors that verify that

$$(M_{XYZ\rightarrow LMS}^{-1} k^{-1} M_C k M_{XYZ\rightarrow LMS} - M_{XYZ\rightarrow LMS}^{-1} \times M_C M_{XYZ\rightarrow LMS})\begin{pmatrix} X_T \\ Y_T \\ Z_T \end{pmatrix} = \begin{pmatrix} 0 \\ 0 \\ 0 \end{pmatrix}. \tag{B6}$$

If we factorize this equation, we obtain

$$M_{XYZ\rightarrow LMS}^{-1} k^{-1}(M_C k - k M_C) M_{XYZ\rightarrow LMS} \times \begin{pmatrix} X_T \\ Y_T \\ Z_T \end{pmatrix} = \begin{pmatrix} 0 \\ 0 \\ 0 \end{pmatrix} \tag{B7}$$

and therefore

$$(M_C k - k M_C) M_{XYZ \to LMS} \begin{pmatrix} X_T \\ Y_T \\ Z_T \end{pmatrix} = (M_C k - k M_C) \begin{pmatrix} L_T \\ M_T \\ S_T \end{pmatrix} = \begin{pmatrix} 0 \\ 0 \\ 0 \end{pmatrix}. \quad \text{(B8)}$$

But, with the substitution hypothesis,

$$(M_C k - k M_C)_{i,j} = \begin{cases} (k_M - k_L)\delta_{i,1}\delta_{2,j} & \text{protanopes} \\ (k_L - k_M)\delta_{i,2}\delta_{1,j} & \text{deuteranopes} \\ (k_L - k_S)\delta_{i,3}\delta_{1,j} & \text{tritanopes, } S = L \\ (k_M - k_S)\delta_{i,3}\delta_{2,j} & \text{tritanopes, } S = M \end{cases}. \quad \text{(B9)}$$

From Eqs. (B8) and (B9) we obtain

$$\begin{aligned} (k_M - k_L) L_T &= 0 && \text{protanopes \& deuteranopes} \\ (k_L - k_S) L_T &= 0 && \text{tritanopes, } S = L, \\ (k_M - k_S) M_T &= 0 && \text{tritanopes, } S = M. \end{aligned} \quad \text{(B10)}$$

If we assume that $k_M \neq k_L \neq k_S$, substituting into Eq. (B1) we reach the following result for protanopes and deuteranopes:

$$\begin{pmatrix} X_S \\ Y_S \\ Z_S \end{pmatrix} = M^{-1}_{XYZ \to LMS} M_C \begin{pmatrix} L_T \\ M_T \\ S_T \end{pmatrix} = M^{-1}_{XYZ \to LMS} M_C \begin{pmatrix} 0 \\ M_T \\ S_T \end{pmatrix} = M^{-1}_{XYZ \to LMS} \begin{pmatrix} 0 \\ 0 \\ S_T \end{pmatrix}. \quad \text{(B11)}$$

That is, the two models predict that the corresponding-pair of stimuli with $L_T = 0$, is the tritanopic confusion point. For tritanopes, we obtain

$$S = L \Rightarrow \begin{pmatrix} X_S \\ Y_S \\ Z_S \end{pmatrix} = M^{-1}_{XYZ \to LMS} M_C \begin{pmatrix} L_T \\ M_T \\ S_T \end{pmatrix} = M^{-1}_{XYZ \to LMS} M_C \begin{pmatrix} 0 \\ M_T \\ S_T \end{pmatrix} = M^{-1}_{XYZ \to LMS} \begin{pmatrix} 0 \\ M_T \\ 0 \end{pmatrix},$$

$$S = M \Rightarrow \begin{pmatrix} X_S \\ Y_S \\ Z_S \end{pmatrix} = M^{-1}_{XYZ \to LMS} M_C \begin{pmatrix} L_T \\ M_T \\ S_T \end{pmatrix} = M^{-1}_{XYZ \to LMS} M_C \begin{pmatrix} L_T \\ 0 \\ S_T \end{pmatrix} = M^{-1}_{XYZ \to LMS} \begin{pmatrix} L_T \\ 0 \\ 0 \end{pmatrix}. \quad \text{(B12)}$$

Thus both models predict that if S = L, all colors with $L_T = 0$ have as corresponding pair the deuteranopic confusion point and that if S = M, all colors with $M_T = 0$ have as corresponding pair the protanopic confusion point.

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