METAMERISM INDEX

Note:
DIN 6172 multiplicative method is used in ColorTools 1.xx, and up to 3.0.5. (older method).

ColorTools 3.1 and newer and Datacolor Tools has both of the DIN 6172 methods included. (the newest method is additive).

DIN 6172 Metamerism Index

Algorithms/Equations:

DIN 6172 (August 1990) metamerism index is given the symbol MI_T. The general equation for MI_T is given as:

\[
MT_T = \sqrt{(L_{1T}^* - L_{2T}^* + K_L)^2 + (a_{1T}^* - a_{2T}^* + K_a)^2 + (b_{1T}^* - b_{2T}^* + K_b)^2}
\]

A new "corrected" color coordinate is calculated that is then differenced from the standard.

\[
L_{3T}^* = L_{2T}^* + K_L, \quad a_{3T}^* = a_{2T}^* + K_a, \quad b_{3T}^* = b_{2T}^* + K_b
\]

and

\[
MT_T = \sqrt{(L_{1T}^* - L_{3T}^*)^2 + (a_{1T}^* - a_{3T}^*)^2 + (b_{1T}^* - b_{3T}^*)^2}
\]

where the correction factors K_L, K_a, K_b form an additive correction to the color coordinates of the samples (sample 1 and sample 2) under the test illuminant (Testlichtart), when the sample pair is not an exact color match under the reference illuminant (Bezugslichtart). Then the additive correction factors are given by:

\[
K_L = L_{2B}^* - L_{1B}^*, \quad K_a = a_{2B}^* - a_{1B}^*, \quad K_b = b_{2B}^* - b_{1B}^*
\]
In an earlier version of this standard, a **multiplicative correction** to the tristimulus values of the batch was recommended. The multiplicative correction factors are given by:

\[
\begin{align*}
    f_X &= \frac{X_{1B}}{X_{2B}}, \\
    f_Y &= \frac{Y_{1B}}{Y_{2B}}, \\
    f_Z &= \frac{Z_{1B}}{Z_{2B}}
\end{align*}
\]

The new tristimulus values are:

\[
X_{3T} = f_X \cdot X_{2T}, \quad Y_{3T} = f_Y \cdot Y_{2T}, \quad Z_{3T} = f_Z \cdot Z_{2T}
\]

L*a*b* values are then calculated for the Test Illuminant and the MI is again calculated.

The required measurement data are thus:

<table>
<thead>
<tr>
<th>Reference Illuminant (B)</th>
<th>Test Illuminant (T)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Sample 1</strong></td>
<td></td>
</tr>
<tr>
<td>X_{1B}</td>
<td>Y_{1B}</td>
</tr>
<tr>
<td>L*_{1B}</td>
<td>a*_{1B}</td>
</tr>
<tr>
<td><strong>Sample 2</strong></td>
<td></td>
</tr>
<tr>
<td>X_{2B}</td>
<td>Y_{2B}</td>
</tr>
<tr>
<td>L*_{2B}</td>
<td>a*_{2B}</td>
</tr>
<tr>
<td><strong>Sample 1</strong></td>
<td></td>
</tr>
<tr>
<td>X_{1T}</td>
<td>Y_{1T}</td>
</tr>
<tr>
<td>L*_{1T}</td>
<td>a*_{1T}</td>
</tr>
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</tr>
</tbody>
</table>

**Curve Fit**

Curve fit is calculated by taking the square root of the sum of the squares (the delta %R) between 2 curves (i.e. the sum of the squares of the differences between the 2 curves).

Curve fit is a number that will determine how close 2 curves are to being the same shape. The greater the number, the greater the difference between the 2 curves.

Curve fit is not weighted by the illuminant/observer functions so it will treat all wavelengths equally (400nm has same effect as 550nm).

**Compare curve fit to a metamerism index like "MI - Root Mean Square"**

This index takes the square root of the sum of the squares (the DE under 3 illuminant/observer conditions) between 2 samples. By using the DE, the curves are weighted by the illuminant/observer condition.