## Independent Histogram Pursuit for segmentation of skin lesions

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Independent Histogram Pursuit for
Segmentation of Skin Lesions

David Delgado Gómez, Constantine Butakoff, Bjarne Kjær Ersbøll, William Stoeker

Abstract

In this work, an unsupervised algorithm called the Independent Histogram Pursuit (IHP), for characterization of dermatological lesions is proposed. The algorithm estimates a set of linear combinations of image bands that enhance different structures embedded in the image. In particular, the first estimated combination enhances the contrast of the lesion to facilitate its segmentation. Given an \(N\)-band image this first combination corresponds to a line in \(N\) dimensions, such that the separation between the two main modes of the histogram obtained by projecting the pixels onto this line, is maximized. The remaining combinations are estimated in a similar way under the constraint of being orthogonal to those already computed. The performance of the algorithm is tested on five different dermatological datasets. The results obtained on these datasets indicate the robustness of the algorithm and its suitability to deal with different types of dermatological lesions. The proposed algorithm can be easily combined with the majority of classification algorithms.

Index Terms

feature extraction, classification, genetic algorithms, exploratory data analysis, projection pursuit, independent component analysis, dermoscopy, boundary detection

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I. INTRODUCTION

Nowadays, the lack of objective methods to evaluate and track the evolution of dermatological lesions is one of the main image processing problems in dermatology. During the last decade, image analysts have tried to provide a solution to this problem. Many research projects have been conducted to automatically and objectively evaluate the severity of the disease [1]–[5]. These studies have provided several measures to describe the lesion such as asymmetry coefficients, border information, color information or differential structures [4], [6], [7].

In order to precisely estimate these indices, segmentation of the lesion is required. Some of the segmentation techniques that have been developed are reviewed in Maglogianis et al. [5]. The simplest approach to lesion segmentation is thresholding, which is based on the difference between the color of the pixels within the lesion and those in the normal skin. The idea of thresholding is to choose a threshold such that the pixels will be separated into two classes: those with the intensity above the threshold as skin (lesion) and those below it as lesion (skin). This threshold value can be obtained, for example, by analyzing the histogram. Based on this approach, some authors have proposed a weighted combination of the segmentation results obtained by thresholding in different color spaces [8].

More elaborate segmentation techniques such as region growing and watershed segmentation include spatial information in the analysis. The general idea of region growing is to spread a set of small regions (sometimes one pixel large) over the image and grow them by adding neighboring pixels with similar properties such as intensity, color or texture descriptors [9]. One technique based on region growing that has been successfully applied to the segmentation of dermatological images is the JSEG algorithm [10], [11]. This technique constructs a new image, called the J-image, where large and small pixel intensity values correspond to possible boundaries and interior regions, respectively. The segmentation is then performed by region growing applied to the J-image. Another technique, called watershed segmentation [12], uses the image intensity gradient in order to define region dynamics by simulating the descent of raindrops on a hill. The resulting regions are then merged according to their similarity [13]. Another segmentation approach, based on the image intensity gradient that has found wide application in medical image processing is the active contour (snake) model. According to this methodology, a curve is placed in the image and is allowed to evolve according to a vector force field, computed from that image, until
a certain equilibrium state is reached. One such approach, called gradient vector flow (GVF) snakes, was proposed to segment skin lesions in [14]. In this method the curve evolution is controlled by the image gradient information to fit the boundary to the contour of the lesion.

The common feature of the majority of these algorithms, though each segments lesions in its own way, is that their accuracy heavily depends on the color representation. The more contrast there is between the lesion and the normal skin in the chosen color space the more accurate the segmentation will be. In order to obtain a color representation that enhances the contrast between the lesion and the normal skin, several works have been conducted to transform the original RGB image into a more suitable color space (in many cases standard and independent of the image). The most common and widely used color spaces are the CIE L*a*b* and CIE L*u*v*, described in [15]. These transformations have been shown to produce good segmentation results for some dermatological diagnoses [16]–[18]. For example in [17], the authors construct a 2D histogram from the u* and v* components of the CIE L*u*v* color space. This histogram is smoothed and initial cluster centers are determined from the histogram peaks using a perceptron classifier. The final segmentation is performed by a modified fuzzy c-Means algorithm.

These color spaces, being too general (i.e. independent of the image or problem), have a reduced applicability. In dermatological images, the selection of the color space depends on the type of diagnosis that needs to be analyzed. It is not likely that the same color space is optimal for different dermatological diagnoses or even for series of images of the same diagnosis acquired by different systems. Therefore, utilizing specific color spaces per case and designing algorithms bound to these color spaces makes most of the algorithms specific to a given set of diagnoses.

Another disadvantage of these transformations is that they are limited to tri-chromatic band images and they cannot be applied to the images collected by new imaging systems [19]–[22]. To obtain a better characterization of the lesion, these systems acquire a multitude of spectral bands, ranging from ultra-violet to near-infrared including the classical RGB. The latter stimulates a search for a transformation that is able to use the information provided by all the bands.

A possible approach to incorporate the information provided by the extra bands is to use features obtained by the principal component analysis (PCA). This approach was introduced by Zagrouba and Barhoum [23]. The shortcoming of this methodology is its reduced capacity to adapt itself to variation of the lesion in different patients.
The principal component direction can vary considerably if the image has other structures such as hair or vessels. Moreover, it is not guaranteed that the component that enhances the lesion will always appear in the same position in the ordered set of all the components. To date there is no general method that can be applied to the majority of dermatological datasets, and many studies are being conducted to improve the existing methods.

To compensate for the disadvantages of the described approaches, we propose here the adaptation of the Independent Histogram Pursuit (IHP) algorithm [24] for finding a suitable image-dependent linear transformation of an arbitrary multispectral color space to aid segmentation and characterization of dermatological images. A typical dermatological image consists of two large classes of pixels: the lesion and the normal skin. Therefore the problem of lesion segmentation can be formulated as that of 2-class segmentation. For an image of $N$ spectral bands, each pixel is represented by an $N$-vector of intensity values sampled from each band. The IHP algorithm is composed of two steps. During the first step, an $N$-vector is estimated, such that the histogram of pixel projections onto this vector is bimodal and the separation between the two modes is maximal. The elements of this vector define a linear combination of the $N$ image bands such that the contrast between the two major classes of objects present in the image is highest. This combination can then be efficiently used to segment the lesion by any clustering algorithm or any classification method, a good survey of which can be found in Duda and Hart [25]. In the second step, the algorithm estimates the remaining $N-1$ informative combinations that enhance less obvious structures of the image. Again the separation between the modes is maximized but a restriction is imposed on the vector, namely it must be orthogonal to the previously estimated vectors. These combinations can be utilized to aid characterization of the lesion and its severity. Note that in this formulation the algorithm is independent of the chosen image representation, whether it is one of the standard color spaces or a multiband image.

II. THE INDEPENDENT HISTOGRAM PURSUIT

Let $X$ be an $m \times n$ image with $N$ bands. Then the $(i,j)$-th pixel of this image can be considered as an $N$-vector $x_{ij} = \left( x_{ij}^{(1)}, ..., x_{ij}^{(N)} \right)^T$. All the pixels $x_{ij}$ of a given image constitute the input data.

The IHP estimates a sequence of $N$ orthogonal $N$-vectors, or components, that constitute a linear transformation of the original color space of the image. The first component is computed so that the histogram of pixels, projected onto it, is bimodal and the concavity between the two modes has the maximum area (the hatched area in Fig. 1).
Fig. 1. A sample bimodal histogram of pixels projected onto \( z \) during optimization. The hatched pattern indicates the area maximized by the algorithm.

During the second step, the remaining \((N-1)\) IHP components are estimated using the same criterion, requiring each component to be orthogonal to those previously estimated.

The algorithm starts by decorrelating the input data. Let \( V \) and \( D \) be the \( N \times N \) matrices of eigenvectors (arranged in columns) and eigenvalues of the covariance matrix \( C \):

\[
C = \frac{1}{nm-1} \sum_{i=1}^{m} \sum_{j=1}^{n} x_{ij}x_{ij}^T
\]

The linear whitening transform is given by [26]:

\[
W = D^{-\frac{1}{2}}V^T
\]

and the whitened pixels are

\[
\tilde{x}_{ij} = Wx_{ij}, \quad \forall \ i, j
\]

The set of IHP components \( \{u_k|k = 1, \ldots, N\} \) is estimated by solving the following optimization problem for each \( k \):

\[
\tilde{u}_k = \arg \max_{x \in \mathbb{R}^N} f \left[ \{ z^T \tilde{x}_{ij} | i = 1, \ldots, m; j = 1, \ldots, n \} \right]
\]

\[
\tilde{u}_k^T \tilde{u}_l = 0, \quad \text{for} \ k > 1 \ \text{and} \ l = 1, \ldots, k - 1
\]

The function \( f \left[ \{ z^T \tilde{x}_{ij} \} \right] \) on the right-hand side of (4) is defined as the area of the concavity between the two modes of the histogram of data \( \tilde{x}_{ij} \) projected onto \( z \), as in Fig. 1. Algorithm 1 provides the necessary steps
Algorithm 1 Computing the concavity area $f\left(\{ z^T \tilde{x}_{ij}\}\right)$

1: Let $H$ be the histogram of whitened pixels $\tilde{x}_{ij}$ projected onto the current estimate of $z$ (i.e. histogram of values $z^T \tilde{x}_{ij}$), and $H (i)$ the value of the $i$-th bin.

2: Smooth $H$ to remove insignificant maxima using 15 iterations of the mean filter with the window length 3.

3: Detect all the local maxima of the smoothed histogram by comparing the value of every bin with the values of the two adjacent bins.

4: if the number of maxima is greater than two then

5: $\text{area} \leftarrow 0$

6: else

7: Let $n_1$ and $n_2$ ($n_1 < n_2$) be the indices (intensity values) of the two bins associated with the two histogram maximum values $A_1$ and $A_2$ (see Fig. 1)

8: $A_{\text{min}} \leftarrow \min\{A_1, A_2\}$

9: $\text{sum} \leftarrow 0$

10: for $i \leftarrow n_1, n_2$ do

11: \hspace{1em} $\text{sum} \leftarrow \text{sum} + \min\{A_{\text{min}}, H (i)\}$

12: end for

13: $\text{area} \leftarrow (n_2 - n_1 + 1) \cdot A_{\text{min}} - \text{sum}$

14: end if

15: return $\text{area}$

to compute this area. Let us briefly outline the important steps of the algorithm. Given a current estimate of a component $z$, all the pixels must be projected onto that vector and the histogram $H$ of projections has to be computed. Then the histogram is smoothed by the mean filter [27] to remove any insignificant extrema, and all the local maxima are found by comparing the value of each bin with its two neighbors. Since we are interested only in bimodal histograms, if there are more than two maxima then $z$ is rejected by setting the area equal to zero. Otherwise the area is computed by integrating over the hatched area in Fig. 1.

The problem (4)–(5) is solved by genetic optimization [28], computing the objective function by Algorithm 1.
Note that the first IHP component is estimated without any constraint. To introduce the orthogonality constraint for each subsequent component $\tilde{u}_k$ ($k > 1$), all the candidate vectors, evaluated at every step of the genetic algorithm, are orthogonalized with respect to the already estimated $\tilde{u}_1, \ldots, \tilde{u}_{k-1}$. The orthogonalization can be performed by any method, the simplest being the Gram-Schmidt algorithm [29], summarized in Appendix II. Note also, that the last component $\tilde{u}_N$ can be computed simply as a vector orthogonal to the rest of $\tilde{u}_l$, $l = 1, \ldots, N - 1$.

Since the obtained set of IHP components $\tilde{U} = [\tilde{u}_1, \ldots, \tilde{u}_N]$ describes projections for the whitened pixels, they have to be transformed by $W^{-1}$ in order to be used with the original pixels. So the final projections are given by:

$$U = W^{-1}\tilde{U}$$

with $U = [u_1, \ldots, u_N]$.

Observing many dermatological images one can notice that the only two structures with the largest difference in color are the lesion (sometimes together with the hair) and the normal skin. These two structures correspond to the two main modes in the histogram of the targeted projection. Therefore, the first, unsupervised, step of the algorithm, that maximizes the area of concavity between the two main modes of the histogram, will provide a direction along which the lesion and the skin have maximum separation in the considered $N$-dimensional space.

In this way, to segment the lesion from the normal skin the pixels must be projected onto the first IHP component $u_1$, and classified by any 2-class clustering algorithm (e.g. k-Means algorithm). This clustering can be performed on whitened data using the projection onto $\tilde{u}_1$ to avoid computing $U$.

By computing the remaining $N - 1$ components, the IHP algorithm aims at separating substructures embedded inside the lesion. Projecting pixels onto one of these components allows enhancing contrast of different elements such as hair, vessels or scales. An example of IHP applied to a 9-band image of a melanoma is presented in Fig. 2. As can be seen, the first estimated combination of the bands in Fig. 2b significantly improves the contrast of the melanoma. On the other hand the combination in Fig. 2d enhances the contrast of its border which can be useful for the diagnosis.
Fig. 2. The first three projections found by IHP. The original 9-band melanoma image (a) projected onto $u_1$ (b), $u_2$ (c) and $u_3$ (d). Images (b)-(d) are grayscale.

III. EXPERIMENTAL RESULTS

A. Segmenting the Lesion

To evaluate the performance of IHP five databases have been chosen. The first database, introduced in Chen et al. [13], contains 100 RGB melanoma images with 70 malignant melanomas and 30 benign cases, mostly dysplastic nevi.

To show that, in contrast to standard color spaces, the IHP is able to find an image-dependent projection well-suited for segmentation we shall compare the lesion segmentation in the individual bands of the standard color spaces such as RGB, CIE L*a*b*, L*u*v* and XYZ (see Appendix I) with the segmentation in the images obtained by projecting the pixels onto the IHP components. In other words, the five above representations are computed for each image and k-Means is applied to each component of each representation: r, g, b, L*, a*, etc. k-Means has been chosen in order to guarantee that the accuracy of the segmentation is due to the properties of the projection and not of the classification algorithm. Table I shows the average segmentation accuracy with respect to the manual segmentation provided by a dermatologist. The names in the table are made up of color space name and component in parenthesis. The numbers represent the average percentage of correctly classified pixels with the corresponding standard error.

It can be seen that the largest correct classification rate is obtained using the first IHP component. Moreover, the
TABLE I

COMPARISON OF LESION SEGMENTATION IN DIFFERENT
COLOR SPACES ON CHEN’S [13] DATABASE. THE BEST
RESULTS FOR EACH COLOR SPACE ARE SHOWN IN BOLD.

<table>
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<th>Component</th>
<th>Error (%)</th>
<th>Component</th>
<th>Error (%)</th>
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<tr>
<td>Red</td>
<td>89.69±0.6</td>
<td>XYZ(X)</td>
<td>93.40±0.4</td>
</tr>
<tr>
<td>Green</td>
<td>94.23±0.4</td>
<td>XYZ(Y)</td>
<td>93.80±0.4</td>
</tr>
<tr>
<td>Blue</td>
<td>95.42±0.5</td>
<td>XYZ(Z)</td>
<td>95.30±0.5</td>
</tr>
<tr>
<td>Lab(L*)</td>
<td>92.52±0.4</td>
<td>Luv(L*)</td>
<td>92.52±0.4</td>
</tr>
<tr>
<td>Lab(a*)</td>
<td>91.92±0.5</td>
<td>Luv(a*)</td>
<td>86.70±1.1</td>
</tr>
<tr>
<td>Lab(b*)</td>
<td>94.24±0.5</td>
<td>Luv(v*)</td>
<td>83.67±1.3</td>
</tr>
<tr>
<td>IHP(1)</td>
<td>96.13±0.2</td>
<td></td>
<td></td>
</tr>
<tr>
<td>IHP(2)</td>
<td>64.78±0.8</td>
<td></td>
<td></td>
</tr>
<tr>
<td>IHP(3)</td>
<td>62.05±0.6</td>
<td></td>
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fact that almost random classification is obtained using the second and the third component points out that most of
the information needed to discriminate the lesion is concentrated in the first one.

It is worth noting that the results presented in Table I can still be improved by pre- and postprocessing. The
preprocessing is a morphological hair removal [30], and the postprocessing is just the morphological closing and
opening with a 5 x 5 square structuring element filled with ones. Since postprocessing is out of scope of this paper,
the choice of the structuring element was purely empirical and therefore not necessarily optimal. The postprocessing
is finished by hole filling and selection of the largest blob, which is assumed to be the lesion. This allows raising
the segmentation precision to 97%.

To compare the IHP to the existing lesion segmentation methods, we have chosen the JSEG [10], [11], Watershed
[12] and GVF Snake [14] reported to be the best three techniques of the four tested by Chen [13]. The comparison
is shown in Fig. 3, where "IHP(p)" stands for IHP with the postprocessing mentioned in the previous paragraph.

An example of segmentation can be seen in Fig. 4 where five images (Fig. 4a) have been selected to exhibit the
differences in redness, size and noise(image with veins) present in the dataset. Fig. 4b-d shows the projection of
pixels of the five images onto the first, second and third IHP components respectively. It is easy to see that the first
component always enhances the contrast of the lesion.

To further evaluate the performance of the algorithm another database has been chosen. This database is composed of 150 melanoma images and was introduced by Ganster [8]. In this case the performance of our algorithm (k-Means segmentation of pixels projected onto the first IHP component) is compared to the segmentation algorithm that has been reported to perform well on this database. This algorithm, proposed by Ganster [8], fuses the results of five different segmentation techniques. These techniques are the global thresholding in the blue component of the RGB image, three dynamic adaptive thresholds in the b component of the CIE-Lab model (mask sizes are $100 \times 100$, $150 \times 150$ and $200 \times 200$) and a 3D color clustering with the X, Y and Z components of the CIE-XYZ color model. As can be seen from the Table II the performance of both algorithms is comparable, but IHP is much simpler in the sense that it uses only one component and k-Means, while Ganster’s algorithm uses five different segmentation techniques.

We tested our algorithm on one more melanoma dataset composed of 57 images. This dataset was introduced in Hintz-Madsen et al. [31]. The authors preprocessed the images with a $11 \times 11$ median filter to remove noise, and applied the Karhunen-Loewe transform to enhance the border of the lesion. After the images were preprocessed, a threshold was applied to segment the lesions. In our experiment, the images do not undergo any preprocessing other than hair removal. The algorithm performed very well, with correct segmentation of all images in the dataset.
Fig. 4. Segmentation demonstration of the five RGB melanoma images chosen from Chen’s [13] database: (a) the original images; (b) the images projected onto the first IHP component; (c) the images projected onto the second IHP component; (d) the images projected onto the third IHP component; (e) segmentation of the lesion using k-Means applied to (b); (f) the morphological postprocessing of the segmented images (e).
indicating robustness of the IHP algorithm to noise. Due to the lack of manual segmentations in this dataset, we were unable to estimate the precision. Again, five images from this dataset that contain considerable noise have been chosen, with segmentation results shown Fig. 5. The first row shows a set of the selected images with noise. The IHP was performed on these images and their pixels were projected onto the first component of the corresponding IHP. The projections and the corresponding histogram of pixels is shown in Fig. 5b-c. As it can be seen from the histograms, IHP succeeded in finding a projection with bimodal distribution of pixels with a good separation between the two modes. The final segmentation, without any postprocessing, by k-Means is demonstrated in Fig. 5d.

To demonstrate that the IHP is not limited to melanoma or RGB images and that it can be also successfully applied to other dermatological images as well as multi-spectral images, two psoriasis datasets have been chosen. The first dataset is a 35-image subset of the database introduced in Delgado et al. [32]. The original dataset has groups of images of the same lesion, collected during the same day, where almost no variation is present. Therefore, it is enough to segment only one image per group to evaluate the algorithm. As a consequence the study is constrained to a subset of images with a high appearance variation. The second dataset is composed of nine multi-spectral images [19]. Each image has nine bands ranging from ultra-violet to near-infrared. So far, dermatological studies based on digital images, have exclusively paid attention to tri-chromatic band images. Only a few works in spectroscopy have considered near-infrared images [20]–[22].

Fig. 6a shows five images taken from these two psoriasis datasets. The first four images are RGB images while the last image is an RGB representation of one of the nine multi-spectral images. Fig. 6bc demonstrate the images of Fig. 6a projected onto the first IHP component together with the corresponding histograms. It can be easily seen that the IHP is able to find a contrast-enhancing combination even in the presence of many image bands. As before,
Fig. 5. Example of segmentation on Hintz-Madsen’s [31] database: (a) original RGB melanoma images; (b) original images projected onto the first IHP component; (c) histograms of the pixels of the projected images; (d) segmentation of the lesion using the k-Means on the projected images (b).

the first IHP component and the k-Means algorithm are used to segment the lesion and the result is displayed in Fig. 6d. Again no postprocessing has been performed.

B. Lesion Substructure Characterization

In the previous set of experiments we were interested only in the properties of the first IHP component, which facilitates lesion segmentation. In this second set of experiments, we want to demonstrate how the other IHP components can be used to characterize the substructures inside the lesion. To achieve these goals Chen’s pigmented lesion dataset [13], the 35-image [32] and the 9-image psoriasis multispectral datasets [19] have been chosen.

The results obtained from the second step of the IHP in the melanoma dataset are shown in Fig. 4cd. It can
Fig. 6. Segmentation of psoriasis images: (a) five sample psoriasis images - the first four images are RGB psoriasis images and the last one is converted to the RGB from the 9-band image; (b) original images projected onto the first IHP component; (c) histograms corresponding to the projected images (b); (d) segmentation of the lesion using k-Means from projections (b).

be seen that the different substructures of the lesion are clearly visible. In particular the first component clearly enhances the lesion itself, and the second enhances its border. The image corresponding to the third component doesn’t carry much information and it can be easily verified that the corresponding histogram is unimodal gaussian, which means that most of the information for segmentation is accounted for by the first two components.

The fact that psoriasis is a more interpretable disease allows for a better evaluation of the performance of the IHP algorithm. Five images from this dataset are shown in Fig. 7a. It is known that psoriasis is characterized by the red area and the scales, which are clearly visible in Fig. 7bd. The second IHP component (Fig. 7c) exhibits other structures, such as vessels (the first image) or hair (third and fourth images).
IV. CONCLUSIONS

In this work, we have proposed the IHP algorithm that estimates a linear multispectral color space transformation optimal for segmentation of dermatological lesions. Projecting the images onto the first IHP component facilitates unsupervised lesion segmentation on these images. The other IHP components can be used to characterize the other different structures embedded in the lesion or in the image. Results have shown that the IHP appropriately segments the lesion in different dermatological datasets. The algorithm can be applied independently of the color space of the image, and the number of image bands. It was also demonstrated that IHP is robust with respect to noise (hair and ink).
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APPENDIX I

A. The CIE XYZ Color Space

The transformation from the RGB color space to XYZ space is defined by [15]

\[
\begin{pmatrix}
X \\
Y \\
Z
\end{pmatrix} =
\begin{pmatrix}
0.49 & 0.31 & 0.20 \\
0.18 & 0.81 & 0.01 \\
0.01 & 0.99 & 0.01
\end{pmatrix}
\begin{pmatrix}
R \\
G \\
B
\end{pmatrix}
\] (7)

B. The CIE 1976 L*u*v* Color Space

The L*u*v* color space is defined by [15]

\[
L^* = \begin{cases} 
116 \cdot \sqrt[3]{\frac{Y}{Y_n}} - 16, & Y/Y_n > 0.008856 \\
903.3 \cdot \frac{Y}{Y_n}, & \text{otherwise}
\end{cases}
\] (8)

\[
u^* = 13 \cdot L^* \cdot (u' - u'_n)
\] (9)

\[
v^* = 13 \cdot L^* \cdot (v' - v'_n)
\] (10)

where

\[
u' = \frac{4X}{X + 15Y + 3Z}; \quad u'_n = \frac{4X_n}{X_n + 15Y_n + 3Z_n}
\] (11)

\[
v' = \frac{9Y}{X + 15Y + 3Z}; \quad v'_n = \frac{9Y_n}{X_n + 15Y_n + 3Z_n}
\] (12)

The values \(X, Y, Z\) are the image coordinates in the XYZ color space and the tristimulus values \(X_n, Y_n, Z_n\) are those of the nominally white object-color stimulus. Usually, the white object-color stimulus is given by the radiant power of one of the CIE standard illuminates, for example \(D_{65}\) or \(A\), reflected into the observer’s eye by
the perfect reflecting diffuser. Under these conditions \(X_n, Y_n,\) and \(Z_n\) are the tristimulus values of the standard illumination with \(Y_n\) equal to 100.

C. The CIE 1976 \(L^*a^*b^*\) Color Space

The \(L^*a^*b^*\) color space is defined by [15]

\[
L^* = 903.3 \cdot \frac{Y}{Y_n} 
\]

\[
a^* = 500 \cdot [f(X/X_n) - f(Y/Y_n)]
\]

\[
b^* = 200 \cdot [f(Y/Y_n) - f(Z/Z_n)]
\]

where

\[
f(x) = \begin{cases} 
3 \sqrt{x}, & x > 0.008856 \\
7.787 \cdot x + \frac{16}{116}, & \text{otherwise} 
\end{cases}
\]

The meaning of the values \(X, Y, Z, X_n, Y_n,\) and \(Z_n\) is the same as in Appendix I-B.

APPENDIX II

GRAM-SCHMIDT ORTHOGONALIZATION

Given a set of \(n\) vectors, \(\{a_1, \ldots, a_n\}\), Gram-Schmidt algorithm builds a set of orthogonal vectors \(\{q_1, \ldots, q_n\}\) by

\[
q_1 = a_1
\]

\[
q_i = a_i - \sum_{j=1}^{i-1} \frac{q_j^T a_i}{q_j^T q_j} \cdot q_j
\]

Notice that the obtained vectors can easily be normalized to obtain a set of orthonormal vectors by \(q_i / ||q_i||\).

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