

**Combined correlation rules to detect skin on colored images based
on dynamic color clustering**

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A detecção de pele desempenha um papel importante em uma ampla gama de aplicações em processamento de imagens e visão computacional. Em suma, existem três abordagens principais para detecção de pele: baseadas em regras, aprendizado de máquina e híbridos. Elas diferem em termos de precisão e eficiência computacional. Geralmente, as abordagens com aprendizado de máquina e as híbridas superam os métodos baseados em regras, mas exigem um conjunto de dados de treinamento grande e representativo, bem como um tempo de classificação custoso, que pode ser um fator decisivo para aplicações em tempo real. Neste trabalho, propomos uma melhoria de um novo método de detecção de pele baseado em regras que funciona no espaço de cores YCbCr. Nossa motivação baseia-se na hipótese de que: (1) a regra original pode ser revertida e, (2) pixels de pele humana não aparecem isolados, ou seja, as operações de vizinhança são levadas em consideração. O método é uma combinação de algumas regras de correlação baseadas nessas hipóteses. Essas regras avaliam as combinações de valores de crominância Cb, Cr para identificar os pixels de pele, dependendo da forma e tamanho dos agrupamentos de cores de pele gerados dinamicamente. O método é muito eficiente em termos de esforço computacional, bem como robusto em cenas de imagens muito complexas.

Palavras-chave: detecção de pele, segmentação de pele humana, modelo de cores YCbCr, regras de correlação, agrupamento dinâmico de cores.

Abstract

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Skin detection plays an important role in a wide range of image processing and computer vision applications. In short, there are three major approaches for skin detection: rule-based, machine learning and hybrid. They differ in terms of accuracy and computational efficiency. Generally, machine learning and hybrid approaches outperform the rule-based methods, but require a large and representative training dataset as well as costly classification time, which can be a deal breaker for real time applications. In this work, we propose an improvement of a novel method on rule-based skin detection that works in the YCbCr color space. Our motivation is based on the hypothesis that: (1) the original rule can be reversed and, (2) human skin pixels do not appear isolated, i.e. neighborhood operations are taken in consideration. The method is a combination of some correlation rules based on these hypothesis. Such rules evaluate the combinations of chrominance Cb, Cr values to identify the skin pixels depending on the shape and size of dynamically generated skin color clusters. The method is very efficient in terms of computational effort as well as robust in very complex image scenes.

Keywords: skin detection, human skin segmentation, YCbCr color model, correlation rules, dynamic color clustering.

Contents

List of Acronyms	ix
List of Symbols	xi
List of Figures	xiii
List of Tables	xv
1 Introduction	1
1.1 Motivação	2
1.2 Trabalhos relacionados	2
1.3 Objetivos	3
1.4 Organização do texto	3
2 Related Work	5
3 Theoretical Background	7
3.1 Color models	7
3.1.1 Munsell color model	7
3.1.2 CIE color model	8
3.1.3 RGB color model	10
3.1.4 CMY color model	10
3.1.5 Color models of the YUV family	11
3.1.6 Color models of the HSI family	12
3.2 Machine learning	14
3.2.1 Support vector machines	16
3.2.2 k -Nearest Neighbors	18
3.2.3 Decision tree	20
4 Proposed Solution	23
4.1 Original Method	23
4.2 Extended Method	26
4.3 Neighborhood Extended Method	26
5 Evaluation	29
5.1 Datasets	29
5.1.1 UCI	29

5.1.2	SFA	30
5.1.3	Pratheepan	30
5.1.4	HGR	30
5.2	Evaluation measures	31
5.3	Primeiro experimento	31
5.4	Segundo experimento	33
6	Plano de Trabalho	37
6.1	Atividades previstas	37
6.2	Cronograma proposto	38
	Bibliography	39

List of Acronyms

AR	Aleix and Robert Face Database
CIE	Commission Internationale de l'Eclairage
CMY	Cyan, Magenta and Yellow
FERET	Face Recognition Technology database
HGR	Hand Gesture Recognition database
HSI	Hue, Saturation, Intensity
HSL	Hue, Saturation, Lightness
HSV	Hue, Saturation, Value
ID3	Iterative Dichotomiser 3
<i>k</i> -NN	<i>k</i> -Nearest Neighbors
NTSC	National Television System Committee
PAL	Phase Alternating Line
RBF	Radial Basis Function
RGB	Red, Green and Blue
SECAM	Sequential Color with Memory
SFA	Skin of FERET and AR Database
SVM	Support Vector Machines
UCS	Uniform Chromaticity Scale
UCI	University of California in Irvine skin/non skin dataset
YIQ	Luma, Hue and Saturation
YUV	Luma and Chrominance
WM	Wang-Mendel method

List of Symbols

L^*	Luminance
a^*	Green/red axis on $L^*a^*b^*$ color model
b^*	Blue/yellow axis on $L^*a^*b^*$ color model
u^*	Green/red axis on $L^*u^*v^*$ color model
v^*	Blue/yellow axis on $L^*u^*v^*$ color model
θ	Hue angle on HSI color model
\max	Max operator
\min	Min operator
$\mu_A(x)$	Membership function
\mathbb{R}	Set of real numbers
σ	Standard deviation of the Gaussian membership function
a_r	r -th attribute of a feature vector
D	Dataset
D'	Dataset in feature space
N	Dataset cardinality
K	Numbers of dataset partitions in cross-validation
α	Lagrange multiplier
ξ	Variável de relaxamento
C	Regularization parameter
Φ	Nonlinear feature expansion function
γ	Polynomial/RBF kernel parameter of a nonlinear SVM
$d(x_i, x_j)$	Distance function between x_i and x_j vectors
argmax	Arguments of maxima operator
$\delta(y, f(x_i))$	Binary function between y and $f(x_i)$ of a training sample x_i in k -NN
$H(D)$	Entropy of dataset D
y_{\oplus}	Positive samples rate
y_{\ominus}	Negative samples rate
$IG(D, a_r)$	Information gain of D partitioning by a_r attribute
$V(a_r)$	Set of all possible values of a_r
D_v	Subset of D where a_r is equal to v

List of Figures

3.1	Munsell color model	8
3.2	CIE 1931 chromaticity diagram	9
3.3	Unit cube representing the colors of the RGB model	10
3.4	CMY subtractive color model	11
3.5	Graphical representation of the HSI model	12
3.6	Decision boundary in the 2-dimensional space	15
3.7	Example of a problem of separable binary classes in a 2-dimensional space	17
3.8	Example of a k -NN application in the classification task in a 2-dimensional space	19
4.1	Graphical representation of the trapezoids as well as its parameters	23
4.2	Computation of Cr_{max} based on Cr values histogram of a 724×526 image	24
4.3	Neighbors evaluation with respect to a pixel P	27
5.1	3-dimensional view of the RGB channels of the UCI dataset	30
5.2	Examples of SFA face image database	34
5.3	Structure of the windows that form the SFA samples	35
5.4	Visão 3-dimensional dos canais RGB do conjunto de dados SFA	35
5.5	Examples of Pratheepan skin dataset	35
5.6	Examples of HGR skin dataset	36

List of Tables

5.1	Excerpt with samples from the UCI dataset	29
5.2	Confusion matrix table used during experiments	31
5.3	Tabela de busca dos parâmetros do estimador ótimo na SVM	32
5.4	Tabela de busca dos parâmetros do estimador ótimo no k -NN	32
5.5	Resultados dos experimentos com k -NN e SVM nos conjuntos de dados UCI e SFA .	32
5.6	Resultados dos experimentos com k -NN e SVM no conjunto de dados SFA em espaços de cores distintos	33
6.1	Disciplinas cursadas no programa de mestrado em Ciência da Computação no IME-USP.	37
6.2	Cronograma das atividades previstas	38

Chapter 1

Introduction

Skin detection can be defined as the process of identifying skin-colored pixels in an image. It plays an important role in a wide range of image processing and computer vision applications such as face detection, pornographic image filtering, gesture analysis, face tracking, video surveillance systems, medical image analysis, and other human-related image processing applications.

The problem is complex because of the numerous similar materials with human skin tone and texture, and also because of illumination conditions, ethnicity, sensor capturing singularities, geometric variations, etc. Because it is a primary task in image processing, additional requirements as real time processing, robustness and accuracy are also desirable.

Skin color is a strong characteristic and it is used in most algorithms for skin detection. It is normally used along with other features such as shape, texture, and geometry, or even as a preliminary step to classify regions of interest in an image.

The human skin color pixels have a restricted range of hues and are not deeply saturated, since the appearance of skin is formed by a combination of blood (red) and melanin (brown, yellow), which leads the human skin color to be clustered within a small area in the color space (Fleck *et al.*, 1996).

The choice of a color space is also a key point of a feature-based method when using skin color as a detection cue. Due to its sensitivity to illumination, the input image is, in general, first transformed into a color space whose luminance and chrominance components can be separate to mitigate the problem (Vezhnevets *et al.*, 2003).

Color has the ability of functioning as a descriptor that often simplifies the identification and extraction of an object in a scene. Moreover, the ability of humans to discern thousands of tonalities and intensities compared to only a few dozen levels of gray, put the color as a strong candidate feature in computer vision and image processing applications (Gonzalez e Woods, 2002).

Basically, there are three approaches for skin detection: rule-based, machine learning based and hybrid. They differ in terms of classification accuracy and computational efficiency. Machine learning and hybrid methods require a training set, from which the decision rules are learned. Such approaches outperform the rule-based methods but require a large and representative training dataset as well as it takes a long classification time, which can be a deal breaker for real time applications (Kakumanu *et al.*, 2007).

In this work we propose an improvement of a novel method on rule-based skin detection that works in the YCbCr color space (Brancati *et al.*, 2017). Our motivation is based on the hypothesis that the original rule can be complemented with another rule that is a reversal interpretation of the one proposed originally. Besides that, we also take in consideration that a skin pixel does not appear isolated, so we propose another variation based on neighborhood operations. The set of rules evaluate the combinations of chrominance Cb, Cr values to identify the skin pixels depending on the shape and size of dynamically generated skin color clusters (Brancati *et al.*, 2017). The method is very efficient in terms of computational effort as well as robust in very complex image scenes.

1.1 Motivação

Há diversos objetos ou observações na natureza que não podem ser classificados com conjuntos clássicos pelo fato de que a relação de pertinência não é bem definida (Pedrycz e Gomide, 1998). Especificamente no campo da visão computacional, vários problemas reais de classificação só podem ser resolvidos quando da análise do contexto onde o problema está inserido.

Sendo assim, a motivação deste trabalho está em analisar problemas reais de visão computacional cujos conjuntos de dados possuem incerteza e imprecisão, modelando-os por meio de conjuntos *fuzzy*, explorando a capacidade desses conjuntos de expressarem transições graduais de pertinência e não pertinência.

1.2 Trabalhos relacionados

Check if we will keep fuzzy part + ML approaches to move this part to next chapter.

Em alguns problemas de classificação, o uso de dados intervalares pode ser uma ferramenta poderosa na obtenção de bons resultados. Intervalos representados por conjuntos *fuzzy* também têm grande valia nesta tarefa. Com base nessa característica, Umano *et al.* (1994) propuseram um algoritmo para gerar uma árvore de decisão *fuzzy*, a partir de dados numéricos, usando conjuntos *fuzzy* previamente definidos. Essa implementação é uma adaptação do algoritmo Divisor Iterativo 3 (ID3) clássico proposto por Quinlan (1986), brevemente discutido na seção 3.2.3. A diferença fundamental para o ID3 está no método de seleção do atributo que particiona o conjunto de dados. Assim como no ID3, aqui também é utilizado o ganho de informação como critério, porém, ao invés de aplicar o valor dos atributos no cálculo, o algoritmo computa pelo grau de pertinência dos conjuntos *fuzzy*. Outra propriedade particular da árvore *fuzzy* está no processo de inferência, pois permite que mais de um ramo seja ativado quando um atributo é testado na avaliação do grau de pertinência.

O *fuzzy* ID3 foi utilizado por Bhatt *et al.* (2009) para segmentação de regiões de pele. O conjunto de dados aplicado no experimento contém os três canais de cores do modelo Vermelho, Verde e Azul (RGB) e também foi utilizado nos experimentos deste trabalho, conforme pode ser visto no capítulo 5. Antes da indução da árvore, os dados de treinamento foram aglomerados em cinco *clusters* por meio do algoritmo *fuzzy c-means* (Bezdek *et al.*, 1984). Os *clusters* foram aproximados com função de pertinência gaussiana. A taxa de erro obtida foi de 94,1%.

Outra variante de árvore de decisão para conjuntos *fuzzy* é a proposta de Cintra *et al.* (2013), porém, baseada na versão clássica C4.5, uma versão estendida do ID3 também criada por Quinlan (1993). Chamado de *FuzzyDT*, o algoritmo igualmente usa a entropia e o ganho de informação do C4.5 como medidas para decidir sobre a importância dos atributos. A estratégia de indução da árvore também é a mesma, ou seja, os dados são particionados recursivamente criando ramos até que uma classe é atribuída a cada folha. Porém, antes da indução da árvore, os atributos contínuos são definidos em termos de conjuntos *fuzzy*. Em outras palavras, a árvore é induzida com os valores dos atributos "discretizados", isto é, transformados em intervalos finitos, ou "discretos". O domínio dos conjuntos *fuzzy* devem ser estabelecidos previamente pelo usuário. Experimentos foram realizados com 16 conjuntos de dados distintos obtidos de Lichman (2013), comparando o desempenho do algoritmo com o C4.5 em termos da taxa de erro, número médio de regras e condições geradas por ambas técnicas. Em resumo, o *FuzzyDT* produziu resultados satisfatórios na maioria dos conjuntos de dados avaliados. O algoritmo foi utilizado para experimentos preliminares que podem ser vistos no capítulo 5.

Vale ressaltar que o *FuzzyDT* contém quatro métodos distintos de estimar o número de conjuntos *fuzzy* para cada atributo do conjunto de dados (Cintra *et al.*, 2011). Um deles define um número de conjuntos *fuzzy* uniforme para todos os atributos. Os demais são flexíveis, ou seja, permitem que o número de conjuntos *fuzzy* para cada atributo seja distinto. Um desses métodos é o ganho de informação, calculado e armazenado para cada atributo após o processo de "fuzzificação" dos valores contínuos. O processo é repetido 8 vezes, utilizando de 2 a 9 conjuntos *fuzzy* para cada atributo.

A base de dados final é, então, formada com o número de conjuntos *fuzzy* que produziram o maior ganho de informação para cada atributo. O segundo método é oriundo do algoritmo RELIEF que mede a utilidade dos atributos com base em sua capacidade de distinguir entre amostras semelhantes pertencentes a classes distintas. Ele produz um ranking de mérito médio dos atributos e funciona tanto em dados discretos como contínuos (Kononenko, 1994). O terceiro método é a implementação da técnica proposta por Wang (2003) e conhecida como Wang-Mendel (WM), onde cada atributo é definido usando de 2 a 9 conjuntos *fuzzy* e, em seguida, usado individualmente para gerar um classificador WM. As taxas de erro obtidas do classificador são usadas como critério para selecionar o número de conjuntos *fuzzy*. Os métodos foram avaliados em 11 conjuntos de dados, sendo que os métodos flexíveis mostraram melhores taxas de erro.

1.3 Objetivos

O principal objetivo deste projeto de mestrado está na avaliação de conjuntos *fuzzy* na aplicação em problemas de classificação em visão computacional, estabelecendo mecanismos comparativos, por meio de indicadores quantitativos e qualitativos, para mensurar seu desempenho em relação aos conjuntos clássicos.

Além disso, a escolha do espaço de cores para a modelagem dos dados como conjuntos *fuzzy* também será analisada com o intuito de compreender sua influência nos resultados obtidos pelo classificador.

1.4 Organização do texto

Quanto à organização deste trabalho, no capítulo 3 são explicitados conceitos fundamentais sobre diferentes modelos de cores, teoria *fuzzy* e classificadores utilizados no desenvolvimento deste estudo. No capítulo 5, são expostos os resultados de experimentos preliminares com conjuntos de dados de pele de seres humanos, bem como a avaliação da influência do modelo de cores escolhido para tratar este tipo de problema de classificação. Por fim, o capítulo 6 apresenta o plano de trabalho com as atividades a serem realizadas no âmbito desta pesquisa.

Chapter 2

Related Work

There are a large number of works of skin detection based on color information and there are a couple of them comparing different techniques and classifiers, mainly from the point of view of performance, color models, skin color modeling and different datasets (Kakumanu *et al.*, 2007; Mahmoodi e Sayedi, 2016; Vezhnevets *et al.*, 2003).

In Jones e Rehg (2002), the authors applied a Bayesian decision rule with a 3-dimensional histogram model constructed from approximately 2 billion pixels collected from 18,696 images over the Internet to perform skin detection. They calculated two different histograms for skin and non-skin in the RGB color space. Using those histograms along with training data, a classifier was derived with the standard likelihood ratio approach of a pixel be skin to not be skin. The best performance at an error rate of 88% was reached for histograms of size 32.

Another method explicitly defines, through a number of rules, the boundaries that delimit the grouping of skin pixels in some color space (Vezhnevets *et al.*, 2003). This was the approach adopted by Kovac *et al.* (2003) in the YCbCr color space, obtaining a true positive rate of 90.66%. They (Kovac *et al.*, 2003) also performed experiments with the chromaticity channels Cb and Cr only. The results showed that the performance of the classifier is inferior in relation to the approach using all Y, Cb and Cr channels. The key advantage of this method is the simplicity of skin detection rules that leads to the construction of a very fast classifier. On the other hand, achieving high recognition rates with this method is difficult because it is necessary to find a good color space and empirically appropriate decision rules (Vezhnevets *et al.*, 2003).

Differently from Kovac *et al.* (2003), the authors of Yogarajah *et al.* (2011) developed a technique where the thresholds defined in the rules are dynamically adapted. The method consists of detecting the region of the eye and extracting an elliptical region to delimit the corresponding face. A Sobel filter is applied to detect the edges of the resulting region which is subjected to a dilation. The resulting image is subtracted from the elliptical image. As a result, there is a more uniform skin region where the thresholds are calculated. The technique was used as a preprocessing step for Tan *et al.* (2012) in a strategy combining a 2-dimensional density histogram and a Gaussian model for skin color detection. The results showed an accuracy of 90.39%.

Naji *et al.* (2012) constructed an explicit classifier in the HSV color space for 4 different skin ethnic groups in parallel. After primitive segmentation, a rule-based region growth algorithm is applied, in which the output of the first layer is used as a seed, and then the final mask in other layers is constructed iteratively by neighboring skin pixels. The number of true positive pixels reported was of 96.5%.

Kawulok *et al.* (2013) combined global and local image information to construct a probability map that is used to generate the initial seed for spatial analysis of skin pixels. Seeds extracted using a local model are highly adapted to the image, which greatly improves the spatial analysis result.

Although color is not used directly in some skin detection approaches, it is one of the most decisive tools that affect the performance of algorithms (Mahmoodi e Sayedi, 2016). Despite the performance of most skin detectors is directly related to the choice of color space, Albiol *et al.* (2001) proved that the optimum performance of the skin classifiers is independent of the color space.

RGB is the most commonly used color space for storing and representing digital images, since the cameras are enabled to provide the images in such model. To reduce the influence of illumination, the RGB channels can be normalized and the third component can be removed, since it does not provide significant information (Kakumanu *et al.*, 2007). This characteristic led Bergasa *et al.* (2000) to construct an adaptive and unsupervised Gaussian model to segment skin into the normalized RGB color space, using only the channels r and g .

In Jayaram *et al.* (2004), a comparative study using a Gaussian approach and a histogram in a dataset of 805 color images in 9 different color spaces has been performed. The results revealed that the absence of the luminance component, which means using only two channels of the color space, significantly impacts the performance as well as the selection of the color space. The best results were obtained in the SCT, HSI and CIELab color spaces with histogram approach.

In Chaves-González *et al.* (2010), the authors compared the performance of 10 color spaces based on the k -means clustering algorithm on 15 images of the Aleix and Robert (AR) face image database (Martínez e Benavente, 1998). According to the results obtained, the most appropriate color spaces for skin color detection are YCgCr, YDbDr and HSV.

In Kaur e Kranthi (2012), an algorithm similar to that proposed by Kovac *et al.* (2003) have been implemented, where the boundaries that delimit the grouping of skin pixels are defined by explicit rules. After segmenting the image with the explicit rules, the algorithm also performs morphological and filtering operations to improve the accuracy of the method. The authors applied the algorithm in the YCbCr and CIELab color spaces, ignoring the Y and L luminance components, respectively. The results were more satisfactory when the algorithm was applied on CIELab. A similar technique was implemented in Shaik *et al.* (2015) and Kumar e Malhotra (2015) in the HSV and YCbCr color spaces, the latter providing the best results in both.

Finally, in Brancati *et al.* (2017), a novel rule-based skin detection method that works in the YCbCr color space based on correlation rules that evaluate the combinations of chrominance Cb, Cr values to identify the skin pixels depending on the shape and size of dynamically generated skin color clusters was proposed. Geometrically, the clusters create trapezoids in the YCb and YCr subspaces that reflect in the inversely proportional behavior of the chrominance components. The method was compared with six well known rule-based methods in literature outperforming them in terms of quantitative performance evaluation parameters. Moreover, the qualitative analysis shows that the method is very robust in critical scenarios.

Chapter 3

Theoretical Background

In this chapter, the theoretical concepts that apply to this research are stated. First, a short introduction to color models is provided in order to give an overview of the main characteristics of some of the most used in the computer vision and image processing area, on which this research is based. Thereafter, some machine learning methods are defined and explained, once they were used in the preliminary experiments of this work.

3.1 Color models

The use of color images in computer vision or image processing can be motivated by two main factors. The first refers to the powerful characteristic of color to function as a descriptor that often simplifies the identification and extraction of an object in a scene. The second is related to the ability of humans to discern thousands of tonalities and intensities compared to only a few dozen levels of gray (Gonzalez e Woods, 2002).

The visual perception of color by the human eye should not vary according to the spectral distribution of the natural light incident upon an object. In other words, the color appearance of objects remains stable under different lighting conditions. This phenomenon is known as color constancy (Gevers *et al.*, 2012).

As an example, the grass of a soccer stadium remains green throughout the day, even at dusk when, from a physical point of view, sunlight has a more reddish appearance.

The human perception of colors occurs by the activation of nerve cells that send signals to the brain about brightness, hue and saturation, which are usually the features used to distinguish one color from another (Gonzalez e Woods, 2002).

The brightness gives the notion of chromatic intensity. Hue represents the dominant color perceived by an observer. Saturation refers to the relative purity or amount of white light applied to the hue. Combined, hue and saturation are known as chromaticity and, therefore, a color must be characterized by its brightness and chromaticity (Gonzalez e Woods, 2002).

Colors can be specified by mathematical models in tuples of numbers in a coordinate system and a subspace within that system where each color is represented by a single point. Such models are known as the color models (Gonzalez e Woods, 2002).

These models can be classified as of two types: the additive models in which the primary color intensities are added to produce other colors and subtractive, where colors are generated by subtracting the length of the dominant wave from the white light.

The following sections briefly describe some of the major color models, as well as their variants and main areas of application.

3.1.1 Munsell color model

Pioneer in an attempt to organize the perception of color in a color space, Albert H. Munsell was able to combine the art and science of colors in a single theory (Plataniotis e Venetsanopoulos,

2000).

The principle of equality of visual spacing between the components of the model is the essential idea of the Munsell color model. These components are hue, value, corresponding to luminance, and chroma, corresponding to saturation (Plataniotis e Venetsanopoulos, 2000).

The model is represented by a cylindrical shape and it can be seen in the figure 3.1. The hue is arranged in the circular axis consisting of five base as well as five secondary colors, the saturation in the radial axis and the luminance in the vertical axis in a range varying from 0 to 10.

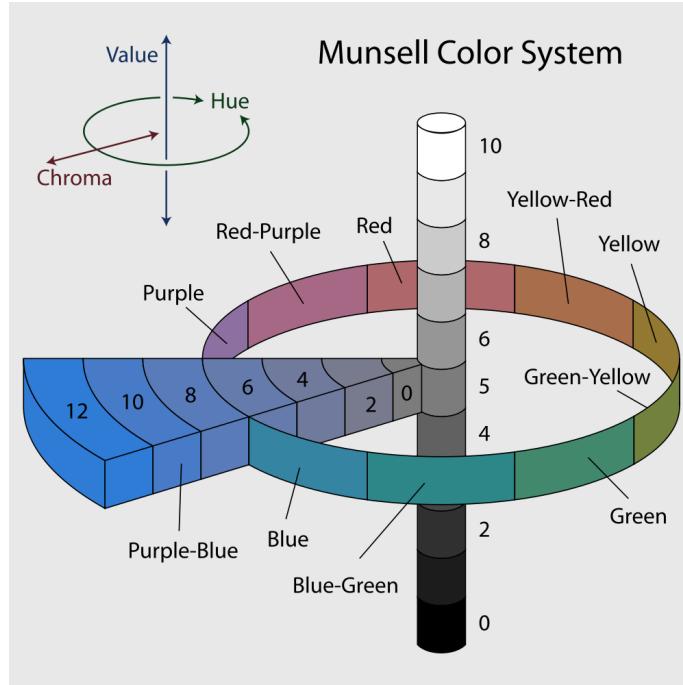


Figure 3.1: Munsell color model represented by a cylindrical shape. The hue is arranged on the circular axis consisting of five base and five secondary colors, the saturation on the radial axis and the luminance on the vertical axis in a range varying from 0 to 10. Source: Rus (2007).

3.1.2 CIE color model

In 1931, the CIE established the first mathematical model of color numerical specification, whose objective was to analyze the relationship between the physical aspects of colors in the electromagnetic spectrum and their perception by the human visual system to determine how an ordinary person perceives the color. A review of this specification was published in 1964 (Gonzalez e Woods, 2002).

The experiment that originated the standard consisted in detecting the colors perceived by an observer from a mixture of three primary colors X, Y and Z called tristimulus values. These coordinates gave rise to the CIE XYZ color space which encompasses all the colors that can be perceived by an ordinary human being. For this reason, it is considered an device independent representation (Plataniotis e Venetsanopoulos, 2000).

The system proposed by the CIE XYZ to describe a color is based on a luminance component Y, and two additional components X and Z, that bring the chromaticity information. This system is formed by imaginary colors that can be expressed as combinations of the normalized measures shown in the equations 3.1, 3.2 and 3.3.

$$x = \frac{X}{X + Y + Z} \quad (3.1)$$

$$y = \frac{Y}{X + Y + Z} \quad (3.2)$$

$$z = \frac{Z}{X + Y + Z} \quad (3.3)$$

where $x + y + z = 1$.

Combinations of negative values and other problems related to selecting a set of real primaries are eliminated. The chromaticity coordinates x and y allow to represent all colors in a two-dimensional plane, also known as a chromaticity diagram, which can be seen in the figure 3.2.

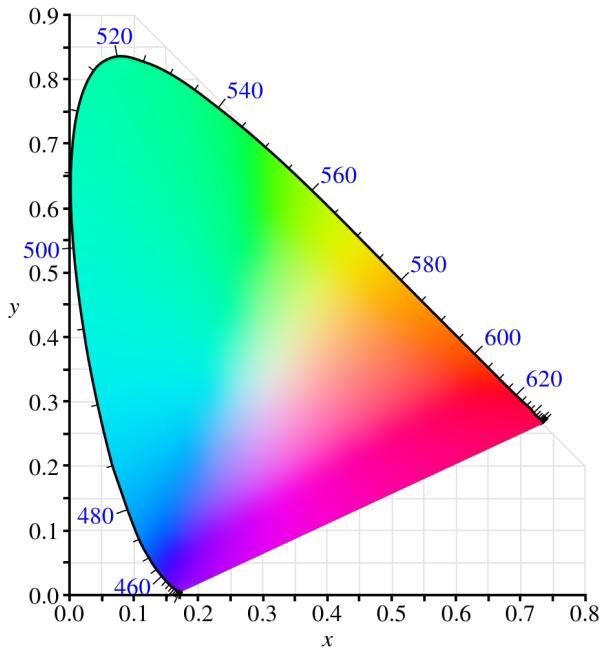


Figure 3.2: CIE 1931 chromaticity diagram. The points representing pure colors in the electromagnetic spectrum are labeled according to their wavelengths and are located along the curve from the right end of the x -axis, corresponding to the red color, to the left end of the same axis, corresponding to the violet color, forming a polygon similar to a horseshoe. The internal points correspond to all possible combinations of visible colors. Source: Ben (2009).

The coordinates $(x = 1/3, y = 1/3)$ correspond to the location of white light, also known as white point, and serve as reference in the process of image capture, coding, or reproduction.

CIE also derived and standardized two other color models based on CIE XYZ specification and, likewise, are device independent. Both are perceptually uniform, which means that equal perceptual distances separate all colors in the system (Vezhnevets *et al.*, 2003). As an example, the gray scale of the space should allow for a smooth transition between black and white.

The first one was designed to reduce the problem of perceptual non-uniformity. Some Uniform Chromaticity Scale (UCS) diagrams were proposed based on mathematical equations to transform the values XYZ or the coordinates x, y into a new set of values (u, v) , which gave rise to the 1960 CIE uv chromaticity diagram (Gevers *et al.*, 2012).

Still with unsatisfactory results, the CIE made a new change by multiplying the v component by a factor of 1.5. In addition, the brightness scale given by the Y component has been replaced by $L^* = [0, 100]$ to better represent the differences in luminosity that are equivalent. This revision originated the CIE 1976 $L^*u^*v^*$ color model, commonly known by the acronym CIELuv (Gevers *et al.*, 2012).

In 1976 the CIE adopted a new color model, based on the L, a, b model, proposed by Richard Hunter in 1948, which best represented the uniform spacing of colors. Named CIE $L^*a^*b^*$ and known by the acronym CIELab, it is a space based on opponent colors ¹ in which the color stimuli

¹Theory started around 1500 when Leonardo da Vinci concluded that colors are produced by mixing yellow and blue, green and red, and white and black. In 1950, this theory was confirmed when optically-colored signals were detected at the optical connection between the retina and the brain (Gevers *et al.*, 2012).

of retina is converted to distinctions between light and dark, red and green, and blue and yellow, represented by the axes L^* , a^* , and b^* , respectively (Gevers *et al.*, 2012).

3.1.3 RGB color model

The RGB model, an acronym for Red, Green, and Blue, is an additive color model in which the three primary colors red, green and blue are added to produce the others (Gonzalez e Woods, 2002).

This system was based on the trichromatic theory of Thomas Young and Hermann Helmholtz in the mid-19th century and can be represented graphically through the unit cube defined on the axes R, G and B, as illustrated in the figure 3.3 (Plataniotis e Venetsanopoulos, 2000).

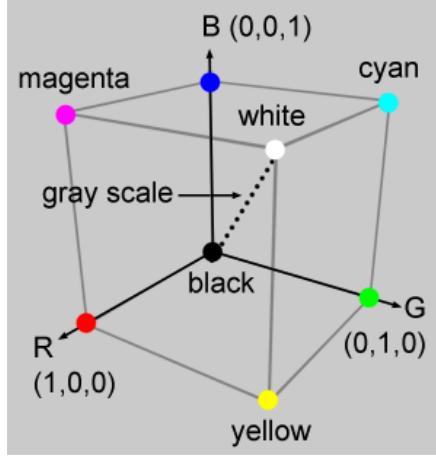


Figure 3.3: Unit cube representing the colors of the RGB model. The origin, given by the vertex $(0, 0, 0)$, represents the black color. The vertex $(1, 1, 1)$, opposite the origin, represents the white color. The highlighted vertices on the axes represent the primary colors and the others are the complement of each. Each point inside the cube corresponds to a color that can be represented by the triple (r, g, b) , where $r, g, b \in [0, 1]$. The shades of gray are represented along the main diagonal of the cube, with each point along this diagonal being formed by equal contributions of each primary color. Source: adapted from Gonzalez e Woods (2002).

It is noteworthy that there are two ways of representing the RGB space: linear and non-linear. The above-mentioned system shows the non-linear model, whose abbreviation is $R'G'B'$, and is most used by devices and applications because of their similarity to the human visual system. In the literature, this system is frequently cited with the acronym RGB, which makes the nomenclature dubious, since the linear model is also called RGB and, therefore, the conversion between color spaces must be done with some caution. It is also important to note that linear RGB values are rarely used to represent an image since they are perceptually highly non-uniform (Plataniotis e Venetsanopoulos, 2000).

3.1.4 CMY color model

The CMY model is based on the complementary primary colors Cyan, Magenta, and Yellow and, unlike RGB, is a subtractive color model in which colors are generated by subtracting the length of the dominant wave from the white light and, therefore, the resulting color corresponds to the light that is reflected (Gonzalez e Woods, 2002).

One way to get the CMY system is:

$$\begin{bmatrix} C \\ M \\ Y \end{bmatrix} = \begin{bmatrix} B \\ R \\ G \end{bmatrix} + \begin{bmatrix} G \\ B \\ R \end{bmatrix} \quad (3.4)$$

or by making a change of coordinates by subtracting the primary colors R, G and B of the white

color $W = (1, 1, 1)$ (Gonzalez e Woods, 2002):

$$\begin{bmatrix} C \\ M \\ Y \end{bmatrix} = \begin{bmatrix} 1 \\ 1 \\ 1 \end{bmatrix} - \begin{bmatrix} R \\ G \\ B \end{bmatrix} \quad (3.5)$$

Likely RGB, CMY is device dependent. The model is widely used in equipment that deposits colored pigments on paper, such as color printers or photocopiers. The figure 3.4 shows how the model components are combined to generate the other colors.

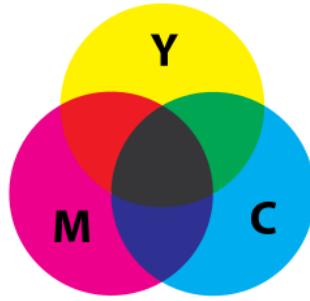


Figure 3.4: CMY subtractive color model. It is interesting to note that the intersection of yellow with magenta generates the red color, magenta with cyan generates the blue color and cyan with yellow generates the green color. Source: Rus (2008).

Overlapping the CMY primary colors in equal amounts to generate the black color typically creates a tint that is close to brown or dark green. To avoid this undesired effect, the black component is usually added to the system, represented by the letter K. This operation gives rise to a new model known as CMYK (Gonzalez e Woods, 2002).

3.1.5 Color models of the YUV family

The acronym YUV stands to a family of color spaces of which the luminance information, represented by the Y component, is coded separately from the chrominance, given by the components U and V. The components U and V are representations of signals of the difference of the blue subtracted from luminance (B-Y) and red subtracted from luminance (R-Y). It is used to represent colors in analogue television transmission systems in the Phase Alternating Line (PAL) and Sequential Color with Memory (SECAM) (Pedrini e Schwartz, 2008).

The transformation of the RGB space to YUV is given by:

$$\begin{bmatrix} Y \\ U \\ V \end{bmatrix} = \begin{bmatrix} 0.299 & 0.587 & 0.114 \\ -0.147 & -0.289 & 0.436 \\ 0.615 & -0.515 & -0.100 \end{bmatrix} \begin{bmatrix} R \\ G \\ B \end{bmatrix} \quad (3.6)$$

where $0 \leq R, G, B \leq 1$.

Analogous to the YUV, the YIQ model was adopted in 1950 by the National Television System Committee (NTSC), an American standard for color television signal transmission. In this model, the Y component corresponds to luminance and the components I (hue) and Q (saturation) encode the chrominance information (Pedrini e Schwartz, 2008).

The transformation of the RGB space to YIQ is given by:

$$\begin{bmatrix} Y \\ I \\ Q \end{bmatrix} = \begin{bmatrix} 0.299 & 0.587 & 0.114 \\ 0.596 & -0.275 & -0.321 \\ 0.212 & -0.523 & -0.311 \end{bmatrix} \begin{bmatrix} R \\ G \\ B \end{bmatrix} \quad (3.7)$$

where $0 \leq R, G, B \leq 1$.

Another color model of the YUV family is the YCbCr, mathematically defined by a coordinate transformation with respect to some RGB space (Pedrini e Schwartz, 2008).

The YCbCr model is widely used in digital videos. In this system, the Y component represents luminance, Cb component gives the measurement of the difference between the blue color and a reference value, similar to the Cr component which is the measurement of the difference between the red color and a reference value (Pedrini e Schwartz, 2008).

The transformation of the RGB space to YCbCr is given by:

$$\begin{bmatrix} Y \\ Cb \\ Cr \end{bmatrix} = \begin{bmatrix} 0.299 & 0.587 & 0.114 \\ -0.169 & -0.331 & 0.5 \\ 0.5 & -0.419 & -0.081 \end{bmatrix} \begin{bmatrix} R \\ G \\ B \end{bmatrix} \quad (3.8)$$

3.1.6 Color models of the HSI family

Hue, Saturation, and Intensity (HSI) models are best suited for image processing applications from the user's point of view, due the correlation with human perception of the color (Plataniotis e Venetsanopoulos, 2000).

In this model, as in YIQ, the intensity given by I component is decomposed from the chrominance information, represented by the hue (H) and saturation (S) (Plataniotis e Venetsanopoulos, 2000). The combination of these components results in a pyramidal structure which can be seen in figure 3.5.

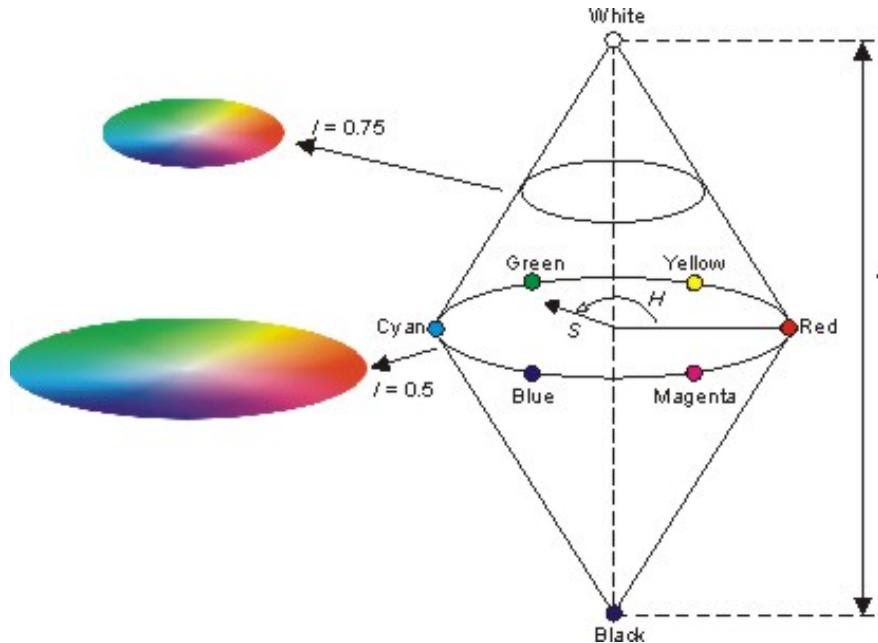


Figure 3.5: Graphical representation of the HSI model. The hue describes the color itself, in the form of an angle θ , where $\theta \in [0, 360]$. Red is at 0 degree, yellow at 60, green at 120, and so on. The saturation component, which varies between 0 and 1, indicates how much color is polluted with white color. The intensity scale is between [0, 1], where 0 means black and 1, white. Source: [Ice \(2016\)](#).

The transformation of the components of the RGB space to HSI is given by the equations:

$$\begin{aligned}\theta &= \cos^{-1} \left(\frac{(R - G) + (R - B)}{2\sqrt{(R - G)^2 + (R - B)(G - B)}} \right) \\ H &= \begin{cases} \theta, & \text{if } B \leq G \\ 360 - \theta, & \text{otherwise} \end{cases} \\ S &= 1 - \frac{3\min(R, G, B)}{R + G + B} \\ I &= \frac{R + G + B}{3}\end{aligned}\tag{3.9}$$

It is important to note that the values R, G and B must be normalized in the interval between 0 and 1. The intensity I and the saturation S are also normalized between 0 and 1.

Another model of this family is formed by the components Hue, Saturation and Value (HSV) and its three-dimensional graphical representation is a hexagonal pyramid derived from the RGB cube (Pedrini e Schwartz, 2008). Value, in this context, is the luminance component.

The various hue shades are represented at the top of the pyramid, the saturation is measured along the horizontal axis and value is measured along the vertical axis, which passes through the center of the pyramid. The hue, which corresponds to the edges around the vertical axis, varies from 0 (red) to 360 degrees and the angle between the vertices is 60 degrees. The saturation varies from 0 to 1 and is represented as the ratio of the purity of a given hue to its maximum purity, that is, when $S = 1$. Value varies from 0, at the peak of the pyramid representing the black color, to 1 at the base, where the intensities of the colors are maximum (Pedrini e Schwartz, 2008).

The transformation of the components of the RGB space to HSV is given by the equations:

$$\begin{aligned}H &= \begin{cases} 60 \frac{(G - B)}{M - m}, & \text{if } M = R \\ 60 \frac{(B - R)}{M - m} + 120, & \text{if } M = G \\ 60 \frac{(R - G)}{M - m} + 240, & \text{if } M = B \end{cases} \\ S &= \begin{cases} \frac{(M - m)}{M}, & \text{if } M \neq 0 \\ 0, & \text{otherwise} \end{cases} \\ V &= M\end{aligned}\tag{3.10}$$

where $m = \min(R, G, B)$ and $M = \max(R, G, B)$. The luminance V and saturation S are normalized between 0 and 1. The H hue ranges from 0 to 360 degrees.

Similarly to HSV, the Hue, Saturation and Lightness (HSL) model is a three-dimensional representation and is formed by two cones of height 1, whose bases are coincident (Pedrini e Schwartz, 2008).

The hue is determined by the points in the circle of the common bases to the cones. The saturation varies from 0 to 1, depending on the distance to the axis of the cone. The lightness is along the vertical axis common to the two cones and varies in the scale $[0, 1]$, where 0 means black and 1, white (Pedrini e Schwartz, 2008).

The conversion of the RGB space to HSL is given by the equations:

$$H = \begin{cases} 60 \frac{(G - B)}{M - m}, & \text{if } M = R \\ 60 \frac{(B - R)}{M - m} + 120, & \text{if } M = G \\ 60 \frac{(R - G)}{M - m} + 240, & \text{if } M = B \end{cases} \quad (3.11)$$

$$S = \begin{cases} \frac{(M - m)}{M + m}, & \text{if } 0 < L \leq 0,5 \\ \frac{(M - m)}{2 - (M + m)}, & \text{if } L > 0,5 \\ 0, & \text{if } M = m \end{cases}$$

$$L = \frac{M + m}{2}$$

where $m = \min(R, G, B)$ and $M = \max(R, G, B)$. The lightness V and saturation S are normalized between 0 and 1. Note that the transformation of the H component is the same as that used in the conversion of the RGB to HSV space in 3.10 and varies between 0 and 360 degrees.

All the color models of this family have the property of thinking of lighter colors, obtained by increasing the brightness or lightness, and darker colors, by the diminution of the same values. The intermediate colors are produced by decreasing the saturation (Pedrini e Schwartz, 2008).

3.2 Machine learning

Machine learning is an area that is concerned with the development of computer programs capable of improving automatically with the experience (Mitchell, 1997). This definition is closely linked to the way humans learn. Research efforts in this area have been carried out with the purpose of bringing this relationship closer.

As an example, in showing the image of a tree to a three-year-old child, she will most likely know how to recognize it, as she must have been exposed to situations where she has seen similar images, and was trained to do so answer. Then, she learned what a tree is by looking at them, not necessarily by precise mathematical definitions. In other words, the learning was done on the basis of data that are often used to obtain empirical solutions to certain problems where there is no possibility of creating an analytical solution (Abu-Mostafa *et al.*, 2012).

Similarly, an algorithm can be trained to differentiate a tree from other objects based on a set of data that has descriptions about the trees, such as height, colors, thickness, length, and so on. These descriptions are also called attributes, properties or features, and are submitted to a classifier that evaluates the presented evidences and makes a decision about the object being analyzed (Duda *et al.*, 2012). This task begins with the definition of a feature vector in a d -dimensional space, of the form (Duda *et al.*, 2012):

$$x = \begin{bmatrix} a_1 \\ a_2 \\ \vdots \\ a_d \end{bmatrix} \quad (3.12)$$

where $x \in X$ and X is the input space, that is, all of the x possible vectors.

The dataset is formed by N of these vectors and, therefore, the problem now is to partition the feature space in such a way that a decision boundary is formed (Duda *et al.*, 2012). We can then assign a specific class or label y for a given vector, where $y \in Y$ and Y is a finite set of classes which, in the binary case, is of the form $Y = \{+1, -1\}$. Figure 3.6 shows partitioning examples of

a 2-dimensional space of skin and non-skin samples from the SFA dataset ².

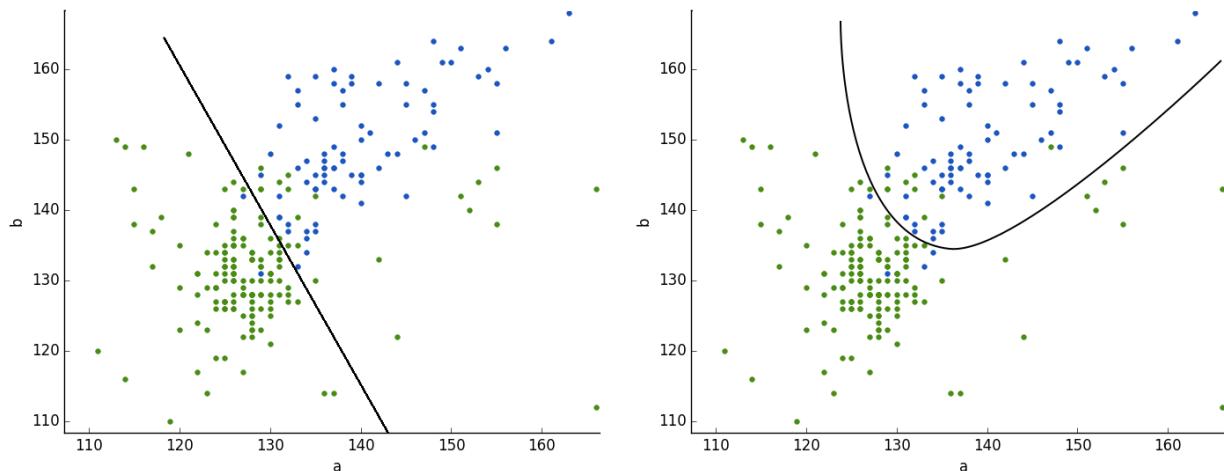


Figure 3.6: Decision boundary in the 2-dimensional space of skin and non-skin samples of the SFA dataset. The axes represent the channels a and b of the Lab color model. The figures on the left and right show the separation of the feature space by linear and non-linear functions, respectively. It is noteworthy that, computational complexity increases significantly in cases where there are many features. Source: proposed by the author.

Note that the decision boundary is a hypothetical function that the learning algorithm must produce based on training data. It should be as close as possible to a target function or objective function $f : X \mapsto Y$ that is unknown (Abu-Mostafa *et al.*, 2012).

This type of approach is characterized as supervised learning, that is, the training data contain explicit samples of how the correct output should be on an input vector (Abu-Mostafa *et al.*, 2012).

In unsupervised learning, also known as clustering, it is unknown what classes the training data belong to. The mission of the classifier, in this case, is to agglomerate input data into natural clusters (Duda *et al.*, 2012). Therefore, unsupervised learning can be seen as a task of finding patterns or structures spontaneously from the input data (Abu-Mostafa *et al.*, 2012).

Another approach is reinforcement learning which, just as in unsupervised learning, does not use labeled input data. The output proposed by the training is used along with a measure of its quality to improve the results of the classifier (Abu-Mostafa *et al.*, 2012).

Still on the results of the classifier, it is important to point out that learning the parameters of a target function and testing it on the same data is a fundamental error because the model would repeat the labels of the samples as soon as they were trained, implying a perfect fit of the data. However, it would not be enough to predict anything useful about new input data. This phenomenon is called over-fitting and to avoid it, the dataset is then partitioned so as to store some of the data for a subsequent test step, in order to find the best-performing estimator (Abu-Mostafa *et al.*, 2012).

Splitting the data into disjoint training and testing subsets is an effective approach when a large amount of data is available. However, when data is limited, retaining part of them for the test set further reduces the number of samples available for training (Mitchell, 1997). Therefore, another approach, known as cross-validation, can be applied so that the entire dataset is used in training and testing.

The cross-validation consists of dividing the dataset D into K disjoint subsets D_1, D_2, \dots, D_K , where each subset has an approximate size of N/K . The model is then trained on each of these subsets, except one that is maintained as a validation set, in which the error measure is calculated. This process is repeated K times, in such a way that each of the subsets has the opportunity to act as the test set. By this reason, this approach is also known as *K-fold*. At the end of all K iterations, the mean error obtained by each estimator is used as the performance measure of the classifier

²This dataset will be detailed in the section 5.1.

(Abu-Mostafa *et al.*, 2012).

Some of the classifiers that were used in the preliminary experiments of the chapter 5 will be briefly discussed in the sections 3.2.1, 3.2.2 and 3.2.3.

3.2.1 Support vector machines

Support Vector Machines (SVM) are a machine learning technique based on the Statistical Learning Theory (Vapnik, 2013), whose objective was to solve problems of classification of patterns. In practice, an SVM has the ability to generate a hyperplane or set of hyperplanes in a space of high or infinite dimensionality, which can be used for classification, regression, or other tasks (Duda *et al.*, 2012).

Derived from the technique name itself, the support vectors are the training set samples that define the optimal hyperplane and are the most difficult patterns to classify (Duda *et al.*, 2012). Intuitively, they are the most relevant patterns for the classification task, since a change in these vectors directly implies in the result of the optimal hyperplane³.

Let the training dataset with N samples of the form:

$$D = (x_1, y_1), (x_2, y_2), \dots, (x_N, y_N) \quad (3.13)$$

where each x_i is a d -dimensional vector of the form given by 3.12, $i = 1, 2, \dots, N$, $y_i \in Y$ and $Y = \{+1, -1\}$. Therefore, the training dataset contain N observations with its respective labels.

Supposing that D is linearly separable, one can separate the data by means of a hyperplane using a classifier, also linear, defined by the equation (Lorena e Carvalho, 2003):

$$w \cdot x + b = 0 \quad (3.14)$$

where $w \cdot x$ is a dot product, w is the normal vector to the hyperplane and b is a bias term. The parameter $\frac{b}{\|w\|}$ determines the offset of the hyperplane in relation to the origin.

From this definition, two other parallel hyperplanes to the optimal hyperplane can be obtained, according to the equations in 3.15, so that a delimited region, known as margin, rises between them.

$$\begin{cases} w \cdot x + b = +1 \\ w \cdot x + b = -1 \end{cases} \quad (3.15)$$

In addition, some constraints are defined to avoid that there are no points between $w \cdot x + b = 0$ and $w \cdot x + b = \pm 1$. Formally, we have (Lorena e Carvalho, 2003):

$$\begin{cases} w \cdot x_i + b \geq +1, & \text{if } y_i = +1 \\ w \cdot x_i + b \leq -1, & \text{if } y_i = -1 \end{cases} \quad (3.16)$$

or, similarly:

$$y_i(w \cdot x_i + b) \geq 1 \quad (3.17)$$

According to Campbell (2000), in the system given by equation 3.16, it is assumed that the margin is always greater than the distance between $w \cdot x + b = 0$ and $|w \cdot x + b = 1|$ and, for this reason, SVMs of this nature are usually referred as hard-margin SVMs. Figure 3.7 shows the graphical representation of these concepts.

Geometrically, the distance between the two parallel hyperplanes to the optimal hyperplane is $\frac{2}{\|w\|}$. Consequently, one can deduce that the distance between the optimal hyperplane and $w \cdot x + b = \pm 1$ is $\frac{1}{\|w\|}$. Then, the minimization of $\|w\|$ maximizes the margin and, thus, we have an optimization problem in which we want to minimize $\|w\|^2$ subject to the constraints in 3.17

³The optimal separation hyperplane of an SVM is that of a class of hyperplanes with the highest separation margin between the two training sets (Cortes e Vapnik, 1995).

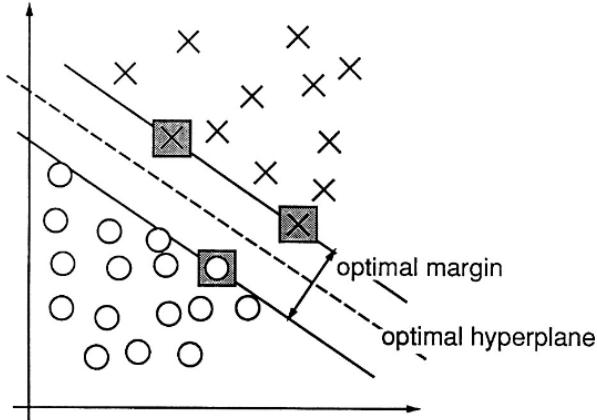


Figure 3.7: Example of a problem of separable binary classes in a 2-dimensional space. The support vectors, marked with gray squares, define the margin with highest separation between the two classes. Source: [Cortes e Vapnik \(1995\)](#).

(Lorena e Carvalho, 2003). Therefore, optimal w and b that solve this problem define the classifier and can be obtained by Lagrange multipliers ([Campbell, 2000](#)):

$$\text{Maximize: } \sum_{i=1}^N \alpha_i - \frac{1}{2} \sum_{i,j=1}^N \alpha_i \alpha_j y_i y_j x_i \cdot x_j \quad (3.18)$$

$$\text{Subject to: } \begin{cases} \alpha_i \geq 0 \\ \sum_{i=1}^N \alpha_i y_i = 0 \end{cases} \quad (3.19)$$

where α are the Lagrange multipliers.

It is important to note that this type of SVM succeeds in linearly separable training datasets. In cases where the data are non-linearly separable, some classification errors are allowed for the training set, by the inclusion of relaxation variables ([Lorena e Carvalho, 2003](#)). These changes were produced by [Cortes e Vapnik \(1995\)](#) and are part of a technique called margin smoothing, and therefore, SVMs of this family are also called soft-margin SVMs. So, the optimization problem becomes ([Lorena e Carvalho, 2003](#)):

$$\text{Minimize: } \|w\|^2 + C \sum_{i=1}^N \xi_i \quad (3.20)$$

$$\text{Subject to: } \begin{cases} \xi_i \geq 0 \\ y_i(w \cdot x_i + b) \geq 1 - \xi_i \end{cases} \quad (3.21)$$

where C is an regularization constant, empirically determined, that imposes a different weight for training in relation to generalization. Thus, the problem can be solved in the same way with the equation in 3.18, but with some changes in the constraints ([Lorena e Carvalho, 2003](#)):

$$\text{Subject to: } \begin{cases} 0 \leq \alpha_i \leq C \\ \sum_{i=1}^N \alpha_i y_i = 0 \end{cases} \quad (3.22)$$

In general, most classification problems prevent linear classifiers from being used because it is not possible to obtain satisfactory results in the partitioning of training data by a hyperplane. However, linear SVMs can be extended to deal with this situation by mapping the input space

into a higher-dimensional feature space, typically much larger than the original space (Duda *et al.*, 2012), of the form:

$$D' = (\Phi(x_1), y_1), (\Phi(x_2), y_2), \dots, (\Phi(x_N), y_N) \quad (3.23)$$

The proper choice of a function Φ makes the training set linearly separable in the transformed space (Lorena e Carvalho, 2003). The shape of the optimal hyperplane is now defined by:

$$w \cdot \Phi(x) + b = 0 \quad (3.24)$$

Therefore, the concepts of support vectors, margin, parallel hyperplanes, and hence, optimization problem to find the solution for the w and b parameters apply here in a similar manner. Formally, the optimization problem can be solved as (Lorena e Carvalho, 2003):

$$\text{Maximize: } \sum_{i=1}^N \alpha_i - \frac{1}{2} \sum_{i,j=1}^N \alpha_i \alpha_j y_i y_j \Phi(x_i) \cdot \Phi(x_j) \quad (3.25)$$

subject to the same constraints given by 3.22.

Now, there is a need to define as the inner product $\Phi(x_i) \cdot \Phi(x_j)$ between two vectors $x_i, x_j \in D$ is realized, whose answer lies in the introduction of the concept of *kernels* (Lorena e Carvalho, 2003).

Kernels are functions that have the purpose of projecting the input vectors in a features space with exponential or infinite number of dimensions (Shawe-Taylor e Cristianini, 2004), of the form:

$$k(x_i, x_j) = \Phi(x_i) \cdot \Phi(x_j) \quad (3.26)$$

Thus, it is possible to apply a *kernel* as described in the equation 3.26 in the SVM optimization step, efficiently calculating the internal product from the input data, without even explicitly computing the mapping of the Φ function (Shawe-Taylor e Cristianini, 2004).

Some of the most commonly used *kernels* are (Lorena e Carvalho, 2003):

(i) Linear *kernel*

$$k(x_i, x_j) = (x_i \cdot x_j) \quad (3.27)$$

The linear *kernel* is the simplest of the *kernel* functions and it is given by the internal product of two vectors x_i and x_j .

(ii) Polynomial *kernel*

$$k(x_i, x_j) = (\gamma x_i \cdot x_j + r)^g \quad (3.28)$$

Where g is the degree of the polynomial and r is a constant term. For this *kernel*, the Φ mappings are also polynomial functions, so the complexity is proportional to the choice of g (Lorena e Carvalho, 2003).

(iii) Gaussian *kernel*

$$k(x_i, x_j) = \exp(-\gamma \|x_i - x_j\|^2) \quad (3.29)$$

Also known as Radial Basis Function (RBF), the Gaussian *kernel* corresponds to a features space of infinite dimension (Lorena e Carvalho, 2003).

For the RBF and polynomial *kernels*, the γ parameter can be seen as the inverse of the radius of influence of samples selected by the model as support vectors (Pedregosa *et al.*, 2011).

3.2.2 *k*-Nearest Neighbors

The *k*-Nearest Neighbors (*k*-NN) is an algorithm based on instances, which means that the target function is not learned based on training samples; they are simply stored, so that the relation

between a new sample and the stored training samples is evaluated, and a target function is then assigned to it (Mitchell, 1997).

As the name suggests, k -NN classifies a new point x by assigning it the highest frequency class of the k closest samples, that is, the decision of the class of x is made by majority of the votes of the k nearest neighbors, and for this reason, it is interesting that the choice of k be an odd number to avoid draws (Duda *et al.*, 2012).

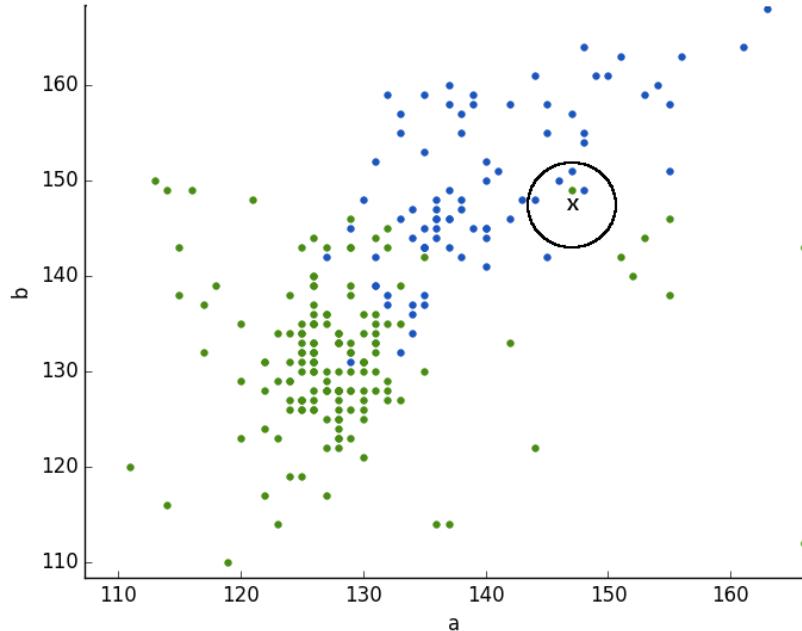


Figure 3.8: Example of a k -NN application in the classification task in a 2-dimensional space. The algorithm evaluates the k samples near x , creating a spherical region, and labels x with the highest frequency class. In this case, $k = 5$ and the class assigned to x must be the same as the blue points. Source: proposed by the author.

Let D be the training dataset with N samples as given in 3.13. Therefore, the distance between two samples x_i and x_j can be obtained in terms of the Euclidean distance, defined as:

$$d(x_i, x_j) = \sqrt{\sum_{r=1}^d (a_r(x_i) - a_r(x_j))^2} \quad (3.30)$$

where a_r refers to the r th attribute of the input vector x and $i, j = 1, 2, \dots, N$. Other distance metrics can be attributed to $d(x_i, x_j)$, such as, Manhattan, Chebyshev, and Minkowski (Duda *et al.*, 2012).

In order to classify a new sample x_q , we take x_1, \dots, x_k instances of the training set, whose distances given by 3.30, are of the k points nearest to x_q . Thus, the function that estimates the class of x_q is given by (Mitchell, 1997):

$$g(x_q) = \operatorname{argmax}_{y \in Y} \sum_{i=1}^k \delta(y, f(x_i)) \quad (3.31)$$

where

$$\delta(y, f(x_i)) = \begin{cases} 1, & \text{if } y = f(x_i) \\ 0, & \text{otherwise} \end{cases} \quad (3.32)$$

It is important to note that $f(x_i)$ is known, that is, it is the class of the sample x_i of the training set.

An obvious variation of the function given in equation 3.31 is the assignment of weights of each neighbor k , according to its distance, to a point x_q being classified (Mitchell, 1997). This variation

implies that points closer to x_q have more influence on its labeling. Formally, we have (Mitchell, 1997):

$$g(x_q) = \operatorname{argmax}_{y \in Y} \sum_{i=1}^k w_i \delta(y, f(x_i)) \quad (3.33)$$

where

$$w_i = \frac{1}{d(x_q, x_i)^2} \quad (3.34)$$

In the case where $d(x_q, x_i) = 0$, that is, x_q and x_i are exactly the same coordinates, $g(x_q)$ can assume the same value of $f(x_i)$. If there are other training samples x_i with the same characteristic, then x_q can assume the class of the one who is the most of them (Mitchell, 1997).

3.2.3 Decision tree

Decision tree is a method for approximation of discrete target functions, in which the learned function is represented by a decision tree or by a set of rules of type *If-Then* that are easy to interpret. It is one of the most popular learning techniques of inductive inference⁴ (Mitchell, 1997).

The samples of a dataset are classified by a decision tree by an iterative process where an attribute (node) is chosen as root to some leaf node, where the class is assigned to the sample. Each branch starting from a node represents one of the possible values of a given attribute (Mitchell, 1997).

There is a family of decision tree algorithms. One of them is the Iterative Dichotomiser 3 (ID3) proposed by Quinlan (1986). The ID3 evaluates each attribute through a statistical test to determine how well it classifies the training samples. The best attribute is selected as the root node of the tree. A descending branch of the root node is created for each possible value of this attribute, and the training samples are classified into the appropriate descendent node. This process is then repeated recursively using the samples associated with each descendent node. This is a greedy search algorithm, since it does not regress to reconsider previous choices (Mitchell, 1997). The algorithm stops when the subset of samples associated with a node is of the same class or when there is no statistical relevance for a new partition (Quinlan, 1986).

To measure the impurity of a partition, ID3 uses the concept of entropy, formally (Quinlan, 1986):

$$H(D) = -y_{\oplus} \log_2 y_{\oplus} - y_{\ominus} \log_2 y_{\ominus} \quad (3.35)$$

where D is the training dataset with N samples of the form presented in 3.13, y_{\oplus} and y_{\ominus} is the proportion of positive and negative samples of D , respectively. It is important to note that the entropy is 0 when all samples of D belong to the same class, 1 when D contains an equal number of positive and negative samples, and a value between 0 and 1 in all other cases (Mitchell, 1997).

Given the entropy as a measure of impurity of a set of training samples, one can define the statistical test, known as information gain, that measures the effectiveness of an attribute in the classification of training data, formally (Quinlan, 1986):

$$IG(D, a_r) = H(D) - \sum_{v \in V(a_r)} \frac{|D_v|}{|D|} H(D_v) \quad (3.36)$$

where $V(a_r)$ is the set of all possible values of the attribute a_r , D_v is the subset of D in which the a_r attribute is equal to v .

It is worth emphasizing that the first term of the equation given in 3.36 is the entropy of the original set D and the second term is the expected value of the entropy after D is partitioned using

⁴The task of induction is to develop a classification rule that can determine the class of any object from the values of its attributes (Quinlan, 1986).

the attribute a_r (Mitchell, 1997). Another important aspect is that the algorithm starts with the original D set, which is replaced by D_v as the recursion deepens.

Named as C4.5, Quinlan (1993) extended ID3 to enable the use of continuous attributes, attributes with missing data, and improved computational efficiency. In addition, this version takes care of issues such as how deep the tree should be to prevent training data from being perfectly classified, that is, when the training set is partitioned until each subset contains only samples of a single class - the over-fitting phenomenon. The strategy adopted by Quinlan (1993) was to prune the tree after the generation of the adjusted tree. This process, although slower than the previous ID3 proposal, made the algorithm more reliable and with greater generalization capacity.

Chapter 4

Proposed Solution

A state of the art skin detection method has been recently developed by Brancati *et al.* (2017). Here, we review the method and extend it adding more rules to enforce the constraints and seeking for a better performance in terms of false positive rate without hurting the performance of the original method.

4.1 Original Method

In order to describe the proposed extensions, we will first transcribe the original method that is based on the definition of image-specific trapezoids, named T_{YCr} and T_{YCb} , in the YCr and YCb subspaces, respectively. The trapezoids are essential to verify a relation between the chrominance components Cb and Cr in these subspaces (Brancati *et al.*, 2017).

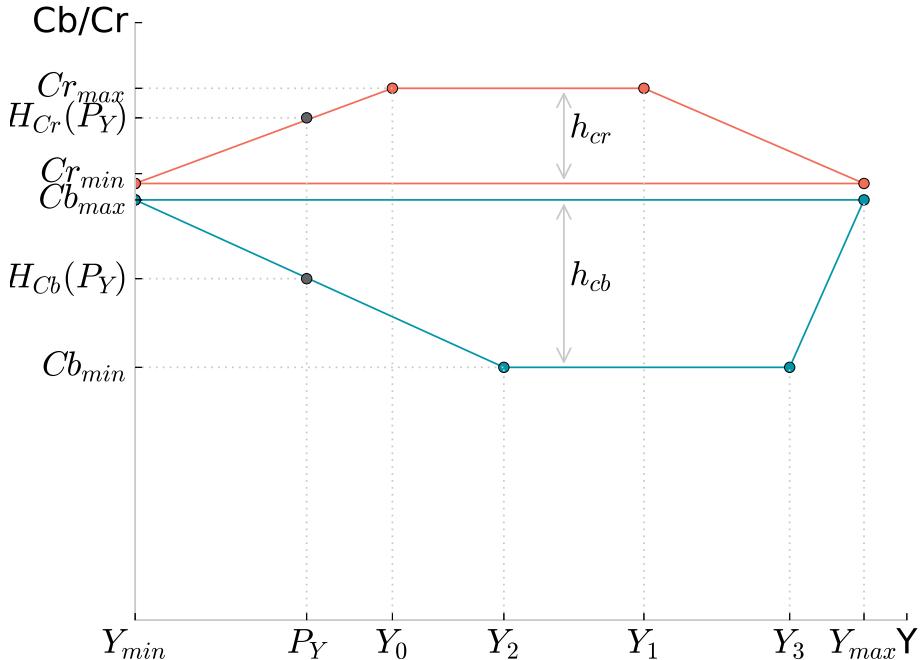


Figure 4.1: Graphical representation of the trapezoids as well as the parameters $Y_{min} = 0$, $Y_{max} = 255$, Y_0 , Y_1 , Y_2 , Y_3 , Cr_{min} , Cr_{max} , Cb_{min} , Cb_{max} , h_{Cr} , h_{Cb} , $H_{Cr}(P_Y)$, $H_{Cb}(P_Y)$. Source: adapted from (Brancati *et al.*, 2017).

The base of the trapezoids T_{YCr} and T_{YCb} (Fig. 4.1) are given by (Y_{min}, Cr_{min}) and (Y_{min}, Cb_{max}) in the YCr and YCb subspaces, respectively. The values $Cr_{min} = 133$, $Cb_{max} = 128$ were selected

according to Chai e Ngan (1999) where a skin color map was designed using a histogram approach based on a given set of training images. Chai and Ngan observed that the Cr and Cb distributions of skin color falls in the ranges [133, 173] and [77, 127], respectively, regardless the skin color variation in different races.

The Cr_{max} parameter is calculated dynamically, taking into account the histogram of the pixels with Cr values in the range $[Cr_{min}, 183]$, looking for the maximum value of Cr associated with at least 0.1%¹ of pixels in the image. The same applies to Cb_{min} , taking the histogram with Cb values in the range $[77, Cb_{max}]$. Y_0 and Y_1 (shorter base of the upper trapezoid) are, respectively, the 5th and 95th percentile of the luminance values associated with the pixels of the image with $Cr = Cr_{max}$. A similar procedure is used to find the values of the shorter base of the other trapezoid, Y_2 and Y_3 (see Fig. 4.2 for an example).

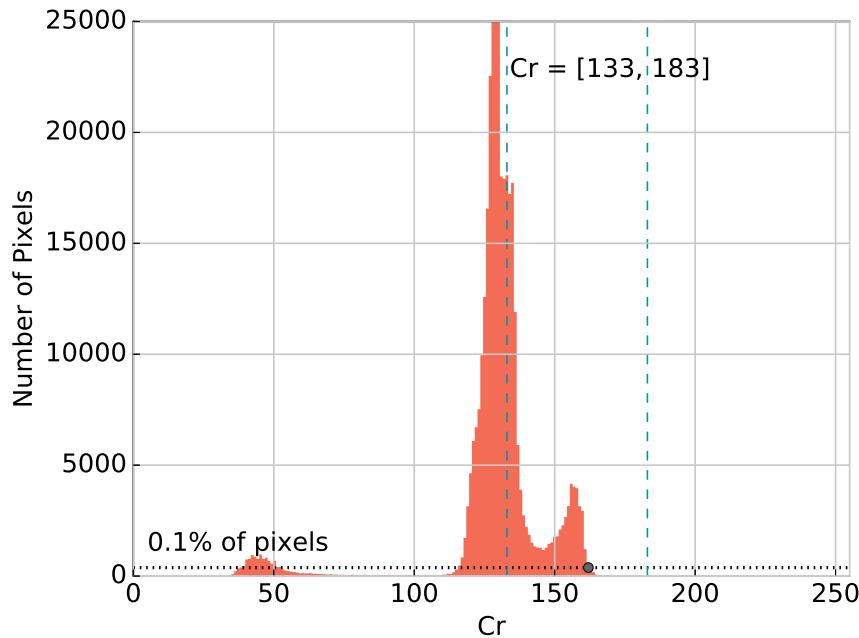


Figure 4.2: Computation of $Cr_{max} = 162$ based on Cr values histogram of a 724×526 image.

The correlation rules between the chrominance components P_{Cr} and P_{Cb} of a pixel P are defined as:

- the minimum difference between the values P_{Cr} and P_{Cb} , denoted I_P ;
- an estimated value of P_{Cb} , namely P_{Cb_s} ;
- the maximum distance between the points (P_Y, P_{Cb}) and (P_Y, P_{Cb_s}) , denoted J_P .

Therefore, to determine if P is skin, the following equations must hold:

$$P_{Cr} - P_{Cb} \geq I_P \quad (4.1)$$

$$|P_{Cb} - P_{Cb_s}| \leq J_P \quad (4.2)$$

The estimated value P_{Cb_s} is given by ²:

$$P_{Cb_s} = Cb_{max} - dP_{Cb_s} \quad (4.3)$$

¹In Brancati *et al.* (2017) this rate is reported to be equal to 10%. However, in the distributed source code we found the value 0.1%, that we are using in the experiments.

² dP_{Cb_s} is the distance between the points (P_Y, P_{Cb_s}) and (P_Y, Cb_{max}) in the YCb subspace, calculated on the basis of dP_{Cr} , observing the inversely proportional behavior of the components. α is the rate between the normalized heights of the trapezoids in relation to the P_Y value.

where ³:

$$dP_{Cb_s} = \alpha \cdot dP_{Cr} \quad (4.4)$$

$$dP_{Cr} = P_{Cr} - Cr_{min} \quad (4.5)$$

The coordinates of the other sides of the trapezoids are given by $[P_Y, H_{Cr}(P_Y)]$ and $[P_Y, H_{Cb}(P_Y)]$, such that:

$$H_{Cr}(Y) = \begin{cases} Cr_{min} + h_{Cr} \left(\frac{Y - Y_{min}}{Y_0 - Y_{min}} \right) & Y \in [Y_{min}, Y_0] \\ Cr_{max} & Y \in [Y_0, Y_1] \\ Cr_{min} + h_{Cr} \left(\frac{Y - Y_{max}}{Y_1 - Y_{max}} \right) & Y \in [Y_1, Y_{max}] \end{cases} \quad (4.6)$$

$$H_{Cb}(Y) = \begin{cases} Cb_{min} + h_{Cb} \left(\frac{Y - Y_2}{Y_{min} - Y_2} \right) & Y \in [Y_{min}, Y_2] \\ Cb_{min} & Y \in [Y_2, Y_3] \\ Cb_{min} + h_{Cb} \left(\frac{Y - Y_3}{Y_{max} - Y_3} \right) & Y \in [Y_3, Y_{max}] \end{cases} \quad (4.7)$$

where $h_{Cr} = Cr_{max} - Cr_{min}$ and $h_{Cb} = Cb_{max} - Cb_{min}$, which are the heights of T_{YCr} and T_{YCb} , respectively.

The computation of those points are useful for the calculation of α . We first compute the distances $\Delta_{Cr}(P_Y)$ and $\Delta_{Cb}(P_Y)$ between the points $(P_Y, H_{Cr}(P_Y))$, $(P_Y, H_{Cb}(P_Y))$ and the base of the trapezoids:

$$\Delta_{Cr}(P_Y) = H_{Cr}(P_Y) - Cr_{min} \quad (4.8)$$

$$\Delta_{Cb}(P_Y) = Cb_{max} - H_{Cb}(P_Y) \quad (4.9)$$

Next, the distances are normalized with respect to the difference in size of the trapezoids:

$$\Delta'_{Cr}(P_Y) = \begin{cases} \Delta_{Cr}(P_Y) \cdot \frac{A_{T_{YCb}}}{A_{T_{YCr}}} & \text{if } A_{T_{YCr}} \geq A_{T_{YCb}} \\ \Delta_{Cr}(P_Y) & \text{otherwise} \end{cases} \quad (4.10)$$

$$\Delta'_{Cb}(P_Y) = \begin{cases} \Delta_{Cb}(P_Y) & \text{if } A_{T_{YCr}} \geq A_{T_{YCb}} \\ \Delta_{Cb}(P_Y) \cdot \frac{A_{T_{YCr}}}{A_{T_{YCb}}} & \text{otherwise} \end{cases} \quad (4.11)$$

where $A_{T_{YCr}}$ and $A_{T_{YCb}}$ are the areas of trapezoid T_{YCr} and T_{YCb} , respectively.

Then, the value of α is given by:

$$\alpha = \frac{\Delta'_{Cb}(P_Y)}{\Delta'_{Cr}(P_Y)} \quad (4.12)$$

Finally, I_P and J_P are given by:

$$I_P = sf \cdot [(\Delta'_{Cr}(P_Y) - dP_{Cr}) + (\Delta'_{Cb}(P_Y) - dP_{Cb_s})] \quad (4.13)$$

$$J_P = dP_{Cb_s} \cdot \frac{dP_{Cb_s} + dP_{Cr}}{\Delta'_{Cb}(P_Y) + \Delta'_{Cr}(P_Y)} \quad (4.14)$$

where:

$$sf = \frac{\min((Y_1 - Y_0), (Y_3 - Y_2))}{\max((Y_1 - Y_0), (Y_3 - Y_2))} \quad (4.15)$$

³ dP_{Cr} is the distance between (P_Y, P_{Cr}) and (P_Y, Cr_{min}) points in the YCr subspace.

4.2 Extended Method

The hypothesis defined in the original method is based on rules that an estimated value of the point P_{Cb} , namely P_{Cr_s} , must hold in order for the correlation to be valid. On the basis of the inversely proportional behavior of the chrominance components, we will rewrite the correlation rules with respect to the P_{Cr} point.

Thus, we have to refactor the correlation rules to put them in terms of the estimated value of P_{Cr} , that we denote as P_{Cr_s} ⁴:

$$P_{Cr_s} = dP_{Cr_s} + Cr_{min} \quad (4.16)$$

where⁵:

$$dP_{Cr_s} = \alpha \cdot dP_{Cb} \quad (4.17)$$

$$dP_{Cb} = Cb_{max} - P_{Cb} \quad (4.18)$$

Next, the constraints given by I_P and J_P in the Eq. 4.13 and 4.14 respectively, can be redefined as:

$$I'_P = sf \cdot [(\Delta'_{Cr}(P_Y) - dP_{Cr_s}) + (\Delta'_{Cb}(P_Y) - dP_{Cb})] \quad (4.19)$$

$$J'_P = dP_{Cr_s} \cdot \frac{dP_{Cb} + dP_{Cr_s}}{\Delta'_{Cb}(P_Y) + \Delta'_{Cr}(P_Y)} \quad (4.20)$$

Therefore, to determine if the pixel P is skin, we have to modify the conditions given by Eq. 4.1 and 4.2:

$$P_{Cr} - P_{Cb} \geq I'_P \quad (4.21)$$

$$|P_{Cr} - P_{Cr_s}| \leq J'_P \quad (4.22)$$

Doing this simple extension, we are now able to apply the method to the same sets of images to evaluate, in fact, the inversely proportional behavior of the chrominance components. More than that, we can combine all these constraints, given by the pair equations 4.1 and 4.2, 4.21 and 4.22, to reinforce the firstly defined hypothesis.

4.3 Neighborhood Extended Method

Both methods presented in Sec. 4.1 and 4.2 can be applied to detect skin pixels, either separated or in a conjunction rule. However, skin pixels do not usually appear isolated and we can improve the method using neighbor pixels information, when evaluating a pixel P , in order to decide if P represents human skin, or not. Let $N_8^-(P)$ the 8-connected neighbors of P that can be reached before P when scanning the image in raster order (blue points in Fig. 4.3).

Thus, we classify P as skin in the following manner: if the constraints given by the pair of equations 4.1 and 4.2, as well as 4.21 and 4.22 hold, then P is classified as skin. When only one of conditions is satisfied, then we check the decision in $N_8^-(P)$. If three or more pixels are skin, then P will also be classified as a skin pixel.

⁴ dP_{Cr_s} is the distance between the points (P_Y, P_{Cr_s}) and (P_Y, Cr_{min}) in the YCr subspace, calculated on the basis of dP_{Cb} , observing the inversely proportional behavior of the components. α is the rate between the normalized heights of the trapezoids in relation to the P_Y value.

⁵ dP_{Cb} is the distance between (P_Y, P_{Cb}) and (P_Y, Cb_{max}) points in the YCb subspace.



Figure 4.3: Neighbors evaluation with respect to P . If the image is scanned in raster order, $N_8^-(P)$ is the set of points that can be reached before P in a 8-connected neighborhood.

Chapter 5

Evaluation

In this section we present some experimental evaluations of the proposed extensions along with the original method in three widely known datasets: SFA, Pratheeepan and HGR. In addition, a brief definition of the evaluation metrics used is shown for the sake of clarity.

5.1 Datasets

5.1.1 UCI

Named UCI in this work, this dataset was proposed by [Bhatt e Dhall \(2012\)](#) and obtained from the machine learning repository of the University of California in Irvine ([Lichman, 2013](#)). The dataset consists of images of various skin and non-skin textures obtained from thousands of arbitrary faces images of different ages, sex and races ([Minear e Park, 2004](#); [Phillips *et al.*, 1996](#)).

The UCI contains 245,057 samples, composed of 3 attributes that constitute the input vector $x = [x_1, x_2, x_3]$, $x \in \mathbb{R}^d$, where d is the space dimension which represents, respectively, blue (B), green (G) and red (R) channels of the RGB color model. In addition, a fourth column determines the class to which the sample x belongs, denoted by y , where $y \in Y$ and $Y = \{+1, -1\}$. In other words, each sample is an RGB pixel with a given label.

The table 5.1 exemplifies a short excerpt from the UCI database. It is worth mentioning that of the 245,057 samples, 194,198 are non-skin pixels and 50,859 pixels with different skin tones. In addition, the images that were used to extract the dataset were not made available by the authors.

B	G	R	Label
74	85	123	1
207	215	255	1
74	82	122	1
202	211	255	1
54	72	125	1
...
166	164	116	-1
148	150	91	-1
29	26	5	-1
167	166	115	-1
180	177	133	-1

Table 5.1: Excerpt with samples from the UCI dataset. Each of the first three columns represents a pixel channel of the RGB color space ranging from 0 to 255. The fourth column is the label assigned to the sample, which can assume +1 if it is skin and -1, otherwise. Originally, the class representing a non-skin pixel had value 2, replaced by -1 for compliance with the experiments.

Since the data are points in the RGB space, it is possible to plot it for a better interpretation of them, as shown in the figure 5.1.

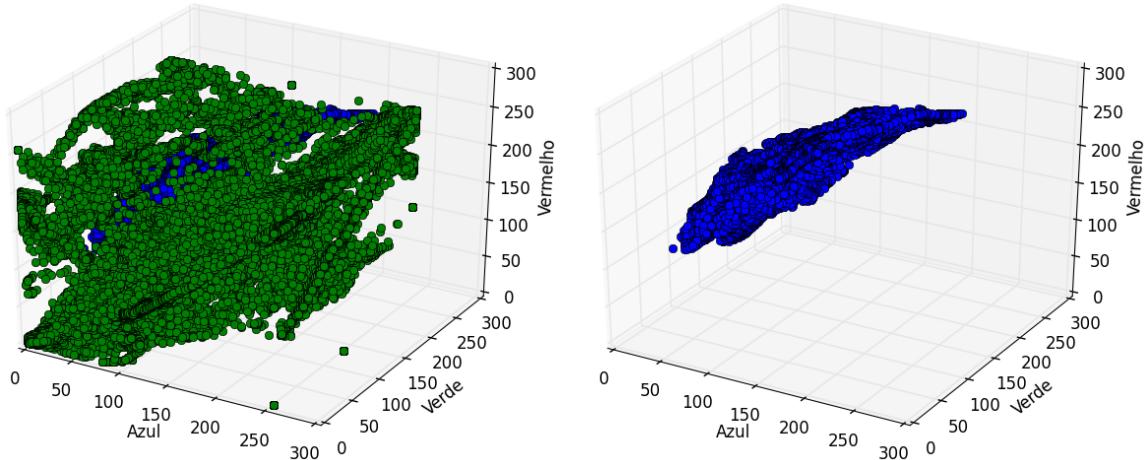


Figure 5.1: 3-dimensional view of the RGB channels of the UCI dataset. The blue points are skin samples and the green ones are non-skin. On the left are all samples of the dataset; to the right only the skin samples. Source: proposed by the author.

5.1.2 SFA

SFA, the name of the dataset proposed by Casati *et al.* (2013), stands for Skin of FERET and AR Database. The SFA is a set of images of frontal faces obtained from two other color image databases: the FERET, created by Phillips *et al.* (1996), and the AR proposed by Martínez e Benavente (1998), which provided 876 and 242 images each, respectively. It is important to notice that AR images have a white background and small variations of skin color. In other words, the environment is more controlled than the images in FERET Casati *et al.* (2013). Figure 5.2 shows some of the 1,118 samples available.

Casati *et al.* (2013) also extracted different window patches of each skin and non-skin samples to facilitate future research. The samples were randomly generated considering the ground truth mask¹ of each image, being three samples of skin and five of non-skin. Each sample is a window of size $n \times n$, where n is odd, with a central pixel, from which other sample sizes have been created, ranging from 1×1 to 35×35 , as can be seen in figure 5.3.

Review A partir das amostras criadas no SFA, um conjunto de dados foi extraído gerando uma base de dados de pele e não pele similar ao UCI na tabela 5.1. O tamanho da janela utilizado foi 9×9 e o espaço de cores também foi o RGB. Portanto, o total de amostras empregado nos experimentos é 724.464, sendo 271.674 de pele e 452.790 de não pele. A classe atribuída à cada amostra tem o mesmo valor que no UCI, ou seja, +1 se for pele e -1, caso contrário. A figura 5.4 mostra a representação gráfica dos dados plotados em 3 dimensões.

5.1.3 Pratheepan

The images in the Pratheepan dataset were downloaded randomly from Google for human skin detection search. There are 78 images of family and face captured with a range of distinct cameras using different color enhancement and under different illumination conditions Tan *et al.* (2012). Figure 5.5 shows some of the 78 samples available.

5.1.4 HGR

The database for Hand Gesture Recognition (HGR) contains the gestures from Polish and American Sign Language. There are 1,558 images acquired in different conditions of background, dimensions and lightening. In addition to original and ground truth binary skin mask images, it

¹Ground truth is the term used to denote an image whose point of interest is properly segmented and highlighted, discarding the remaining pixels giving them uniform colors.

includes hand feature points location in separate files. Figure 5.6 shows some of the 1,558 samples available (Grzejszczak *et al.*, 2016; Kawulok *et al.*, 2014; Nalepa e Kawulok, 2014).

The images within were acquired in three different series. A set of 899 was captured in uncontrolled background and lighting. A small set of 85 was obtained in gray (44) and (41) uncontrolled background; the lighting was uniform. The third group contains 574 images in controlled background (green tone), using uniform lighting conditions (Grzejszczak *et al.*, 2016; Kawulok *et al.*, 2014; Nalepa e Kawulok, 2014).

5.2 Evaluation measures

Precision, *Recall*, *Specificity* and *F-measure* have been used as evaluation metrics. They are the same used in Brancati *et al.* (2017) to compare the performance with state-of-the-art methods. They are also widely used by the scientific community. These metrics are given by the following formulas:

$$\text{Precision} = \frac{TP}{TP + FP}$$

$$\text{Recall} = \frac{TP}{TP + FN}$$

$$\text{Specificity} = \frac{TN}{TN + FP}$$

$$F - \text{measure} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}$$

where TP, TN, FP, FN are, respectively, the number of true positive, true negative, false positive, and false negative pixels counted in the image, which are obtained from the confusion matrix (see table 5.2).

		prediction outcome	
		skin	non-skin
ground truth	skin	True Positive	False Negative
	non-skin	False Positive	True Negative

Table 5.2: Confusion matrix table used to count the number of true positive, true negative, false positive, and false negative pixels in the image during experiments. These numbers are fundamental input for evaluation measures.

5.3 Primeiro experimento

O primeiro experimento foi realizado com *k*-NN e SVM, disponíveis no pacote *scikit-learn* (Pedregosa *et al.*, 2011). O espaço de cores usado originalmente foi o RGB, como citado na descrição dos conjuntos de dados em 5.1. Em ambos os casos, a estratégia escolhida de validação cruzada foi a *10-fold*, que é uma escolha comum desta abordagem na prática (Abu-Mostafa *et al.*,

2012). Além disso, a técnica de tabela de busca do *scikit-learn* também foi utilizada com o objetivo de encontrar os parâmetros mais adequados para cada classificador.

A tabela de busca é usada no *scikit-learn* para encontrar os parâmetros ótimos de um classificador quando eles não podem ser aprendidos pelo estimador, tais como, *kernel* e γ na SVM ou número de vizinhos no *k*-NN (Pedregosa et al., 2011). As tabelas de parâmetros utilizadas no treinamento da SVM e *k*-NN podem ser vistas em 5.3 e 5.4. Os parâmetros de cada linha são combinados na tentativa de encontrar o estimador ótimo. Por exemplo, uma escolha no treinamento da SVM seria *kernel*=rbf, $C=100$, $\gamma=1e-4$. Todas as combinações possíveis são exploradas, sendo que a melhor delas é retornada (Pedregosa et al., 2011).

<i>kernel</i>	<i>C</i>				<i>gamma</i>			<i>degree</i>
rbf	1	10	100	1000	1e-3	1e-4	1e-5	
poly	1	10	100	1000		1e-4	1e-5	3
linear	1	10	100	1000				4

Table 5.3: Tabela de busca dos parâmetros do estimador ótimo na SVM. A coluna *kernel* refere-se aos kernels usados no treinamento que são gaussiano, polinomial e linear, respectivamente. *C* é um parâmetro de regularização que diz à SVM a quantidade de erro admitido no treinamento. Gamma é um parâmetro usado somente nos kernels gaussiano e polinomial, conforme citado em 3.2.1. Degree é o grau do polinômio; usado somente no kernel polinomial (Pedregosa et al., 2011).

<i>n_neighbors</i>										<i>weights</i>	<i>algorithm</i>	
3	5	9	15	25	50	100	200	400	800	distance	uniform	auto

Table 5.4: Tabela de busca dos parâmetros do estimador ótimo no *k*-NN. A coluna *n_neighbors* refere-se ao número de vizinhos considerado no treinamento. Weights é a função peso usada na predição, onde uniform indica que os pontos têm pesos iguais e distance indica que o inverso da distância é aplicado na classificação, conforme citado em 3.3.4. A terceira coluna indica qual algoritmo deve ser utilizado; auto significa que o algoritmo será decidido com base nos dados (Pedregosa et al., 2011).

Os resultados deste experimento podem ser vistos na tabela 5.5. Vale ressaltar que o treinamento foi executado com 10 tarefas em paralelo em ambos os classificadores e 30% dos dados, aleatoriamente, foram separados para teste.

Conjunto de dados	Classificador	Modelo de cores	Precision	Recall	F1-score
UCI	<i>k</i> -NN	RGB	0,9995	0,9995	0,9995
	SVM	RGB	0,9995	0,9995	0,9995
SFA	<i>k</i> -NN	RGB	0,9672	0,9669	0,9670
	SVM	RGB	0,9643	0,9628	0,9638

Table 5.5: Resultados dos experimentos com *k*-NN e SVM nos conjuntos de dados UCI e SFA. Os parâmetros ótimos do *k*-NN no treinamento com UCI foram *n_neighbors*=3, *weights*=uniform e com SFA *n_neighbors*=15, *weights*=uniform. Os parâmetros ótimos da SVM no treinamento com UCI e SFA foram *kernel*=rbf, $C=100$ e $\gamma=1e-3$.

Como pode ser visto na tabela 5.5, o *k*-NN teve resultados ligeiramente melhores que a SVM no conjunto de dados SFA. Ambos classificadores tiveram medidas de qualidade muito altas no conjunto de dados UCI, próximas a 100%, o que, provavelmente, é uma situação de sobreajuste. Uma causa possível está na separação dos dados de treinamento e teste. Há muitas repetições entre as amostras, logo, é possível que amostras já vistas pelo classificador durante o treinamento sejam utilizadas na etapa de teste. Por essa razão, os experimentos subsequentes foram realizados somente com o SFA.

5.4 Segundo experimento

Este experimento, de maneira similar ao realizado na seção 5.3, também foi realizado com k -NN e SVM. Porém, o conjunto de dados SFA foi transformado para os espaços de cor HSV, Lab e YCbCr com o objetivo de compreender a influência nos resultados. Além disso, o atributo referente ao componente de luminância foi ignorado para que um teste somente com os componentes de crominância fosse realizado. Novamente, a estratégia escolhida de validação cruzada foi a *10-fold*.

Como o objetivo deste experimento é avaliar a performance do classificador em espaços de cores distintos, os parâmetros ótimos obtidos no experimento 5.3 foram fixados aqui.

Os resultados podem ser vistos na tabela 5.6. Vale ressaltar que o treinamento foi executado com 10 tarefas em paralelo em ambos os classificadores e 30% dos dados, aleatoriamente, foram separados para teste.

Modelo de cores	Classificador	Precision	Recall	F1-score
RGB	k -NN	0,9672	0,9669	0,9670
	SVM	0,9643	0,9628	0,9638
HSV	k -NN	0,9676	0,9673	0,9674
	SVM	0,9718	0,9677	0,9679
HS	k -NN	0,9215	0,9194	0,9199
	SVM	0,9305	0,9302	0,9302
Lab	k -NN	0,9671	0,9660	0,9670
	SVM	0,9675	0,9665	0,9672
ab	k -NN	0,9444	0,9439	0,9440
	SVM	0,9451	0,9447	0,9446
YCbCr	k -NN	0,9679	0,9677	0,9677
	SVM	0,9635	0,9633	0,9632
CbCr	k -NN	0,9487	0,9482	0,9483
	SVM	0,9496	0,9492	0,9493

Table 5.6: Resultados dos experimentos com k -NN e SVM no conjunto de dados SFA em espaços de cores distintos. As linhas com os modelos de cores HS, ab e CbCr indicam que o componente de luminância não foi utilizado no treinamento.

Os melhores resultados com a SVM e k -NN foram obtidos nos espaços de cores HSV e YCbCr, respectivamente. Dentre aqueles onde o componente de luminância foi ignorado, o CbCr teve a melhor performance.

É interessante observar que os indicadores de qualidade do modelo mostram que ambos classificadores tiveram taxas ao redor de 96% em todos os espaços de cor, quando aplicado com os 3 canais. Além disso, quando o canal de luminância foi ignorado, o desempenho foi inferior - aproximadamente 4 pontos percentuais no pior caso. Por outro lado, a perda de performance pode ser compensada pela redução da complexidade do modelo, já que uma dimensão pode ser descartada, mantendo, ainda, medidas de qualidade relativamente significativas.

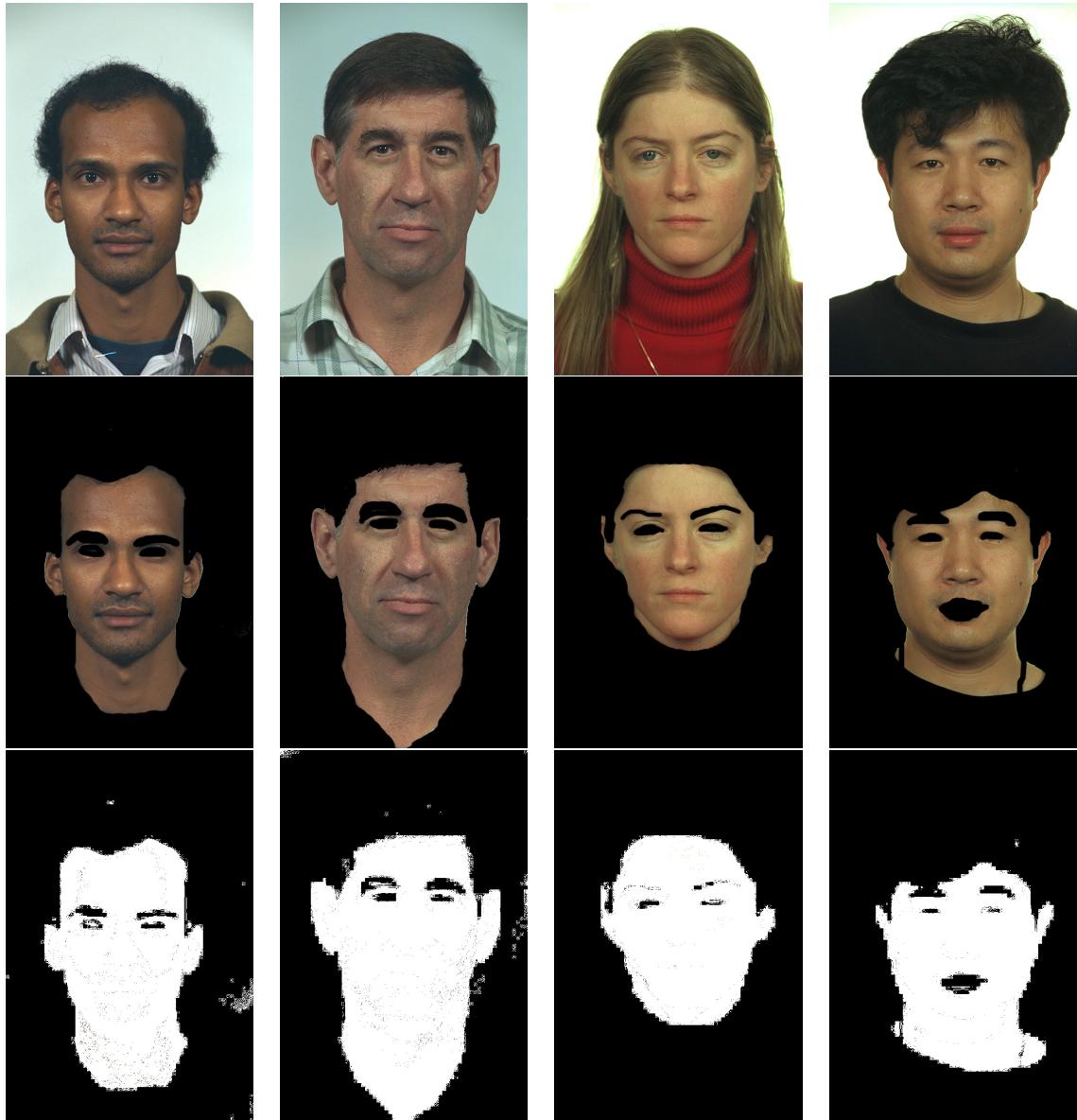


Figure 5.2: Examples of SFA face image database. First row are the original images and the second contain the colored ground truth with the skin color pixels annotated manually. The black color $RGB = (0, 0, 0)$ was assigned to all pixels in the background. In the third row we have the binary ground truth images. We generated these samples based on the colored ground truth, by creating a mask, assigning $(255, 255, 255)$ for the pixels which were not background $(0, 0, 0)$. One can see some noise in the results, but the samples were enough for further experiments. In addition, the original images were not perfectly annotated. Therefore, some salt noise can be seen in non-skin regions. Source: [Casati et al. \(2013\)](#).

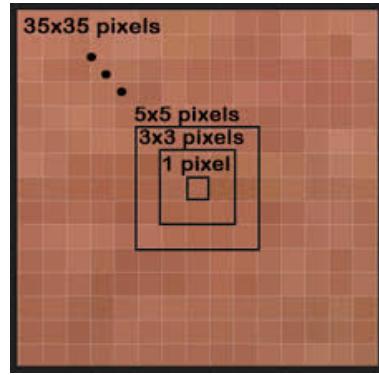


Figure 5.3: Structure of the windows that form the SFA samples. In total, there are 3,354 skin samples and 5,590 non-skin samples for each window size. Source: Casati et al. (2013).

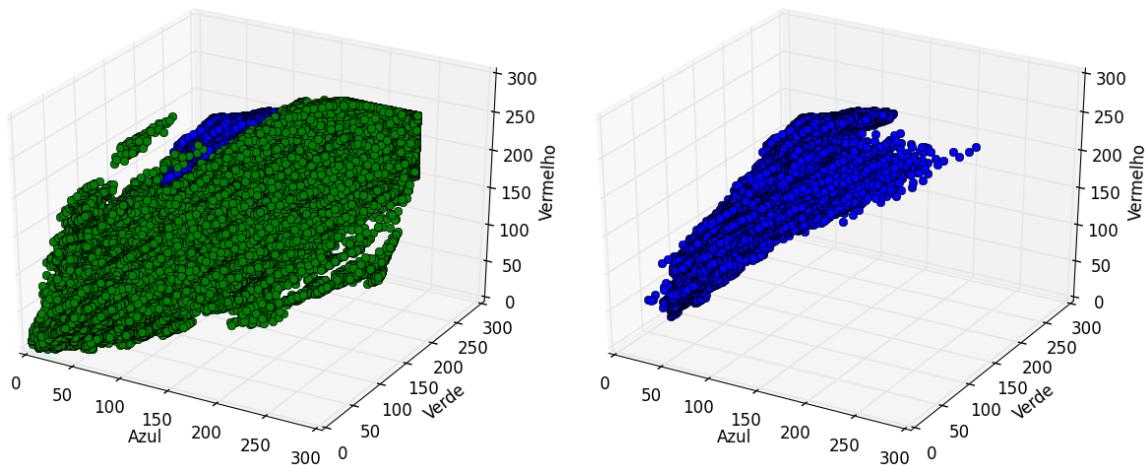


Figure 5.4: Review Visão 3-dimensional dos canais RGB do conjunto de dados SFA. Os pontos em azul são amostras de pele e os verdes de não pele. À esquerda tem-se todas as amostras do conjunto de dados gerado; à direita apenas as amostras de pele. Fonte: proposto pelo autor.



Figure 5.5: Examples of Pratheepan skin dataset. At the top is the original image and at the bottom the ground truth with the skin color pixels annotated. Here, the ground truth are binary images, where the black color $RGB = (0, 0, 0)$ was assigned to all pixels in the background. Source: Tan et al. (2012).



Figure 5.6: Examples of HGR skin dataset. At the top is the original image and at the bottom the ground truth with the skin color pixels annotated. Differently from Pratheeepan and SFA, the ground truth is also binary images, but the black color $RGB = (0, 0, 0)$ was assigned to all pixels when they represent skin patches. Source: Grzejszczak et al. (2016); Kawulok et al. (2014); Nalepa e Kawulok (2014).

Chapter 6

Plano de Trabalho

Os créditos em disciplinas necessários para o programa de mestrado em Ciência da Computação no IME-USP foram cumpridos de fevereiro de 2015 até junho de 2016, conforme a tabela 6.1. Em meados de 2015, iniciou-se a pesquisa bibliográfica para o desenvolvimento deste projeto. Durante esse período, até o presente momento, foram realizados os experimentos preliminares que estão incorporados neste texto para a etapa de qualificação. Após apresentação, as recomendações da comissão julgadora serão ponderadas e devem ser refletidas nas atividades subsequentes listadas na seção 6.1.

Código	Disciplina	Término
MAC5832	Aprendizagem Computacional: Modelos, Algoritmos e Aplicações	jun/2015
MAC5744	Introdução à Computação Gráfica	jun/2015
MAC5768	Visão e Processamento de Imagens - Parte I	jun/2015
MAC5711	Análise de Algoritmos	nov/2015
MAC6914	Métodos de Aprendizagem em Visão Computacional	nov/2015
MAC4722	Linguagens, Autômatos e Computabilidade	jun/2016
MAC5714	Programação Orientada a Objetos	jun/2016

Table 6.1: Disciplinas cursadas no programa de mestrado em Ciência da Computação no IME-USP.

6.1 Atividades previstas

1. **Revisar leituras adicionais:** outras referências deverão ser adicionadas ao presente trabalho, principalmente, conteúdo relacionado a métodos de *kernel*, que servirão de embasamento para compreender e estudar a técnica de *kernels* em conjuntos *fuzzy* proposta por Guevara *et al.* (2014).
2. **Incorporar novos conjuntos de dados:** essa atividade consiste em analisar e integrar novos conjuntos de dados ao projeto para utilização nos experimentos, tanto de bancos de imagens de cor de pele, como outros conjuntos de imagens coloridas onde a classificação de dados intervalares possa ser aplicada.
3. **Investigar características passíveis de uso em classificadores de dados intervalares:** os classificadores treinados durante a etapa de experimentos preliminares consistiam apenas da informação de cor da imagem, independente do espaço de cores escolhido. Portanto, essa atividade visa compreender o papel de outros atributos, tais como textura e características locais, durante o treinamento e se a inclusão de tais atributos, de fato, pode acarretar em melhoria de performance.
4. **Desenvolver novas ferramentas:** novas ferramentas devem ser desenvolvidas para dar suporte aos experimentos subsequentes, tais como a tabela de busca implementada para otimiza-

ção de parâmetros do *FuzzyDT*. Todo software criado por este projeto de pesquisa será disponibilizado para toda a comunidade científica em formato de código livre.

5. **Elaborar novos experimentos:** com base nas ferramentas desenvolvidas e conjuntos de dados estabelecidos, elaborar e executar novos experimentos.
6. **Analizar os resultados:** os resultados obtidos deverão ser avaliados e reportados no projeto de pesquisa e em publicações a serem realizadas. Eventualmente, correções nas ferramentas desenvolvidas e/ou nos experimentos também serão agregadas nesta etapa.
7. **Publicar resultados:** artigos científicos com os resultados obtidos devem ser publicados em revistas ou conferências sobre processamento de imagens, classificação ou outras áreas relacionadas com o contexto do projeto de pesquisa.
8. **Escrever a dissertação:** a dissertação deverá ser escrita assim que as demais atividades tiverem sido concluídas, principalmente em relação aos experimentos e análise de resultados, o que fornecerá dados consolidados para a conclusão do projeto de pesquisa.

6.2 Cronograma proposto

As atividades listadas na seção 6.1 serão realizadas de acordo com o cronograma disposto na tabela 6.2. As tarefas foram divididas dentro de um período de onze meses de execução e a previsão de defesa da dissertação é outubro de 2017.

Atividade	Meses 2016/2017										
	dez	jan	fev	mar	abr	mai	jun	jul	ago	set	out
1	X	X	X								
2	X	X									
3		X	X								
4			X	X	X	X					
5					X	X	X				
6						X	X	X			
7							X	X			
8								X	X	X	X

Table 6.2: Cronograma das atividades previstas

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