

An Elliptical Boundary Model for Skin Color Detection

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Abstract

Automatic skin detection has been intensively studied for human-related recognition systems. A Gaussian model for skin detection is a well-known approach with its simplicity and generality. In this paper, we discuss limitations of the Gaussian model and suggest a new statistical color model for skin detection, called an elliptical boundary model. The suggested model overcomes the limitations of the Gaussian model with better performance. From the experiment performed on six chrominance spaces, it gives the much higher correct detection ratio than a single Gaussian model. As compared to the mixture of Gaussian model suggested to improve the correct detection ratio of a single Gaussian at the expense of slower speed, the elliptical boundary model still gives the better correct detection ratio with faster speed.

Keywords: skin detection, skin color model, elliptical boundary model, Gaussian model

1. Introduction

Many research results on automatic skin detection have been published [1, 2, 3, 4, 5, 6, 7, 8, 9]. The well-known statistical color models to estimate skin density in chrominance space may be the single Gaussian model [4, 5, 6], the mixture of Gaussian model [8, 9], and histograms [2, 3]. The histogram model based on local approximation is simple and fast but becomes effective only when training data is sufficiently large to be dense. Moreover, it requires additional memory to keep the histograms. The Gaussian model based on the global feature of distribution has the advantage of generality. Specially a single Gaussian model is simple and fast. It

however does not adequately represent the variance of the skin distribution occurred in the situation where illumination condition varies. To overcome this drawback, the mixture of the Gaussian model has been suggested. It is however hard to be trained and slow.

In this paper, we suggest a new statistical color model for skin detection, called an elliptical boundary model. This elliptical boundary model can be easily constructed from training data in a fast speed and its performance is better than both the single and the mixture of Gaussian model.

2. Chrominance Histograms

To devise the appropriate model for skin detection, we investigate the characteristics of skin and non-skin distributions in terms of chrominance histograms. The normalized 2D chrominance space is derived from the original 3D color space by eliminating intensity [4]. The skin and non-skin chrominance histograms are then constructed from 2,000 skin images and 4,000 non-skin images in Compaq database which contains 4,675 skin images and 8,965 non-skin images randomly collected from the World Wide Web [2]. Histograms are computed with 400×400 bin resolution in six different chrominance spaces, r-g, CIE- u^*v^* , CIE- a^*b^* , CIE-xy, I-Q, and Cb-Cr. From these histograms, the following three characteristics have been observed. For the lack of space, we present histograms in two, r-g and CIE- u^*v^* , of the six chrominance spaces, in Figure 1 and Figure 2.

First, most non-skin chrominances

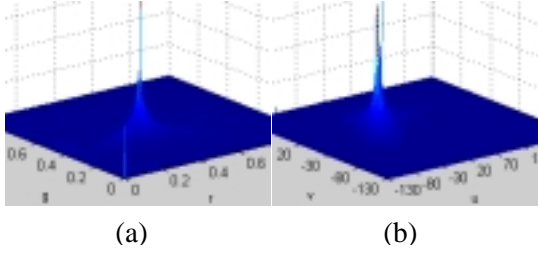


Figure 1. Non-skin chrominance histograms. (a) r-g space. (b) CIE-u*v* space.

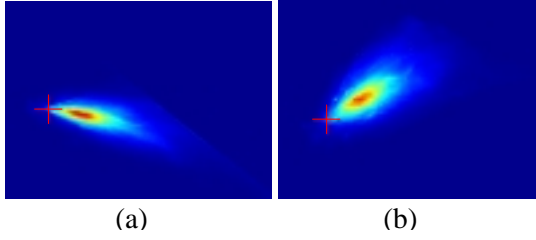


Figure 2. Skin chrominance histograms. Each cross mark denotes gray point. (a) r-g space. (b) CIE-u*v* space.

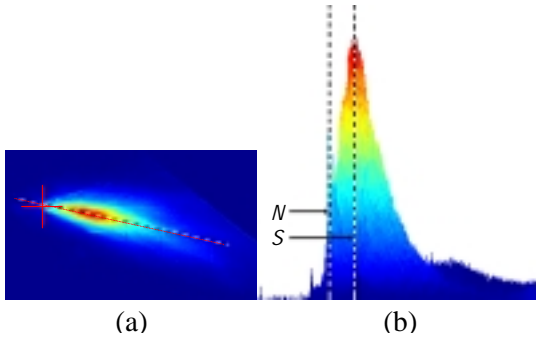


Figure 3. (a) Skin histogram in r-g chrominance space. (b) A side view of (a). N denotes non-skin density peak and S denotes skin density peak.

concentrate on one point, so called a gray point ($r=g=1/3$ in the r-g space, and $u^*=v^*=0$ in the CIE-u*v* space). It implies that the performance of an object detection system based on color information strongly depends on the degree of overlapping between object color area and the gray point area in chrominance space. Secondly, skin cluster is simple-shaped despite of the unconstrained nature of web images. This is due to both color normalization and a large amount of data. Finally, skin density looks

like a normal distribution but with a skew peak toward the gray point. It is because the dark skin color is unstable and diffuses toward red over the wide surface area [7]. We can observe this asymmetry more clearly with a side view of histogram in Figure 3.

Any color model for skin detection should thus reflect these characteristics to give the better performance. In the next section we briefly review the Gaussian models and discuss its limitations.

3. Gaussian Models

3.1 A Single Gaussian Model

Assuming that the skin density is modeled by a single Gaussian, the skin likelihood of an input chrominance vector X is given by

$$P(X) = \frac{1}{2\pi|\Lambda|^{1/2}} \exp\left[-\frac{1}{2}\lambda^2\right] \quad (1)$$

where λ is the Mahalanobis distance defined as

$$\lambda^2 = (X - \mu)^T \Lambda^{-1} (X - \mu) \quad (2)$$

The mean vector μ and covariance matrix Λ of the density are estimated from a training set. Given threshold λ_t^2 , X is classified as skin chrominance if $\lambda^2 < \lambda_t^2$ and as non-skin chrominance otherwise. The inequality $\lambda^2 < \lambda_t^2$ defines an elliptical area whose center is given by μ and whose principal axes are by Λ . This area however does not meet tightly the skin chrominance distribution since μ is skewed toward the gray point as mentioned in section 2. Moreover it contains the gray point, which results in large false detections. Figure 4 illustrates this situation.

3.2 A Mixture of Gaussian Model

In a mixture of Gaussian suggested to overcome the limitation of a single Gaussian,

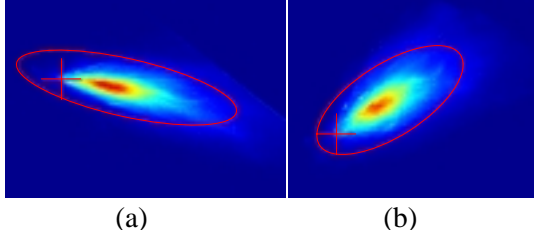


Figure 4. Class boundaries formed from a single Gaussian model with 95% skin detection rate. (a) r-g chrominance space. (b) CIE-u*v* chrominance space.

the skin likelihood of an input chrominance vector X is given by

$$P(X) = \sum_{i=1}^t w_i g(X; \mu_i, \Lambda_i) \quad (3)$$

where $g(X; \mu, \Lambda)$ is a 2-dimensional Gaussian density with mean vector μ and covariance matrix Λ , and the w_i are the mixing parameters of the Gaussians meeting $\sum w_i = 1$. These model parameters can be estimated by means of the Expectation-Maximization (EM) algorithm [10].

Although the mixture of Gaussian can model arbitrarily complex densities, it is computationally expensive in training and evaluation: The mixture model is hard to be trained since the EM algorithm needs very high time complexity and the skin detection takes long time since each of the Gaussians used for the mixture model should be evaluated to generate the skin likelihood of the chrominance [2]. In the next section we suggest a new statistical color model which may overcome these limitations.

4. An Elliptical Boundary Model

The skin density is simple-shaped as discussed in section 2 and the skin area in each chrominance space fits well an ellipse. This can be observed visually from Figure 2. With this observation, we suggest a new statistical color model for skin detection, called an elliptical boundary model. This

model is trained from a set of training data in two steps, preprocessing and parameter estimation. In preprocessing step we remove outliers so that the trained model reflects the main density of the underlying data set. In parameter estimation step we estimate model parameters from the preprocessed data set.

1) Training Data Set: Initially training data set consists of skin chrominance samples.

2) Preprocessing: Outliers are removed by eliminating k % sample data from the training set which have low frequency. The value of k , where $0 \leq k \leq 5$, is determined by the amount of noise and negligible data in the training set.

3) Parameter Estimation: Let X_1, \dots, X_n be all the distinctive chrominance vectors of the preprocessed training data set and $f(X_i) = f_i$ ($i=1, \dots, n$) be the number of samples with chrominance value of X_i . An elliptical boundary model $\Phi = (X; \psi, \Lambda)$ is then defined as

$$\Phi(X) = [X - \psi]^T \Lambda^{-1} [X - \psi] \quad (4)$$

where the two model parameters, ψ and Λ are given by

$$\psi = \frac{1}{n} \sum_{i=1}^n X_i \quad (5)$$

$$\Lambda = \frac{1}{N} \sum_{i=1}^n f_i (X_i - \mu)(X_i - \mu)^T \quad (6)$$

and where $N = \sum_{i=1}^n f_i$ is the total number of samples in the preprocessed training data set and the vector $\mu = \frac{1}{N} \sum_{i=1}^n f_i X_i$ is the mean of chrominance vectors.

Given threshold θ and input chrominance X of a pixel, X is classified as skin chrominance if $\Phi(X) < \theta$ and as non-skin chrominance otherwise. Note that the value of threshold θ trades off

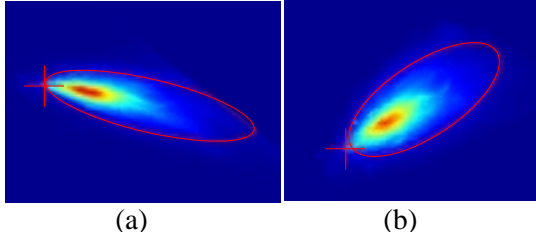


Figure 5. Class boundaries formed from an elliptical boundary model with 95% skin detection rate. (a) r-g chrominance space. (b) CIE-u*v* chrominance space.

correct detections by false detections. As the value of threshold increases, the number of correct detections increases but the number of false detections also does.

The equality $\Phi(X) = \theta$ defines an elliptical boundary between skin chrominance and non-skin chrominance whose center is given by ψ and whose principal axes are by Λ . This boundary meets well the skin chrominance distribution as shown from Figure 5. It includes most of skin chrominance area and the least non-skin chrominance area especially near the gray point. Note that this model is not affected by the degree of skew of skin distribution since ψ is the center of distribution area computed from distinctive data not counting their frequencies.

5. Experimental Results

In this section, we compare the performance of the elliptical boundary model to those of the single and the mixture of Gaussian model. Each model has been trained from 2,000 skin images and tested by 2,000 skin and 4,000 non-skin images from Compaq database [2]. The test skin images are distinct from the training ones. In training the elliptical model, the value of k for removing outliers is set to 1. The mixture model constructed from six Gaussians has been trained using the EM algorithm [10].

Figure 6 shows the ratios of correct detection and false detection for each of the three models in six different chrominance

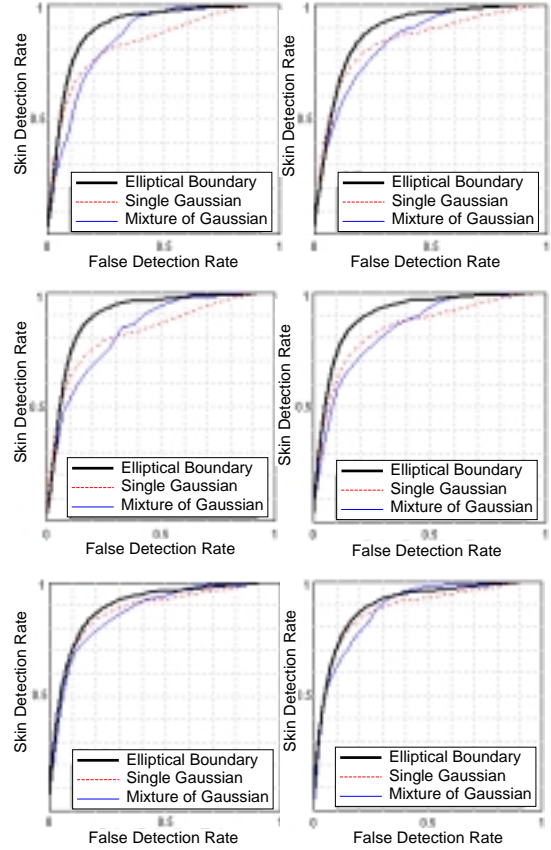


Figure 6. ROC curves in six different chrominance spaces for elliptical boundary model, single Gaussian model, and mixture of Gaussian model. From top to bottom and left to right: r-g, CIE-a*b*, CIE-xy, CIE-u*v*, Cb-Cr, and I-Q spaces.

spaces, r-g, CIE-u*v*, CIE-a*b*, CIE-xy, I-Q, and Cb-Cr. We can see that the elliptical boundary model gives the best performance in every chrominance space. As expected, the single Gaussian gives the worst performance. The mixture of Gaussian gives better performance than that of the single Gaussian but worse than that of the elliptical model, in average, as shown in Table 1.

In terms of time complexity, the suggested elliptical model is as fast as the single Gaussian but much faster than the mixture of Gaussian: In order to classify one pixel, the elliptical model needs evaluate Equation (4) only and the single Gaussian model needs Equation (2). The mixture model however needs evaluate Equation (3)

Table 1. Selected ratios of correct detection and false detection. *SD* is skin detection rate and *FD* is false detection rate.

	Elliptical Boundary Model		Single Gaussian Model		Gaussian Mixture Model	
	<i>SD</i>	<i>FD</i>	<i>SD</i>	<i>FD</i>	<i>SD</i>	<i>FD</i>
Average	90.0%	23.3%	90.0%	47.0%	90.0%	38.4%
	95.0%	35.7%	95.0%	67.8%	95.0%	47.8%
r-g	90.0%	21.3%	90.0%	54.4%	90.0%	34.3%
	95.0%	32.4%	95.0%	68.5%	95.0%	39.8%
CIE-a*b*	90.0%	25.3%	90.0%	52.0%	90.0%	41.4%
	95.0%	37.0%	95.0%	71.1%	95.0%	52.1%
CIE-xy	90.0%	20.9%	90.0%	58.5%	90.0%	42.4%
	95.0%	31.2%	95.0%	72.2%	95.0%	52.0%
CIE-u*v*	90.0%	22.3%	90.0%	50.4%	90.0%	45.2%
	95.0%	34.0%	95.0%	69.7%	95.0%	52.6%
Cb-Cr	90.0%	25.0%	90.0%	33.3%	90.0%	37.1%
	95.0%	39.7%	95.0%	62.7%	95.0%	52.0%
I-Q	90.0%	25.0%	90.0%	33.3%	90.0%	30.0%
	95.0%	39.7%	95.0%	62.7%	95.0%	38.0%

which is much more complicated and time-consuming than Equation (4).

6. Conclusions

As exhibited in the experiments, the elliptical boundary model outperforms both the single Gaussian model and the mixture of Gaussian model in six chrominance spaces. Moreover, it is simple and fast. One drawback of the suggested model is that its usage is limited to binary classification, where the continuous information given by probability density function is not preserved.

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