A NOVEL TWO-TIER BAYESIAN BASED METHOD FOR HAIR SEGMENTATION

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ABSTRACT

In this paper, a novel two-tier Bayesian based method is proposed for hair segmentation. In the first tier, we construct a Bayesian model by integrating hair occurrence prior probabilities (HOPP) with a generic hair color model (GHCM) to obtain some reliable hair seed pixels. These initial seeds are further propagated to their neighborhood pixels by utilizing segmentation results of Mean Shift, to obtain more seeds. In the second tier, all of these selected seeds are used to train a hair-specific Gaussian model, which are combined with HOPP to build the second Bayesian model for pixel classification. Mean Shift results are further utilized to remove holes and spread hair regions. The experimental results illustrate the effectiveness of our approach.

Index Terms— Hair Segmentation, Two-tier Bayesian Model, GMM, Gaussian Model, Mean Shift.

1. INTRODUCTION

Human hair related applications, such as hair modeling [1], editing [2], rendering [3], synthesis [4] and animating [5] have attracted increasing interest in recent years, since hair plays a significant role in the overall appearance of an individual. To achieve these tasks, hair segmentation is generally the first prerequisite step. However, to our knowledge, in most previous studies, hair is assumed segmented already or manually labeled. Furthermore, besides the above hair-related applications, many computer vision tasks can also benefit from segmented hair. For instance, it provides an important clue for gender classification, since hair styles of male and female are generally different. Hair can also facilitate age estimation since hair distribution and color gradually changes with the increase of age, especially for old men/women. Hair information can even contribute a lot to face recognition, considering that the hair style of one normal subject does not abruptly change frequently. To sum up, more attention should be paid to automatic hair segmentation.

Detecting and segmenting hair within images represents a significant challenge due to the diversity of hair patterns and background variability. To our knowledge, only few works have been done on automatic hair segmentation [6-9]. Among them, the early work [6] performs the segmentation via classification of image pixels based on textural and geometrical features. In [7], hair is segmented by mainly exploiting a simple color model accounting for highlights and shadows that often affect the brightness of hair color. However, the method cannot work under complex background and the performances are evaluated subjectively. One recent work in [8] applies matting method based on a hair interaction mask resulting from frequential and color analysis. However, in [7, 8], hair color model is built on sample windows, like top of the face, which are defined by experience. Hence seed regions cannot be controlled quantitatively and maybe inaccurate. More recently, in the method in [9], Markov Random Field is used and optimized by extending traditional segmentation algorithms such as Graph-Cut and Loopy Belief Propagation for hair and face segmentation.

In this paper, we present a novel two-tier Bayesian based method for hair segmentation. The basic idea is as follows: first, we select some seed pixels which we believe are hair pixels with very high probability, by using a Bayesian model combining two prior clues: the hair occurrence prior probability (HOPP) of each position (relative to the detected face region), and a generic hair color model (GHCM); then, the hair seed pixels are propagated to their neighborhoods with the help of Mean Shift [10] segmentation results, thus more seeds are obtained; finally, by training on all seeds, a color model specific to the current hair is built for another Bayesian model which also combines the HOPP. Mean Shift results are utilized again to spread hair pixels.

2. OVERVIEW OF THE PROPOSED METHOD

Fig. 1 illustrates the block diagram of the proposed method for hair segmentation and Fig. 2 illustrates an

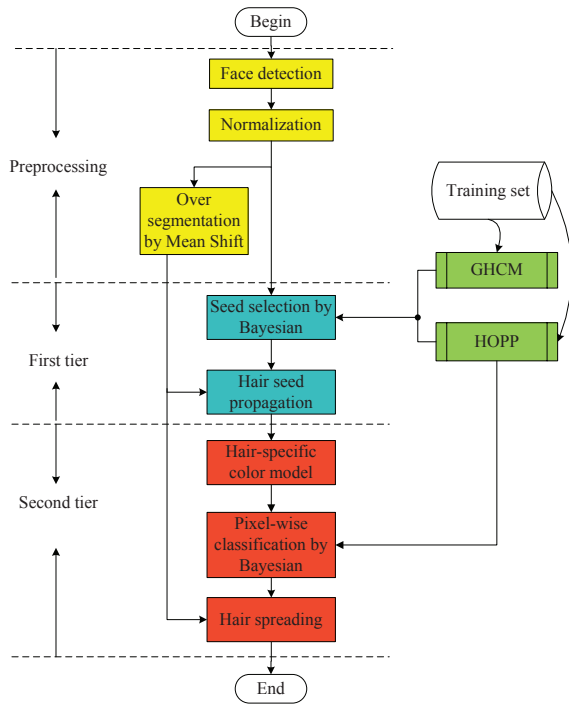example of the segmentation procedure. In the following, we briefly explain our method based on the figures.

Fig. 1. Block diagram of the proposed method.

Given a human image, face detection and eye localization are first performed automatically to obtain eye centers. After that, the image is normalized by aligning eye centers in order to make use of the HOPP. Then, as shown in Fig. 2(c), an over-segmentation with Mean Shift is performed on the normalized image and the results are stored for the sequent procedures.
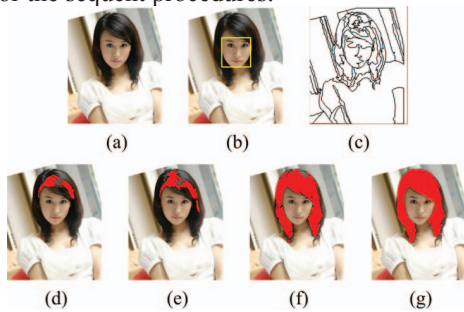

Fig. 2. An example of hair segmentation: (a) Input image. (b) Detected face. (c) Results of Mean Shift segmentation. (d) Initial hair seeds. (e) Hair seed propagation with Mean Shift results. (f) Pixel-wise hair classification. (g) Hair spreading with Mean Shift results.

We then turn to the selection of initial hair seeds combining the HOPP and likelihood from a GMM-based GHCM. A small number of reliable hair seeds are selected, as shown in Fig. 2(d). Then, more hair seeds, in Fig. 2(e), are obtained by further propagating from the initial seeds by using the region information provided by the Mean Shift.

With all these hair seeds, a hair-specific Gaussian model is built and combined with HOPP to form the second tier Bayesian model, which is adopted to classify pixels. Finally, segmentation results of Mean Shift are used again for hair regions spreading.

3. HAIR SEED SELECTION

In this section, we will introduce the hair seed selection by using the first tier of the proposed approach. It is composed of a Bayesian model and seed propagation stage. We now show how to learn GHCM and HOPP.

3.1. Hair Color Model and Occurrence Prior Probability

The statistics tell that most hair color values scatter within certain ranges and obey specified principles. In the current implementation, we assume that the distribution of hair color values obey Gaussian Mixture Model (GMM). The GMM employed in this paper is trained on a prepared generic dataset containing a number of images with hair labeled manually. And the number of GMM components is determined by experience.

Hair generally surrounds the face. Therefore, the HOPP at each location with respect to the eyes can be an important clue for hair segment. We learn these probabilities from a prepared dataset with hair region labeled. The images contain human faces with a large range of pose variations, hair styles and backgrounds. All images are normalized to a specified size, e.g., 300×400, with eye centers aligned. Then the HOPP for each pixel location are calculated by counting the hair occurrence frequency. Fig. 3 visualizes the learned probabilities in different locations, which is evidently very consistent with our common sense.

Fig. 3. Visualization of HOPP at different locations with respect to the two eye centers. The larger intensity implies the higher probability being hair.

3.2. Bayesian Model for Initial Hair Seeds Selection

As mentioned in Section 2, we first need to seek for some seeds with very high probability being hair pixels. To achieve this, the probability of each pixel should be estimated first. Formally, for each pixel (x, y) (with respect to eye centers), according to Bayesian rules, its posterior probability being a hair pixel can be computed by:

$$P(S \mid f(x,y)) = \frac{P(f(x,y) \mid S)P(S)}{P(f(x,y))}, \qquad (3.1)$$

where $f(x,y)$ is the color (e.g., in RGB space) value. The conditional probability of hair, $P(f(x,y)|S)$, can be reasonably replaced by the pre-learned GMM-based GHCM. We rewrite it as $P(f(x,y)|\theta_g)$, with θ_g, the parameter of GMM. And, the HOPP of location (x,y) can be naturally used as the prior probability $P(S)$. So the posterior probability can be computed as:

$$P(S|f(x,y)) = \frac{P(f(x,y)|\theta_g)P(S_{x,y})}{P(f(x,y))}. \quad (3.2)$$

In order to reduce the computation cost, we first get a "mask" by setting a threshold on HOPP. Only the pixels within the mask are involved in the computation of the posterior probabilities. Finally, a small number of pixels with highest posterior probabilities being hair will be selected as initial hair seeds.

Compared with the methods in [7, 8] where seeds are selected from the assumed sample windows without an exact measure, in our proposed approach, seed pixels are selected according to Bayesian rule.

3.3. Seed Propagation Based on Mean Shift Results

The utilization of Mean Shift results is inspired by the fact that hair seeds generated from Section 3.2 are apt to be precise, which, however, are scattered and far from enough to learn hair-specific color model. On the other hand, usually the pixels around the selected seeds are also hair, according to spatial correlation. Mean Shift segments an image into regions, each of which consists of either hair pixels only or non-hair pixels only, with very high accuracy. Therefore, we elegantly integrate the results of Mean Shift and the scattered seed pixels to propagate seeds. The basic idea is to take all pixels in the same region as hair seeds, if and only if the proportion of hair seeds in the region is larger than a threshold.

Another way of seed propagation is that, given a desired number of seeds, we keep selecting the regions with higher HOPP, until the number is reached or the HOPP of the rest regions is too low. Anyway, more seeds will be obtained, which greatly facilitate the sequent hair-specific color model.

4. HAIR SEGMENTAION

In this section, to capture the particularity, we present the second tier Bayesian model which utilizes a hair-specific color model for hair segmentation.

4.1. Bayesian Model for Pixel Classification

Based on the selected hair seeds in Section 3, a Gaussian model with parameter θ_s, reflecting the particularity of hair color in the current image, can be constructed. Then, another Bayesian model, similar to the seed selection stage, can be built. If the two eye centers are fixed, the hair-specific Bayesian model is defined to be:

$$P(H|f(x,y)) = \frac{P(f(x,y)|\theta_s)P(H_{x,y})}{P(f(x,y))}, \quad (4.1)$$

where the prior probability $P(H_{x,y})$ is again defined as the HOPP of (x,y), and the conditional probability $P(f(x,y)|\theta_s)$ is computed on the hair-specific Gaussian model.

Finally, we classify the pixels according to the following rule:

$$C(x,y) = \begin{cases} 1, & \text{if } P(H|f(x,y)) > \delta_h \\ 0, & \text{otherwise} \end{cases}, \quad (4.2)$$

where $C(x,y) = 1$ means the pixel (x,y) is hair.

4.2. Hair Spreading Based on Mean Shift Results

Due to the same reason as described in Section 3.3, Mean Shift results are also used to spread the hair pixels obtained by Eq. (4.2). A region will be labeled as hair region or non-hair region by the criteria:

$$R_i = \begin{cases} 1, & \text{if } \dfrac{Number_{hair}}{Total_{pixel}} > \delta_r \\ 0, & \text{otherwise} \end{cases}, \quad (4.3)$$

where $i = 1,...,N$ and N represents the total number of regions segmented by Mean Shift. In this way, a large portion of hair holes are removed and dispersive hair pixels are connected. On the other hand, if the proportion of hair pixels is low, the region contains less or no hair. Here, the thresholds δ_r and δ_h mentioned in 4.1 are both set by experience.

5. EXPERIMENTAL RESULTS

In our experiments, two databases are used: the first one is the public Caltech database used in [8]; the second one is collected by us from Internet. The Caltech database used in [8] only contains frontal face images of 10 women, and each of them wears a unique hair style respectively. For further evaluation of our method, a more challenging database is collected from Internet. The images are with a large range of variations in head pose, hair styles, and backgrounds. There are totally 1000 images, 500 females and 500 males.

In our implementation, each image in Caltech is normalized to 900×650 and the number of hair seed pixels selected is no less than 8000. The thresholds δ_h and δ_r are set to be 0.88 and 0.6 respectively. To evaluate the method, two performance measurements, False Reject Rate (FRR) and False Accept Rate (FAR), are calculated in term of pixels. Experimental results on the two sets are shown in Table 1.

Table 1. Experimental results on two databases.

Database	Method	FRR	FAR
Caltech	Rousset, *et al*	4.8%	38.7%
	Our method	3.7%	36.6%
Our database	Our method	11.3%	32.7%

It takes 0.5s in average to perform our algorithm on each 300×400 image with known eye centers, using unoptimized VC code on Intel Core 2 Duo 2.26G CPU. In the table, the results of Rousset, *et al* are taken from [8] directly. It can be observed that our method achieves comparable results on Caltech to those in [8]. It is worth pointing out that our 'ground truth' hair pixels are labeled manually, whereas those in [8] are generated by mixing manual entries and automatic processing. Despite a few differences between the two 'ground truth', they should be considered well matched. Furthermore, FAR and FRR are statistics based on millions of pixels, which will not be influenced fundamentally by the few differences.

Fig. 4. Segmentation examples of our method. The first three rows show successful segmentations and the bottom row shows some failed examples.

Some intuitive results are shown in Fig. 4. It is observed that our proposed method is robust to different hair styles, and exhibits somewhat tolerance to small pose variation. Of course, it sometimes does not work well on images containing large pose variation or background similar to hair, e.g. the bottom row of Fig. 4.

6. CONCLUSION

A two-tier Bayesian based method for hair segmentation is proposed in this paper. In the first tier we utilize a Bayesian model and Mean Shift results to obtain a number of reliable hair seed pixels. The Bayesian model combines hair occurrence prior probabilities (HOPP) and generic hair color model (GHCM). In the second tier, likewise, we perform hair segmentation by combining a hair-specific color model learned from the reliable hair seeds and HOPP. Additionally,

Mean Shift results are employed to spread hair regions. Experimental results demonstrate the effectiveness of the proposed method.

Hair segmentation is indeed a challenging task, it is clear that our method only provides a primary study on the problem. In the future, hair color information should be further studied, and texture information should be explored as well for more accurate segmentation.

8. REFERENCES

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