

Automatic Facial Feature Extraction by Applying Genetic Algorithms

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Abstract

An automatic facial feature extraction algorithm is presented in this paper. The algorithm is composed of two main stages: the face region estimation stage and the feature extraction stage. In the face region estimation stage, a second-chance region growing method is adopted to estimate the face region of a target image. In the feature extraction stage, genetic search algorithms are applied to extract the facial feature points within the face region. It is shown by simulation results that the proposed algorithm can automatically and exactly extract facial features with limited computational complexity.

1 Introduction

Facial feature extraction plays an important role in many applications, such as very low bit-rate video coding [1] and human face recognition [2]. In very low bit-rate video coding, the variation of facial features (the so-called local motion) carries much more information than the other parts of the target image do. In order to obtain higher coding gain, the facial feature areas are usually separated from the target image, and then special coding schemes are performed on these areas. As for human face recognition, facial features are extracted as the major analyzed targets, because they compose basic characteristics of a human face.

Although lots of facial feature extraction algorithms have been proposed so far [3, 4], facial feature extraction is still a handicap to the prescribed applications due to its high complexity. In the existed algorithms, all the pixels within the face region were evaluated to find the best ones, that is, they didn't apply any fast searching method. Genetic algorithms (GAs) [5] are adopted in our work to solve the most troublesome task of facial feature extraction, the template matching. Due to its good reputation in the applications of searching and optimization, good template matching performance

(in terms of speed and matching error) can be expected. Although the results are not guaranteed to be global optima by applying GAs in searching, the expected feature points can always be extracted, in our simulations, with the aids of some intrinsic geometric relations among facial feature points.

2 An automatic facial feature extraction algorithm

Fig. 1 shows the block diagram of the proposed facial feature extraction algorithm. The system is composed of three main components: (1) **pre-processing**, (2) **first stage feature extracting**, and (3) **second stage feature extracting**. The details are described in the following subsections.

2.1 Pre-processing

The purpose of the pre-processing stage is to find out the face region. Because the face region locates roughly on the center of a head-and-shoulder image, region growing can be performed to estimate that region by selecting the central point of the image as an initial seed. If the size of the region grown from the initial seed is beyond a range, either a new seed should be selected, or the threshold should be adjusted, to generate another region whose size is in the range.

In order to make sure that the forehead region is contained in the grown region, the intensities of three extended points above the region are compared with that of a pivot point in the region. If the difference is less than a threshold, they will be selected as new seeds. The new regions grown from the new seeds are checked and combined with the original region. The checking process prevents from including the hair region or the background region into the face region. This second-chance region growing process avoids the possibility of losing the forehead region from the face region.

When the combined region is extracted, a minimum rectangle is found to surround that region. The following feature extraction algorithm will be performed within the so-obtained square area to find the facial features.

2.2 Genetic search of facial features

The solution space S is a 2-D image subregion, and each image pixel in the subregion is an element in S . If the coordinate of the central point of S is (\hat{x}, \hat{y}) , the i th chromosome C_i in the population is defined as

$$C_i = \begin{bmatrix} m_i \\ n_i \end{bmatrix} = \begin{bmatrix} a_{i,k-1} & a_{i,k-2} & \dots & a_{i,1} & a_{i,0} \\ b_{i,k-1} & b_{i,k-2} & \dots & b_{i,1} & b_{i,0} \end{bmatrix}, \quad (1)$$

where k represents the codeword size of each coordinate component whose value is dependent on the region size. If the maximum value of the width and the height of the region is w , the value k will be $\lceil \log_2 w \rceil$. The values of the genes are derived from the coordinate of the chromosome, (x_i, y_i) , that is, $a_{i,j} = \lfloor \frac{m_i + 2jw}{2^j} \rfloor \bmod 2$, and $b_{i,j} = \lfloor \frac{n_i + 2jw}{2^j} \rfloor \bmod 2$, where $m_i = x_i - \hat{x}$, and $n_i = y_i - \hat{y}$.

An initial population is formed before the evolution. In most GA-based applications, the initial population is created by randomly selecting elements from the solution space. To reduce the necessary iteration number, in our approach, the initial chromosomes (x_i, y_i) are selected from the solution space as

$$(x_i, y_i) = (x_0 + s \cdot X_i, y_0 + s \cdot Y_i), \quad (2)$$

$$X_i = (-1)^m \cdot ([i - m(m+1)] \cdot [1 - ((2\sqrt{i}) \bmod 2)] + \lceil \frac{1}{2}m \rceil), \quad (3)$$

$$Y_i = (-1)^m \cdot ([i - m(m+1)] \cdot [(2\sqrt{i}) \bmod 2] - \lceil \frac{1}{2}m \rceil), \quad (4)$$

where $m = \lfloor \sqrt{i} \rfloor$, $s = \lceil \frac{d \cdot \max(X_{N-1}, Y_{N-1})}{4} \rceil$, and d is the length of the region.

Each chromosome has an associated fitness value which is defined as

$$f_i = U_{F(x_i, y_i) - \hat{F}_k} \cdot (F(x_i, y_i) - \hat{F}_k) + \delta_{F(x_i, y_i) - \hat{F}_k}, \quad (5)$$

where $F(x_i, y_i)$ is the matching value of the i th chromosome, and \hat{F}_k is the k th maximum matching value among all the N matching values, and δ is a delta function. The constant k determines how many chromosomes could be selected at most as the seeds in the reproduction stage for producing a rival population. The chromosomes with larger fitness values in the current population have larger probability to be selected as seeds for the next generation.

The reproduction method used in this work is similar to the weighted roulette wheel method [5]. For each chromo-

some, an interval r_i is calculated as

$$r_i = \left[\frac{\sum_{k=0}^{i-1} f_k}{\sum_{k=0}^{N-1} f_k}, \frac{\sum_{k=0}^i f_k}{\sum_{k=0}^{N-1} f_k} \right), 0 \leq i \leq N-1, \quad (6)$$

where f_k is the fitness value of the k th chromosome in the population, and '[' and ')' denote closing and opening boundaries, respectively. When the interval of each chromosome has been determined, N real numbers, α_i , are randomly generated, where $0 \leq \alpha_i < 1$ and $0 \leq i \leq N-1$. The value of α_i will be bounded by some r_j , that is, $\alpha_i \in r_j$. The chromosome C_j is then selected as a seed to generate the rival population. It is possible that one chromosome can be selected twice or more. Because N real random numbers are generated, N seeds could be selected and placed in the mating pool.

For every two seeds selected from the mating pool, two new chromosomes are produced by performing uniform crossover operations [6]. Crossover is applied only when the mutation operation is performed on the most significant genes of the chromosomes.

In the mutation stage, assume the current seed to be processed is $[m'_i \ n'_i]^t$, where $m'_i = [a'_{i,k-1} \ a'_{i,k-2} \ \dots \ a'_{i,0}]$ and $n'_i = [b'_{i,k-1} \ b'_{i,k-2} \ \dots \ b'_{i,0}]$. In the j th generation, the two genes $a'_{i,z}$ and $b'_{i,z}$ are varied, where $z = k - 2 - (j \bmod k)$. There are eight mutation operators, $\{(\zeta_p, \eta_p) = (X_{p+1}, Y_{p+1}) | 0 \leq p \leq 7\}$, that can be applied in our implementation, i.e., $a''_{i,z} = a'_{i,z} + \zeta_p$, and $b''_{i,z} = b'_{i,z} + \eta_p$, where p is a random integer number whose value is between 0 and 7.

There are N chromosomes in the mating pool after performing the genetic operations. Along with the original chromosomes in the current generation, N chromosomes are selected from these $2N$ chromosomes according to their fitness values. Each chromosome can only be selected at most once. The chromosomes with larger fitness values will be picked up as the members of the population in the next generation, and go through the next iterations of the genetic evolution. Although the sorting operation is needed in the survival competition stage, the overhead is not high because the population size is usually not large in this case.

The chromosome with the maximum fitness value is selected from the current population as the possible solution. The possible solution might be replaced by the other ones from a generation to the other generations. The iteration will be terminated if the solution is not updated for a predetermined period of iterations.

2.3 First stage feature extracting

Basically, the face region can be divided into three subregions, R_a , R_b , and R_c . The right eye, left eye, and mouth feature points are expected to appear in different subregions.

Because the face rotation angle is normally not large, the main feature points will not cross the boundaries of their associated subregions. By applying GAs on searching the possible feature points and find the one with the best matching value in each subregion, the three main feature points of a human face can always be extracted.

2.4 Second stage feature extracting

After the main features have been extracted, the other feature points are searched in the three new subregions which can be specified according to main feature points. The points with best matching values are extracted as the secondary feature points.

3 Experimental results

The proposed algorithm has been implemented, on a SUN SPARC-10 workstation under Unix environment, at the Communication and Multimedia Lab., National Taiwan University. Figs. 2 and 3 show some of the experimental results.

The two images in Fig. 2 were captured by a normal V8 camera and transferred into digital form by an A/D converter. There was no special lighting when the images were captured. That is, the images were captured in a normal environment without any special equipment. With the proposed algorithm the facial features of the two images can be extracted successfully.

We also applied the proposed algorithm to typical head-and-shoulder images. The sequence "Claire" is shown here. Each image in the sequences was processed by the proposed algorithm and as expected the facial features had been extracted exactly. The simulation results are shown in Fig. 3. Notice that the eye features can still be extracted even though the eyes on the target images are closed.

Table 1 shows the ratios of the average number of searched points to the total number of candidate points. According to the table, it is known that most of the unnecessary evaluations are avoided. Therefore, the computational complexity is largely reduced, although some overheads are required for applying GAs in the searching process.

4 Conclusion

In this paper, an automatic facial feature extraction algorithm is proposed. In order to extract facial features from a head-and-shoulder image, the face region is first estimated by a second-chance region growing method. The facial feature points are then searched based on genetic algorithms within the face region. The necessary search numbers are reduced, so the whole system is very efficient. The

proposed algorithm has been applied to lots of head-and-shoulder images. It is shown by computer simulations that the facial features can always be extracted exactly by applying the proposed algorithm.

References

- [1] M. Wollborn, "Prototype prediction for colour update in object-based analysis-synthesis coding," *IEEE Trans. Circuits Syst. Video Technol.*, Vol. 4, No. 3, June 1994, pp. 236–245.
- [2] R. Chellappa, C. L. Wilson, and S. Sirohey, "Human and machine recognition of faces: a survey," *Proceedings of the IEEE*, Vol. 83, No. 5, May 1995, pp. 705–740.
- [3] G. Yang, and T. S. Huang, "Human face detection in a complex background," *Pattern Recognition*, Vol. 27, No. 1, 1994, pp. 53–63.
- [4] L. C. Desilva, K. Aizawa, and M. Hatori, "Detection and tracking of facial features," in *SPIE Symposium on Visual Communications and Image Processing*, Taipei, Taiwan, May 1995, pp. 1161–1172.
- [5] D. E. Goldberg, *Genetic Algorithms in Search, Optimization & Machine Learning*. Reading: Addison-Wesley, 1989.
- [6] G. Syswerda, "Uniform crossover in genetic algorithms," in *Proc. 3rd Int. Conf. Genetic Algorithms and Applications*, CA, 1989, pp. 2–9.

Sequence	Ratio
Tseng	0.11
Chou	0.12
Miss America	0.22
Claire	0.43

Table 1. The ratios of the averaged number of searched points to the total number of candidate points.

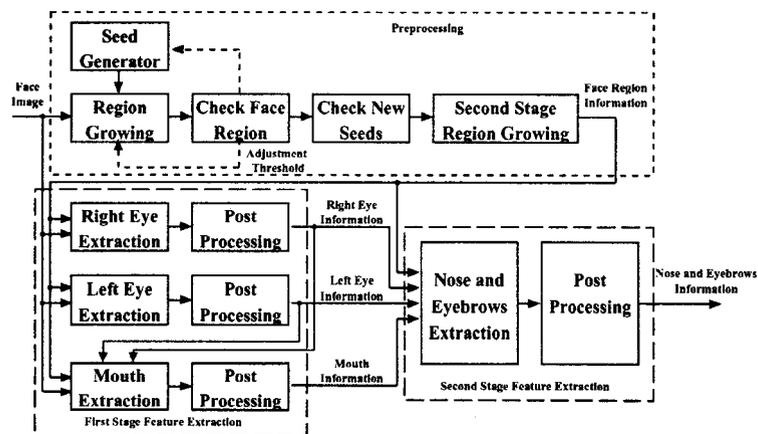


Figure 1. The block diagram of the proposed automatic feature extraction algorithm.



Figure 2. Simulation results of two captured images.

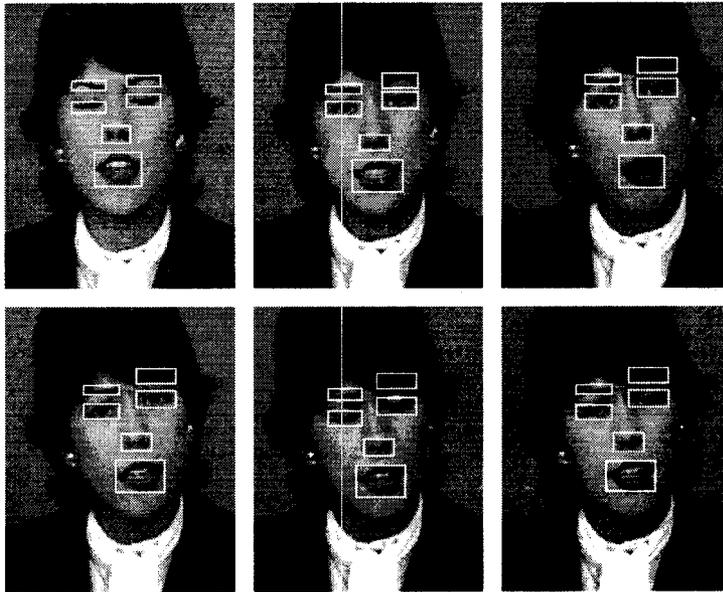


Figure 3. Simulation results of the 8th, 31th, 71th, 76th, 83th, and 86th frame from the “Claire” sequence. Notice that the eyes in the 8th and the 83th frames are closed. Moreover, the eyebrows of the second layer images are covered by hair.