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Radical recognition of handwritten Chinese characters using GA-based kernel active shape modelling

D. Shi, G.S. Ng, R.I. Damper and S.R. Gunn

Abstract: A key property of Chinese characters is that they are composed of fundamental parts called radicals. In this paper, a method to recognise (offline) the radicals of handwritten Chinese characters is proposed that is an extension of the authors' previous work based on active shape modelling. Three stages are involved: a set of example radicals is first described by landmarks using (mostly) automatic landmark labelling, then radicals are modelled as active shapes using kernel principal component analysis, and finally unseen radicals are matched to the reference models using a genetic algorithm to search for the optimal shape parameters. Experiments are conducted on a 430,800 character subset of the freely-available HITPU database, a collection of 751,000 loosely-constrained handwritten Chinese characters. Results show that this new method outperforms existing representative radical approaches, including the authors' own earlier work. Improvements on the previous work are made in two aspects: automatic landmark labelling, which renders this methodology more practical, and the use of a genetic algorithm which finds the optimal shape parameters more effectively, leading to the best results so far reported on this dataset.

1 Introduction

Since the Chinese writing system is used by a high proportion of the world's population, it is obviously important to develop computer systems applications featuring user interaction based on Chinese characters. As such, the topic of Chinese language processing has been of interest to many people for a long time. One way of inputting Chinese characters to computers is to employ optical character recognition for the (offline) reading of newspapers, printed transcripts and so forth. However, there is also a requirement for online recognition of handwritten characters. This is generally viewed as an extremely difficult problem, even for humans. The difficulties come from many sources, the most obvious of which are variety in shape between writers, variations by the same writer from time to time, and the writing instrument employed. The fundamental goals in writer-independent handwriting recognition are to capture both inter- and intra-writer shape variations.

In computer vision, there has been growing interest in deformable models, or active shape models (ASMs), [1], that are able to approximate a target object by adjustment of their controlling parameters. Such models are capable of capturing the natural variability within a class of shapes, and can be used in object extraction. Deformable templates are

closely related to the active contour models known as snakes [2]. Snakes are usually free to take up almost any smooth boundary with few constraints on their overall shapes. The idea of fitting by using image evidence to apply forces to the model and minimising an energy function has proved very effective. The fundamental difference between the two is the amount of prior knowledge which is incorporated: A snake only has generic prior knowledge, such as smoothness, whereas a much greater amount of prior information can be recovered from training sets and encoded within deformable templates.

Although there are many different Chinese characters in use, it is fortunate that most can be decomposed into a few fundamental parts, called radicals [3, 4]. These radicals have different sizes and are placed in specific positions with respect to each other to make a legitimate character. Most approaches to Chinese character recognition are based on stroke extraction. To avoid ambiguity caused by stroke extraction, as well as to discover structural information within the Chinese characters in a statistical way, Shi, Gunn and Damper [5, 6] built up a deformable model for each radical using both linear and nonlinear active shape modelling. The output of the radical extraction stage is a set of radicals ranked by their recognition scores. Treating Chinese character composition as a discrete Markov process corresponding to a sequential composition of radicals, the optimal radical combination is equivalent to the best path in a graph made up of all possible radical combinations [7, 8].

As the peripheral information in a character is more discriminative, it attracts greater interest from researchers [9]. In fact, there is less interconnection within the peripheral structures than within inner structures in a typical Chinese character. In this work, all the peripheral radicals are sorted into nine types: left-hand side, right-hand side, upper ('up'), lower ('down'), surrounding and four diagonal corner radicals. So any mean radical has its own initial location. This treatment simplifies the matching
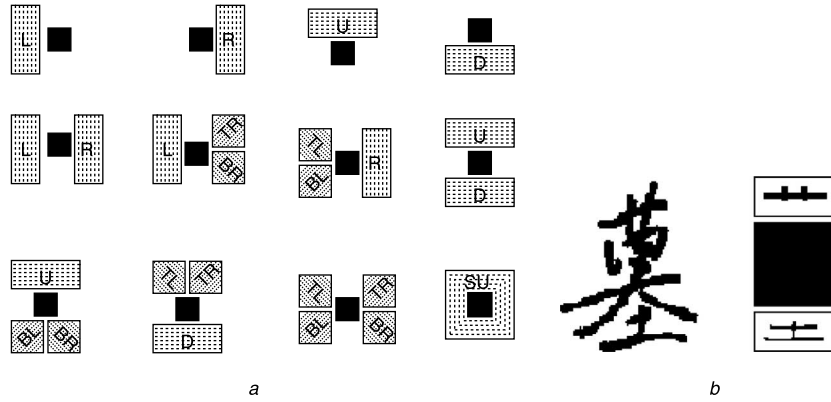
Fig. 1 *Twelve basic structures of Chinese characters and an example character*

a Twelve basic structures of Chinese characters composed from nine peripheral radicals. Black rectangles represent possible inner structures

b An example Chinese character which can be decomposed into one *U* radical, one *D* radical and some inner parts

phase in which we do not need to search over the whole character image.

Let *L*, *R*, *U*, *D*, *SU*, *TL*, *TR*, *BL* and *BR* denote left, right, up, down, surrounding, top-left, top-right, bottom-left, and bottom-right radicals, respectively. Figure 1*a* shows the basic structures and composition rules of radicals to produce characters. The twelve basic structures shown can be used to simplify the radical matching and combination procedures. Wang and Fan [10] identified ten patterns of composition for Chinese characters, but they are only a general description. Figure 1*b* shows an example Chinese character, which can be decomposed into two peripheral radicals and some inner parts. The inner parts can be further decomposed after the recognition of peripheral radicals.

2 Automatic landmark labelling

Active shape modelling requires some landmark points to capture shape constraints in training and to construct plausible new shapes for matching. Chinese characters consist of strokes: in printed characters, these are straight lines but handwritten characters will have curves also.

We used 60 examples of each radical for training. The process of labelling landmark points for training examples is carried out as follows:

Step 1: To bootstrap the automatic process, we first have to label the landmarks of a single example of each radical (called the reference) manually. The reference radicals were selected from among the training examples to be typical of their class. Then, the two terminating points of each stroke were manually identified. A total of 10 points were then spaced approximately equally along each stroke to produce the final landmark-labelled reference radical.

Step 2: To label the remaining training radicals automatically, we superimpose a reference radical upon all the training character examples of the same class. Rotation, translation and scaling are applied around the origin within the following ranges: rotation from $-30°$ to $+30°$ at $5°$ steps; translation from -5 to $+5$ pixels at 1 pixel steps; scaling from $\times 0.5$ to $\times 2$ at $\times 0.1$ steps.

Step 3: Find the best matched radical. The best match for each stroke is the one with minimal sum of geometric distance from all of its 10 control points to their nearest target image pixels. The best matched radical is the one with minimal sum of distance from the varied reference radical points to their nearest target image pixels.

3 Kernel principal component analysis (KPCA)

The original ASMs are only suitable for representing linear variations. However, nonlinear shape variations are common in handwriting. For example, handwritten characters vary widely from person to person (inter-person variation), and from the same person at different times (intra-person variation). Many researchers have been trying to extend ASMs to their nonlinear case. Romdhani, Gong and Psarrou [11] were the first to apply KPCA to active shape models. Recently, Twining and Taylor [12] proved that the treatment of Romdhani *et al.* is not generally valid. In this Section, we will analyse the workings of KPCA, and conclude that the method of Twining and Taylor is not suitable for active shape modelling. The drawback is that differentiation in the feature space cannot be indicators for shape optimisation in the input space. In the following discussion, any Chinese character or radical is a binary skeleton image or sub-image.

Principal component analysis (PCA) is a powerful technique for extracting structure from possibly high-dimensional datasets. It aims to find a low-dimensional representation, by an orthogonal transformation of the coordinate system, which explains the majority of the variance. It is readily performed by solving an eigenvalue problem, or by using iterative algorithms that estimate principal components.

Given a set of *M* examples for a radical $\{\mathbf{e}_1, \mathbf{e}_2, \ldots, \mathbf{e}_M\}$, which are represented by *N* landmark points, i.e., $\mathbf{e}_k = \{\mathbf{x}_{k1}, \mathbf{y}_{k1}, \mathbf{x}_{k2}, \mathbf{y}_{k2}, \ldots, \mathbf{x}_{kN}, \mathbf{y}_{kN}, \}$, the mean radical of the set is given by $\boldsymbol{\Psi} = (1)/(M) \sum_{k=1}^{M} \mathbf{e}_k$. By principal component analysis yielding eigenvectors $\mathbf{U}$ and eigenvalues λ, a radical $\boldsymbol{\Gamma}$ can be generated by:

$$\boldsymbol{\Gamma} = \boldsymbol{\Psi} + \mathbf{Ub} \qquad (1)$$

Here, $\mathbf{b}$ is the vector of shape parameters, which can be adjusted to vary the shape. Usually, only a small number of principal components is sufficient to account for most of the structure variance. The shape parameters $\mathbf{b}$ are typically limited in the range $-3\sqrt{\lambda_i} < b_i < 3 < \sqrt{\lambda_i}$ for the *i*th component with eigenvalue λ_i.

Kernel PCA [13] provides a way to extend linear PCA to nonlinear subspaces of the data. Here, linear PCA is performed in some high-dimensional feature space which is related to the input space by a nonlinear map Φ. The nonlinear map needs no explicit construction. Instead, it can be specified by the dot product in terms of Mercer kernel functions.

The projections of a data point $\mathbf{e}$ onto the eigenvectors $\mathbf{V}^k$ in the feature space can be defined as:

$$\beta_k(\mathbf{e}) = (\mathbf{V}^k)^T \tilde{\mathbf{\Phi}}(\mathbf{e}) = \sum_{i=1}^{M'} \alpha_i^k \tilde{K}(\mathbf{e}_i, \mathbf{e}) \qquad (2)$$

where M' is the number of principal components, $\tilde{\mathbf{\Phi}}(\mathbf{e})$ is the centralised point in the feature space corresponding to the mean vector $\mathbf{\Psi}$, α_i^k is the coefficient for the kth eigenvector, and $\tilde{K}(\mathbf{e}_i, \mathbf{e})$ is the centralised kernel matrix.

Both Romdhani *et al.* and Shi *et al.* follow the strategy to generate active shape models in the feature space and then find their pre-images in the input space. The generation of active shape models can be considered as linear operations on the mean vector $\mathbf{\Psi}$, denoted as $P_{M',b}(\tilde{\mathbf{\Phi}}, (\mathbf{\Psi}))$ which includes truncation and shape parameter adjustment on the mean vector. Given an input observation vector $\mathbf{e}$, the active shape model in the input space $\mathbf{\Gamma}$ is approximated by minimising $\| P_{M',b}(\tilde{\mathbf{\Phi}}, (\mathbf{\Psi})) - (\tilde{\mathbf{\Phi}}, (\mathbf{\Gamma})) \|$. However, Romdhani *et al.* did not provide any effective minimisation method suitable for active shape modelling, whereas Shi, Damper and Gunn [8] applied the dynamic tunnelling algorithm [14].

Twining and Taylor [12] concentrate on the case of a Gaussian kernel function:

$$\tilde{K}(\mathbf{e}_i, \mathbf{e}) = \exp\left(-\frac{\|\mathbf{e}_i - \mathbf{e}\|^2}{2\sigma^2}\right) \qquad (3)$$

From (3), it can be seen that all the nonlinear components for these points will approach zero as the points recede from the data, and all points far from the data in input space will map to the vicinity of the origin in KPCA space. Hence, Twining and Taylor [12] conclude that the treatment of Romdhani *et al.* [11] is invalid, because the latter defined valid shape regions by placing an upper bound on the modulus of each of the normalised KPCA components.

As depicted in Fig. 2, points in the input space will be mapped to points (shown as asterisks) on a hyperplane in the feature space. However, linear operations (e.g., component truncation and shape parameter adjustment) will move points in the feature space away from this hyperplane (as shown by the circles). But such points not on the hyperplane do not have a pre-image in the input space. Hence, the pre-image will be approximated by the one corresponding to the nearest point on the hyperplane in the feature space.

On the basis of the above analysis, we can see that the differentiation of (3) in the feature space cannot be an indicator to search for the optimal shape model in the input space. In other words, the gradient information in the feature

space cannot be applied in the input space. In this respect, Twining and Taylor's method [12] is not suitable for active shape modelling. Also, the Romdhani *et al.* treatment [11] lacks an appropriate means to search for the optimal shape parameters in the input space.

One feasible approach to kernel active shape modelling is to generate an active shape model in the feature space and then find its nearest pre-image in the input space. The distance between the generated model and the target image can be an indicator leading to the optimal solution. In the next Section, further analysis will show why our previous dynamic tunnelling algorithm has to be replaced by another more suitable optimisation technique.

4 Radical matching with a genetic algorithm

Given a radical model, we can employ gradient descent to adjust the shape parameters $\mathbf{b}$, to fit the character image. Now, a good basin of attraction is required to find the shape parameter efficiently. The chamfer distance transform [15] can help to achieve this. The most significant property of the chamfer distance transform is its ability to handle noisy and distorted data, as the edge points of images are transformed by a set of parametric transformation equations that describe how the images can be distorted geometrically in relation to one another. The transform approximates global distances by propagating local distances at image pixels.

Shi *et al.* [5] search for the optimal shape parameters by considering the gradient:

$$\frac{\partial E(\mathbf{\Gamma})}{\partial \mathbf{b}} = \sum_{i=1}^{N} \frac{\partial I_{\text{cham}}(x_i, y_i)}{\partial \mathbf{b}}$$

$$= \sum_{i=1}^{N} \left(\frac{\partial I_{\text{cham}}(x_i, y_i)}{\partial \mathbf{b}} u_{2i-1} + \frac{\partial I_{\text{cham}}(x_i, y_i)}{\partial \mathbf{b}} u_{2i} \right) = 0$$

$$(4)$$

where $E(\mathbf{\Gamma})$ is the energy of a model, $I_{\text{cham}}(x_i, y_i)$ is the chamfer distance between the generated model and the target image at the landmark point (x_i, y_i) and $\mathbf{U} = [u_1, u_2 \ldots u_{2N}]$ is the eigenvector. Shi *et al.* [7, 8] used the dynamic tunnelling algorithm to overcome problems with local minima in gradient descent search. The dynamic tunnelling algorithm is based on a physical analogy to the quantum-mechanical tunnelling of a particle through a potential barrier. Also, the degree of tunnelling is a function of time, increasing during iterative search. After converging to a local minimum, the procedure can jump to another basin of attraction where the new starting point for the search is even lower in energy. From this new starting point, gradient
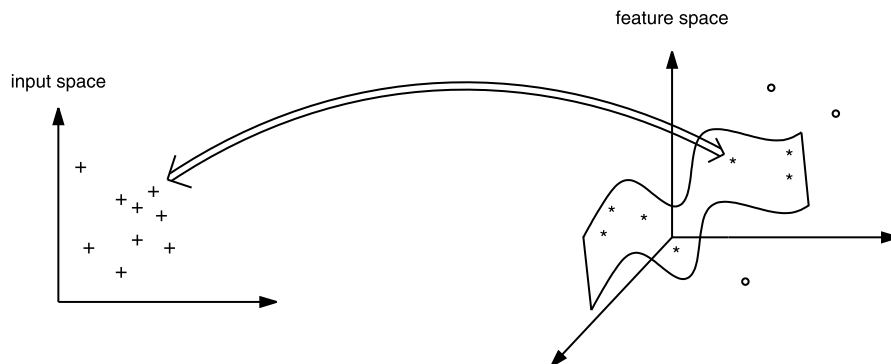

Fig. 2 *Illustration of kernel PCA*
Points in the input space map to a hyperplane in the feature space. Points not on this hyperplane in the feature space do not have a pre-image in the feature space

descent can again be used. For linear active shape modelling, we can get gradient descent information from (3), since the energy in input space is a function of **b**.

However, there is no gradient information available from the image differentiation for kernel active radical modelling (ARM). In this case, the energy is computed in the input space but the shape parameters **b** are defined in the feature space. The energy is not an explicit function of **b**. Hence, the dynamic tunnelling algorithm in the nonlinear case is more like a multi-start point random search within a range limited by the eigenvalues. A more effective methodology to find global minima is needed to address this problem.

Loosely simulating biological evolution, genetic algorithms (GAs) offer a class of global search techniques based on the selective adaptation of a population of individuals [16]. Each individual represents a potential solution to a given problem. We have used a GA to search for the optimal shape parameters in kernel ARM; the cost function used is the chamfer distance.

As mentioned earlier, the eigenvectors and eigenvalues are obtained through PCA. Let $\lambda = \{\lambda_1, \lambda_2, \ldots, \lambda_M\}$ be the set of all the eigenvalues in decreasing order. Active shape models can be generated with the first M' principal components (usually $M' \ll M$). The shape parameters $\mathbf{b} = (b_1, b_2, \ldots, b_{M'})$ control the shape, where M' the smallest integer value that satisfies $\left(\sum_{i=1}^{M'} \lambda_i\right) / \left(\sum_{i=1}^{M} \lambda_i\right) > 90\%$. The chosen M' varies from radical to radical, but is typically five or six.

Finding the optimal model is equivalent to finding the-optimal shape parameters. The fitness of any possible shape parameter is calculated as:

$$E(\mathbf{\Gamma}, \mathbf{b}) = \frac{1}{N} \sum_{j=1}^{N} I_{\text{cham}}(x_j, y_j) + \rho \frac{\|\mathbf{b}\|^2}{M'} \qquad (5)$$

The first term on the right hand side is the chamfer distance between the model $\mathbf{\Gamma}$ and the target image, and the second term is introduced to penalise the model's deviation from its mean position. The coefficient ρ is used to limit the contribution from the second term. The bigger ρ is, the more sensitive a model is to the variation. However, the appropriate penalties to apply to the shape parameters are different from dimension to dimension; it is difficult to estimate an empirical coefficient for each dimension. Moreover, the main contribution of the energy must come from the first term, i.e., the chamfer distance. So here, ρ is set to a small value (0.0001), which was found to give good results.

The optimal active radical model can be found by genetic algorithm as follows:

1. Let the population size be $100 \times M'$.
2. Set the search range for each shape parameter to $-3\sqrt{\lambda_k} < b_k < 3\sqrt{\lambda_k}$, with step size 0.001.
3. Generate active shape models and compute the fitness of the individuals using (5).
4. Let the probability of crossover be 0.8 and the probability of mutation be 0.05.
5. Terminate the search when the number of different individuals is $1000 \times M'$.

There was little difference in the execution time of the GA against dynamic tunnelling. In both cases, it took approximately 0.6 s to match the 200 radicals.

5 Experiments and results

In this work, we have used the HITPU handwritten Chinese character database. It was collected by Harbin Institute of Technology and Hong Kong Polytechnic University, and comprises a collection of 751,000 loosely-constrained handwritten Chinese characters, consisting of 3755 categories written by 200 different writers. HITPU is freely-available from http://www.ntu.edu.sg/home/asdmshi/hitpu.htm and is expected to become a benchmark dataset for researchers in this area. We have used it for all evaluations of our previous work.

In the current experiments, the radical training sets include 200 radical classes, which cover 2154 commonly-used Chinese characters. A lexicon of these 2154 characters has been built up, in which each character is a 9-dimensional feature corresponding to nine types of radical (*L*, *R*, *U*, *D*, *SU*, *TL*, *TR*, *BL* and *BR* as in Fig. 1). If the best-matching candidate radical extracted from the character image in a particular position is the same as the relevant one in the lexicon, the matching is treated as correct. On this basis, the matching rate is 97.4% radicals correct, on the 2154 character classes×200 writers=430,800 characters, where each character is composed of from 1 to 4 radicals. There are approximately 1.1 million radicals in total.

To assess the effectiveness of our proposed method (designated Method 1), we have compared it to some existing representative approaches to Chinese character recognition, namely:

Method 2: Our best previous result [8] using manual landmark labelling and the dynamic tunnelling algorithm [14].

Method 3: The stroke-based approach of Wang and Fan [10].

Method 4: The method of Chung and Ip [17] that uses snakes to partition a character into radicals, then uses a structure-based recogniser to classify them.

To allow comparison on the same database, Methods 3 and 4 were carefully reimplemented by the second author.

From Table 1, it is seen that kernel active radical modelling as in Methods 1 and 2 is far better than stroke analysis in Method 3 and snake decomposition in Method 4. Our method achieves the best correct matching rate. Note that the differences seen between all the figures are highly significant on the basis of a binomial test as described in [6, p. 280]. The advantage of our method is not only the avoidance of straight-line stroke extraction, but also the ability to capture the inter- and intra-writer variations with only a small number of shape parameters. As a matter of fact, it is difficult to implement stroke extraction within a handwritten Chinese character because there is considerable interconnection among the strokes as well as many broken strokes resulting from image capture and preprocessing. Our method has significant advantage in this respect, since any break in a stroke has only a small, local effect on chamfer distance matching.

Figure 3 illustrates the result of using the two search algorithms—dynamic tunnelling (Fig. 3*a*) and genetic algorithm (Fig. 3*b*)—to extract the lower radical from a

Table 1: Performance comparison of representative radical approaches to Chinese character recognition

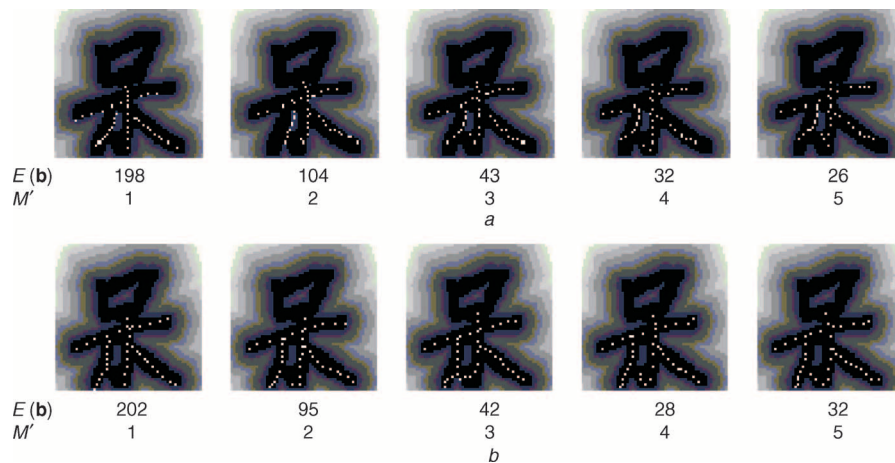|	Description	Correct radical matching rate (%)
Method 1	Kernel ARM+GA	97.4
Method 2	Kernel ARM+DTA	96.5
Method 3	Stroke analysis	93.2
Method 4	Snake decomposition	89.8

Fig. 3 *Performance of optimal shape parameter search with number of principal components varying from 1 to 5*

The result of extracting the lower radical from the target chamfer-transformed image is illustrated
a Active models found by dynamic tunnelling algorithm
b Active models found by genetic algorithm

typical character. In this Figure, the background is the chamfer-transformed test image, and the best-matching model is shown superimposed. In this case, the best-matching model is also the correct one. As can be seen, the genetic algorithm finds generally lower-energy solutions (that are also slightly superior visually).

6 Conclusions

Offline recognition of handwritten Chinese characters is a very hard pattern recognition problem. Here, we report the best results so far achieved on a large subset (430,800 characters, ~1.1 million radicals) of the freely-accessible HITPU database. Active radical modelling (ARM), featuring kernel PCA, offers improved performance over other representative approaches by its avoidance of problematic stroke extraction, by its use of prior knowledge about radical position and shape, and by its ability to encode the statistics of shape variation in example data, so capturing inter- and intra-writer variation. In particular, our previously proposed nonlinear ARM is significantly improved. One new feature of the present work is automatic landmark labelling, which reduces the overhead of manual labelling and greatly improves prospects for practical use. We also point out that one of the most recent approaches to KPCA is not suitable for active shape modelling, because gradient information in the feature space cannot be used in the search for matching radical models in the input space. Thus, genetic algorithms are introduced to search for the optimal shape parameters in the feature space, the cost function being the chamfer distance in the input space.

At present, the impact of automatic landmark labelling on performance is unknown and remains to be tested in future work. We are, however, heartened by the overall improvement we have seen in this work. We also intend to extend our work to the full set of radicals and characters in the HITPU database. This extension will be greatly facilitated by automatic labelling.

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