On-line Handwritten Character Recognition Selectively Employing Hierarchical Spatial Relationships among Subpatterns

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Abstract

This paper proposes an on-line handwritten character pattern recognition method that examines spatial relationships among subpatterns which are components of a character pattern. Conventional methods evaluating spatial relationships among subpatterns have not considered characteristics of deformed handwritings and evaluate all the spatial relationships equally. However, the deformations of spatial features are different within a character pattern. In our approach, we assume that the distortions of spatial features are dependent on the hierarchy of character patterns so that we selectively evaluate hierarchical spatial relationships of subpatterns by employing Bayesian network as a post-processor of our sub-stroke based HMM recognition system. Experiments on on-line handwritten Kanji character recognition with a lexicon of 1,016 elementary characters revealed that the approach we propose improves the recognition accuracy for different types of deformations.

Keywords: on-line handwriting recognition, sub-stroke HMM, Bayesian network, distorted handwriting, spatial relationships among subpatterns

1. Introduction

As the popularity of PDAs, tablet PCs, and other pen-based or paper-based systems increases, the demand for high-performance on-line handwriting recognition even for deformed handwriting is increasing. However, handwritings with deformation of spatial relationships among strokes and subpatterns such as radicals are difficult to recognize. As a representation method for relationships among subpatterns, "Attributed Relational Graphs (ARG)", where each node denotes a subpattern and each arc denotes a relationship between nodes, are commonly employed [1]-[4]. Recently, Bayesian network, a statistical-structural representation scheme, has been proposed to tolerate the shape variation of input patterns [5]. However, these previous studies are based on the assumption that the deformations are caused equally among all subpatterns, though the deformations among strokes and those among radicals are not always

the same within character patterns. Moreover, there are various deformations depending on writing style. For example, scribbled handwritings tend to connect adjacent strokes. On the other hand, in blind handwritings written without visual-feedback, subpatterns tend to overlap.

In order to solve these problems, we focus on the structures of Kanji character patterns. Kanji character patterns, ideographic character patterns of Chinese origin, are mostly composed of multiple subpatterns. Very often subpatterns are shared among several Kanji character patterns as shown in Figure 1. According to the characteristics of the deformations and the Kanji pattern structures, we assume that deformations of spatial relationships among subpatterns are different in each level of the Kanji character patterns' hierarchy. Based on this assumption, we propose a method for evaluating spatial relationships by selecting hierarchical spatial features according to the deformations of the input patterns.

In this study, in order to evaluate spatial relationships among subpatterns, we extract subpatterns from each character pattern by a sub-stroke HMM [6]. The sub-stroke HMM has the advantages that the total size of the models is very small and that the recognition speed is faster compared to conventional whole character HMMs in the case of character patterns recognition with large categories such as Japanese or Chinese Kanji character set. This approach is robust to deformations of strokes and variations of stroke-number and stroke orders [6][7].

Evaluation methods for spatial relationships among subpatterns based on the HMM framework have already been proposed [5][8]. However, these approaches only evaluate spatial relationships between preceding strokes and the current stroke rather than those between the current stroke and its succeeding strokes because they evaluate them while extracting subpatterns from each character pattern. Moreover, these approaches are very sensitive to wrong stroke orders. We thus decided to evaluate subpattern relationships after performing the evaluation by the sub-stroke HMM, and make use of a Bayesian network which is a well-known framework for statistically modeling relationships among strokes and is very robust to deformations.
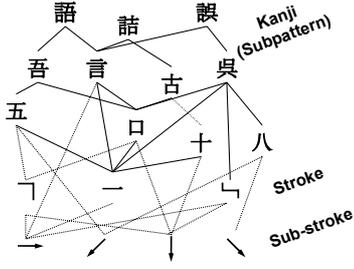
Figure 1. Hierarchical structure of Kanji patterns.

This paper is organized as follows. Section 2 describes the outline of a sub-stroke HMM. Section 3 proposes an evaluation method for spatial relationships among subpatterns based on a Bayesian network. In Section 4, we expand the method proposed in Section 3 by considering deformations of each character pattern. Section 5 shows experimental results and Section 6 concludes this work.

2. Recognition System for Time-Sequential Pattern based on Sub-stroke HMM

A recognition system based on sub-stroke HMM basically consists of a feature extraction module, sub-stroke models (HMMs), a hierarchically structured dictionary and a decoder. In this section, we show the outline of this system.

2.1. Time-Sequential Feature Extraction

We use a sequence of pen-tip positions (x_t, y_t), $t=1, \cdots, T$, sampled at a certain interval from a pen tablet as the pen-coordinate features. Moreover, we extract the displacement $(\Delta x_t, \Delta y_t) = (x_t - x_{t-1}, y_t - y_{t-1})$ from two consecutive pen-tip positions and use $o_t = (r_t, \theta_t)$ as a feature vector, where $r_t = \sqrt{\Delta x_t^2 + \Delta y_t^2}$ and θ_t denote the velocity and the direction of the pen movement, respectively. We then denote by $O = o_1, o_2, \cdots, o_T$ the feature sequence representing each character pattern.

2.2. Sub-stroke HMMs

We have defined 25 sub-strokes of eight directions as shown in Figure 2: eight long sub-strokes (`A'~`H'), eight short sub-strokes (`a'~`h'), eight pen-up movement ('1'~'8') and one pen-up-down movement ('0') based on the knowledge of distinctive features of Kanji character patterns. The HMMs of these sub-strokes have a left-to-right topology as shown in Figure 3. The pen-down models have three states representing the changes of sub-stroke velocity, while pen-up models have only one state without self-loop probability.

Here, let $\lambda^{(k)} = (A^{(k)}, B^{(k)}, \pi^{(k)})$ be the set of HMM parameters of a sub-stroke k, with the following notations:

$A^{(k)} = \{a_{ij}^{(k)}\}$: set of all the state-transition probability distributions from state S_i to S_j,

$B^{(k)} = \{b_i^{(k)}(o_t)\}$: set of all the probability distributions of observing symbol o_t at state S_i,
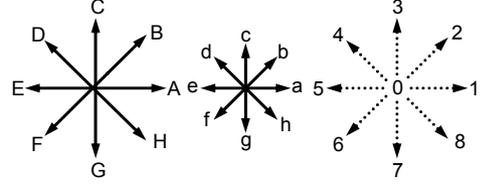

Figure 2. Sub-stroke categories: A-H (a-h) are long (short) sub-strokes and 0-8 are the direction of off-strokes.
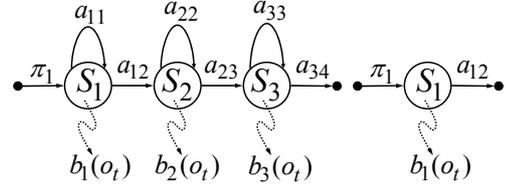

Figure 3. Sub-stroke HMMs : (Left) pen down model, (Right) pen up model.

$\pi^{(k)} = \{\pi_i^{(k)}\}$: initial state probability distributions.

The observation probability distributions are represented by mixtures of M Gaussian distributions given by

$$b_i(o_t) = \sum_{m=1}^{M} c_{im} \frac{\exp(-\frac{1}{2}(o_t - \mu_{im})^t \Sigma_{im}^{-1} (o_t - \mu_{im}))}{\sqrt{(2\pi)^n |\Sigma_{im}|}} \qquad (1)$$

with mean vectors μ_i, covariance matrices Σ_i (n is the dimension of the observation feature vector o_t) and weighting coefficients c_{im}. Here, the direction feature θ has a continuous probability distribution with 2π cycle. These parameters can be trained through the Viterbi training or the Baum-Welch algorithm. Moreover, we employ context-dependent sub-stroke HMMs [7] to enhance robustness to deformations of strokes.

2.3. Hierarchically Structured Dictionary

A hierarchically structured dictionary is useful to define stroke-order rules common to many characters systematically [6]. As shown in Figure 4, six Kanji characters (“語”, “言”, “吾”, “五”, “口”, “一”) can be defined by nine sub-stroke models (`A', `F', `a', `g', `h', `2', `3', `5', `6'). The rule “語=言 2 吾” means that Kanji “語” is defined by combining “言” and “吾” with pen-up model `2', where Kanji “言” and Kanji “吾” are treated as parts of Kanji “語”.

Since the recognition method is sensitive to stroke order variations, we employ a dictionary which defines 300 additional different stroke-order-rules of subpatterns [6]. These additional rules are statistically chosen from training patterns.

2.4. Decoder

According to the description in the hierarchically structured dictionary, the decoder concatenates the sub-stroke HMMs to generate an HMM of each candidate character pattern, and then calculates the probability that the input pattern is produced from the HMM. This

W	=	語 | 言 | 吾 | 五 | 口 | 一		¬	=	a g
語	=	言 2 吾		一	=	A
言	=	、 6 一 6 - 6 – 6 口		-	=	a
吾	=	五 6 口		ノ	=	F
五	=	一 5 ノ 3 ¬ 5 一		|	=	g
口	=	| 3 ¬ 5 -		、	=	h

Figure 4. Hierarchically structured dictionary of six Kanji character patterns.

火	=	ソ 4 人
火*	=	人 4 ソ
火**	=	、 2 人 3 ノ
ソ	=	、 2 ノ
人	=	g F 2 H
、	=	h
ノ	=	f

Figure 5. Bayesian network and definitions in hierarchically structured dictionary for Kanji pattern "火" (* denotes a definition with wrong stroke-order.).

operation is effectively done by the Viterbi search algorithm of a sub-stroke network [6].

3. Bayesian Network Modeling of Subpatterns and their Relationship

A Bayesian network is a well-known stochastic graph efficient in modeling dependencies. Cho et al. [5] have successfully applied it to Hangul character pattern recognition where nodes correspond to point models and each arc represents their dependencies. In this section, we propose a Bayesian network framework to model subpatterns and their relationships.

3.1. Bayesian Network

A Bayesian network is a graph model whose nodes represent random variables and arcs represent dependencies between the random variables with conditional probabilities. It is represented as a directed acyclic graph (DAG) so that all edges are directed and there is no cycle when edge directions are followed.

Here let $\{X_1,\cdots,X_N\}$ be random variables in a Bayesian network. The dependency from $\pi(X_i)$ to X_i ($1 \le i \le N$) is represented by the directed edge: $\pi(X_i) \rightarrow X_i$ in the Bayesian network and $P(X_i|\pi(X_i))$ is a conditional probability distribution, where $\pi(X_i)$ denotes the parent nodes of X_i. The joint probability of all the nodes is given by the multiplication of their conditional probabilities, and the joint probability of $\{X_1,\cdots,X_N\}$ is then:

$$P(X_1,\cdots X_N) = \prod_{i=1}^{N} P(X_i | \pi(X_i)) \qquad (2)$$

3.2. Spatial Feature Extraction

In order to evaluate spatial relationships among subpatterns, we extract a spatial feature. First of all, we normalize the size of an input character pattern with a sequence of pen-tip positions (x_t,y_t), $t=1,\cdots,T$, while preserving the aspect ratio (width/height). For the normalized character pattern, we extract three feature points $(\tilde{x}_i, \tilde{y}_i)$: the starting point, the center of gravity and the ending point for each subpattern, and use them as spatial features s_i in the Bayesian network. In order to extract the s_i, we need the segmentation points of each subpattern, which has been obtained by the Viterbi segmentation in the sub-stroke HMM framework. In the previous work by Cho et al. [5], fine spatial features such as stroke points had to be used to evaluate the time
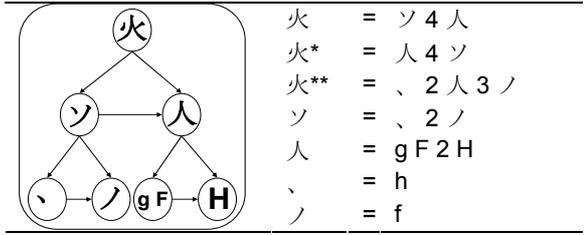
sequence features and the spatial relationships among subpatterns, while we are able to evaluate spatial relationships by employing coarse features thanks to the sub-stroke HMM pre-processing. By doing so, we can speed up the evaluation process in the Bayesian network framework.

Moreover, even if the stroke order of the input character pattern is different from the standard one, we can easily extract subpatterns. For example, as shown in Figure 5, the Kanji "火" whose standard stroke order is "火 = ソ 4 人" has two types of wrong stroke-orders: "火*" and "火**". In the case of the character pattern with wrong stroke-order "火* = 人 4 ソ", we can easily extract subpatterns: "人" and "ソ" by looking at permutations in the stroke order. On the other hand, in the case of the character pattern with wrong stroke-order "火** = 、2 人 3 ノ", the subpattern: "ソ" can not be extracted. In this case, we can generate quasi-subpatterns by connecting subpatterns "、" and "ノ" which belong to a lower hierarchy level than them.

3.3. Subpattern Relationship Modeling

For each character pattern, a Bayesian network is constructed according to the hierarchically structured dictionary mentioned in Section 2.3. Figure 6 shows a Bayesian network for the Kanji character pattern "語". When we construct a Bayesian network, we assume that each node except a character pattern node is affected by the character patterns or subpatterns in which it is used parent nodes and by subpatterns it follows inside a chararacter pattern. According to these assumptions, we set directed arcs among relevant nodes, and then normalize each hierarchy level to give equivalent weights to subpatterns with the same size during the evaluation of their spatial relationships. This normalization is performed by computing for each node a weight α, defined as follows: α=(number of strokes of the subpattern) / (number of strokes of the character pattern). The weight of the top hierarchy level is then 1.0 and that of the lowest hierarchy level is 0.0.

As mentioned in Section 3.2, we extract three spatial feature points from each subpattern. Assuming that each center of gravity is affected by the starting point and each ending point is affected by the other two points, we obtain the detail of the Bayesian network described in Figure 6 is shown in Figure 7. Since the starting or the
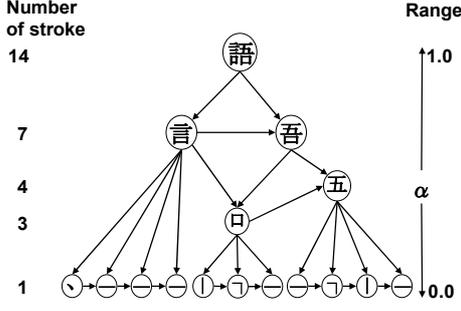
Figure 6. Bayesian network of Kanji "語".

ending point can be the same inside a pair of subpatterns which belong to adjacent hierarchy levels (for example, the starting points of the character pattern "語" and of the subpattern "言" are the same), we only take into account the influence of the center of gravity of a subpattern belonging to the upper hierarchy level on a subpattern of a lower hierarchy level. Therefore, the total number of nodes in the Bayesian network is three times bigger than the number of subpatterns inside the main character pattern, and if we denote by N_w the total number of nodes of the Bayesian network associated to a character pattern w, we have to extract $S=\{s_1,\cdots,s_{Nw}\}$.

3.4. Evaluation using a Bayesian Network

In the Bayesian network associated to a character pattern w, the joint probability of random variables $\{X_1,\cdots,X_{Nw}\}$ for the spatial feature set $S=\{s_1,\cdots,s_{Nw}\}$ is given by

$$P_{BN}(X_1,X_2,\cdots,X_{N_w}\mid w)=\prod_{i=1}^{N_w}P(X_i\mid\pi(X_i),w). \qquad (3)$$

Since the random variables are supposed to be continuous, a conditional probability table is not adequate because continuous values should be quantized and the table size would grow exponentially with the number of dependencies among variables. For these reasons, we use a conditional Gaussian distribution for each random variable X_i as follows:

$$P(X_i = s_i\mid\pi(X_i)=q_i)$$
$$=\frac{1}{\sqrt{(2\pi)^d\mid\Sigma_i\mid}}\exp(-\frac{1}{2}(s_i-\mu_i(q_i))^t\Sigma_i^{-1}(s_i-\mu_i(q_i))) \qquad (4)$$

where the spatial feature set $q_i=\{\hat{s}_1,\cdots,\hat{s}_N\}\in S$ corresponds to the random variable $\pi(X_i)$, d is the dimension of the spatial features, $\mu_i(q_i)$ is the mean vector and Σ_i is the covariance matrix of the Gaussian distribution. The mean vector $\mu_i(q_i)$ is computed using the vector $Z_i=[\hat{s}_1,\cdots,\hat{s}_k,1]$ and a regression matrix R_i as follows:

$$\mu_i(q_i)=R_iZ_i^t \qquad (5)$$

where Z_i is a $(d\times k+1)$-dimensional feature vector and R_i is a $2\times(d\times k+1)$-dimensional linear regression matrix.
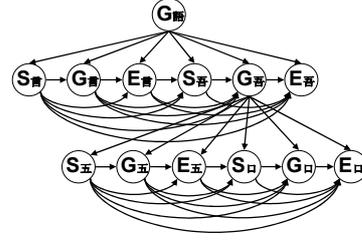

Figure 7. Detailed structure of nodes among 語 and 言 and 吾 and 五 and 口 in Figure.6. S, G and E denote the starting point, the center of gravity and the ending point of each subpattern, respectively.

3.5. Estimation of the Bayesian Network's Parameters

The parameters of a Bayesian network, including the multiple regression matrix R_i can be trained using the following equations:

$$\overline{R}_i=(\sum_{m=1}^{M}s_m^tZ_m)(\sum_{m=1}^{M}Z_mZ_m^t)^{-1} \qquad (6)$$

$$\overline{\Sigma}_i=\frac{1}{M}\sum_{m=1}^{M}(s_m-\overline{R}_iZ_m)(s_m-\overline{R}_iZ_m)^t \qquad (7)$$

where M denotes the total number of training tokens. If no feature vectors: Z_i are given, the above equations become equivalent to the parameter estimation for a standard Gaussian distribution.

4. Selectively Evaluating Hierarchical Spatial Relationships among Subpatterns

In this section, we propose a method that selectively evaluates hierarchical spatial relationships between subpatterns by employing a Bayesian network as a post-processing of the sub-stroke HMM we introduced.

4.1. Combining Sub-stroke HMM and Bayesian Network

For the observation of an input character pattern w whose time-sequential feature is $O=o_1,\cdots,o_T$ (T is the length of O) and spatial feature is $S=\{s_1,\cdots,s_{Nw}\}$ (Nw is the total number of nodes in the Bayesian network), by combining the probability P_{HMM} of the sub-stroke HMM with the probability P_{BN} of the Bayesian network, we obtain the following evaluation formula:

$$(1-\gamma)\frac{\log P_{HMM}(O\mid w)}{T}+\gamma\frac{\log P_{BN}(S\mid w)}{N_w} \qquad (8)$$

where γ is a weighting coefficient that we set to $\gamma=0.92$. By dividing P_{HMM} by T and P_{BN} by Nw, we can normalize the total score among different character patterns for which T or Nw are different.

4.2. Evaluating Range

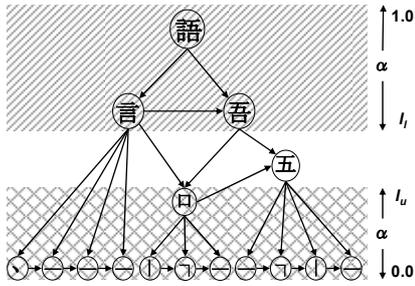To evaluate spatial relationships among subpatterns except for hierarchy levels where spatial relationships

Figure 8. Evaluating Range

Figure 9. Handwriting samples.

are too distorted, we employ the hierarchical value α, which range is $0.0 \leq \alpha \leq 1.0$ as introduced in Section 3.3. We can define an upper limit l_u and evaluate spatial relationships among subpatterns whose hierarchical value α lies in the range $0.0 \leq \alpha \leq l_u$, or define a lower limit l_l and evaluate spatial relationships among subpatterns whose hierarchical value lies in the range $l_l \leq \alpha \leq 1.0$ as shown in Figure 8.

We should note however that when evaluating only a part of the Bayesian network by defining l_l or l_u, we should delete the arcs connecting unevaluated nodes, and in order to do so, we would need to reestimate the regression matrix R_i, which cannot be considered in a practical realization. Therefore, we will leave this problem for future research and will not consider it in this paper.

5. Experiments

We conducted experiments to investigate the efficiency of our approach for Japanese Kanji recognition.

5.1. Description of the Handwriting Database

The database we considered, called the JAIST IIPL (Japan Advanced Institute of Science and Technology, Intelligence Information Processing Laboratory) database, consists of several kinds of datasets. Among them, we used the datasets written in two kinds of deformed handwritings: the ε set (which we will refer to as scribbled handwritings) and the δ-$1a$ set, written in no visual-feedback condition (which we will refer to as blind-handwritings). In the former, there are many patterns whose adjacent strokes are connected, while in the latter there are many patterns with overlaps of separated strokes. Some examples depicted in Figure 9. Blind-handwriting dataset also has slanted or rotated handwritings which deteriorate the recognition performance. Though we can recognize those patterns by applying a rotation-free recognition method [10], we rejected those handwritings in this study since we would

like to evaluate the performance of our approach for the deformation of spatial relationships.

Each dataset covers 83 Hiragana, 86 Katakana, 62 Alpha-numeric characters and 1,016 old and new educational Kanji character patterns with free stroke order. In the experiment, we used only the Kanji character patterns. Scribbled handwritings from 34 writers were used to estimate the parameters of the sub-stroke HMMs and the Bayesian networks, and those from 17 other writers were used to determine the weighting coefficient γ mentioned in Section 4.1. The scribbled handwritings from the remaining 17 writers and the blind-handwritings from 30 writers were used for test.

5.2. Examination about Deformations of Spatial Relationships among Subpatterns

In order to examine how the deformations of spatial relationships among subpatterns depend on the hierarchy of character patterns, we at first carried out recognition experiments by varying an evaluating range for a Bayesian network.

Table 1 shows the recognition results for scribbled handwritings and Table 2 shows those for blind-handwritings. The rate in each table denotes correct recognition accuracy when varying the limit l_l or l_u by 0.2 intervals. For l_l=0.0 or l_u=1.0, all the nodes in the Bayesian network are evaluated. On the other hand, l_u=0.0 means that only spatial relationships among small subpatterns such as adjacent strokes are evaluated. This corresponds to an evaluation performed using the sub-stroke HMM only.

In the case of scribbled handwritings, l_l=0.0 or l_l=0.2 gave the highest recognition accuracy. This results show that, as we assumed, there are many patterns whose adjacent strokes are connected in the scribbled handwritings and the recognition accuracy can be improved by removing those hierarchies from evaluating range. On the other hand, in the case of blind handwritings l_u=0.6 gave the highest recognition accuracy. Even though for blind-handwritings with only a slight overlap of separated subpatterns such as "状" in Figure 9 can be recognized even if we evaluate all the

Table 1. Recognition rate of scribbled handwritings for each evaluating range.

Evaluating range	Correct recognition rate [%]					
	0.0	0.2	0.4	0.6	0.8	1.0
$l_l \leq \alpha \leq 1.0$	**91.4**	**91.4**	90.9	90.6	90.6	90.6
$0.0 \leq \alpha \leq l_u$	90.2	90.7	90.9	91.2	91.2	**91.4**

Table 2. Recognition rate of blind-handwritings for each evaluating range.

Evaluating range	Correct recognition rate [%]					
	0.0	0.2	0.4	0.6	0.8	1.0
$l_l \leq \alpha \leq 1.0$	89.8	89.4	88.7	87.9	87.5	87.5
$0.0 \leq \alpha \leq l_u$	88.6	89.4	89.9	**90.1**	90.0	89.8

Table 3. Recognition rates according to the selection mode of the evaluating range. (1)~(3) denote the evaluating range. (1):all hierarchy levels, (2): l_l or l_u which gives the highest recognition accuracy as shown in Table 1 and Table 2, (3):automatically selected.)

Database	Correct recognition rate [%]		
	(1)	(2)	(3)
Scribbled handwritings	91.40	91.40	**91.83**
Blind-handwritings	89.83	90.05	**90.31**

Table 4. Examples of character patterns correctly recognized by automatically selecting the evaluating range.

Input	Misrecognized character patterns (Reduction of error recognition rate)
困	囲(29.4%⇒ 0.0%), 国(5.9%⇒ 0.0%)
室	実(23.5%⇒ 0.0%), 宝(5.9%⇒ 0.0%)
飼	銅(23.5%⇒ 0.0%), 情(5.9%⇒ 0.0%)
特	持(23.5%⇒ 5.9%), 時(5.9%⇒ 0.0%)
宝	定(41.2%⇒ 0.0%), 宙(5.9%⇒ 0.0%)

hierarchy levels, the recognition accuracy for seriously distorted blind-handwritings such as "穀" and "秋" in Figure 9 is improved by not evaluating upper hierarchy levels in the Bayesian networks.

Moreover, we can see that the recognition accuracy for both scribbled handwritings and blind-handwritings deteriorates when l_l is larger than 0.2 in $l_l \le \alpha \le 1.0$. This is due to the following misclassifications: when the lower limit l_l is large, there are misclassifications among character patterns which have similar structure, because only spatial relationships among large subpatterns such as radicals are evaluated.

5.3. Automatically Selecting of Evaluating Range

From the results in Section 5.2, as we assumed, recognition accuracy changes according to the evaluating range and can be improved by selecting it properly. However, the proper evaluating range changes according to the handwriting deformations and it is not practical to select it manually. Then we select evaluating range which gives the best score among all evaluating ranges considered automatically. From the discussion of Section 5.2, we set the variation range of α using l_l =0.2, meaning that α can vary in the range $\alpha_l \le \alpha \le 1.0$ for any α_l such that $0.0 \le \alpha_l \le 0.2$ in the case of a lower bound, and that α can vary in the range $0.0 \le \alpha \le \alpha_u$ for any α_u such that $0.0 \le \alpha_u \le 1.0$ in the case of an upper bound. In this experiment, to reduce the computation costs, we chose to let the upper and lower bounds α_u and α_l on α vary by 0.2 intervals.

Table 3 shows the recognition results, and we see that the recognition accuracy has been improved by automatically selecting the evaluating range for each Bayesian network. From our analysis, there were two types of improvements: one is discussed in Section 5.2, the other can be observed for both scribbled handwritings and blind-handwritings. Some Kanji character patterns that used to be misrecognized but were correctly recognized with our method are shown in Table 4. In Table 4, the automatically selected evaluating range of "困" and "室" was α_u=0.8 and that of the other character patterns was α_l=0.2. These character patterns have similar subpatterns. In the former, subpatterns of the upper hierarchies are similar. On the other hand, in the latter, subpatterns in the lower hierarchies are similar. By not evaluating the spatial relationships among those similar subpatterns, the misrecognition among character patterns was reduced.

6. Conclusion

In this paper, we have proposed a method that selectively evaluates hierarchical spatial relationships of subpatterns by employing Bayesian network as a post-processing of a sub-stroke HMM we designed. Through the experiments, we have shown that our approach improves the recognition accuracy for different types of deformations (scribbled handwritings and blind-handwritings).

Acknowledgement

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