Deformed trademark retrieval based on 2D pseudo-hidden Markov model☆

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Abstract

A new deformed trademark retrieval method based on two-dimensional pseudo-hidden Markov model (2D PHMM) is proposed in this paper. Most trademark retrieval systems focus on color features, shape silhouettes, or the combination of color and shape. However, these approaches adopted individual silhouettes as shape features, leading to the following two crucial problems. First, most trademarks have various numbers of decomposed components, while the silhouette-based approaches cannot handle the variety correctly. Second, the infringement cases in which trademarks are changed by non-rigid deformation, in particular nonlinear deformation, may escape detection. Thus, our method focuses on the overall appearance of trademarks and incorporates color and shape features into 2D PHMM to tackle the above two problems. The reason to involve 2D PHMM is that it has high tolerance to noise and distortion, moreover, contextual information can be incorporated into it in a natural and elegant way. However, 2D PHMM is computation intensive and sensitive to rotation, scale and translation variations. Thus, it is the main originality of this paper to include the advantages of 2D PHMM but to exclude its disadvantages. As a result, similar trademarks can be retrieved effectively, even those with different numbers of components or non-rigid deformation. Various experiments have been conducted on a trademark database to prove the effectiveness and practicability of the proposed method. © 2001 Pattern Recognition Society. Published by Elsevier Science Ltd. All rights reserved.

Keywords: Deformed trademark; Similarity measure; Color; Shape; Color quantization; Log-polar mapping; Invariance; 2D hidden Markov model

1. Introduction

Trademark recognition is an important research issue since the increasing number of registered trademarks puts a heavy burden on manual examiners. Hence, it is imperative to develop similar trademark retrieval for automatic trademark recognition, which in turn speeds up manual examination process.

The developed trademark recognition methods in the literature include those using color features [1], shape features [2–5], or both of them [6–9]. However, most shape features used in these approaches are restricted to silhouettes, thus resulting in two crucial problems related to composition and deformation resemblances. The composition resemblance means that two images may look alike although the numbers of components included in the images may be different. Two examples are shown between Figs. 1(a) and (b). The deformation resemblance can be defined in the similar way except that the difference between two images is caused by deformation. Six examples are shown between Figs. 1(a) and (c), (d) and (f). Past approaches might derive low similarity values between the images having either the composition or deformation resemblances due to the weaknesses listed below.

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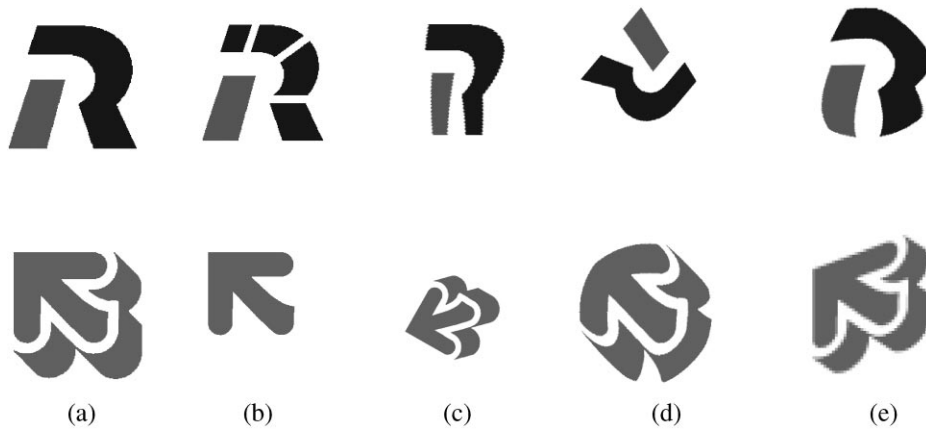*E-mail address:* cschen@cs.yzu.edu.tw (S.-Y. Chen).

Fig. 1. Some resemblance examples. (a) Two original trademarks; (b) composition resemblances of (a); (c), (d) and (e) deformation resemblances of (a).

First, although some approaches concerned more than one silhouettes, the techniques used to handle differences in the numbers of components such as hierarchical representation [2], combination summation [3,4,6–8], histogram intersection method [9] or maximum and average terms of similarities [5] are too rough to tackle the composition resemblance problem correctly. Second, most approaches took into account mild non-rigid transformation rather than the general non-rigid and nonlinear deformation.

Our method copes with the two problems by focusing on overall appearance rather than individual silhouettes. More specifically, we incorporate color and shape features into 2D PHMM to tackle the problems. The hidden Markov model is a popular stochastic method used for attacking problems such as matching observed signal patterns [10,11], character recognition [12] and color image retrieval [13]. The retrieval method in Ref. [13] is effective and flexible. Moreover, it can handle the varieties of images by 2D PHMM, thus its matching performance is better than that of template matching. However, 2D PHMM is computation intensive and sensitive to rotation, scale, and translation variations. Thus, it is the main originality of the proposed method to include the advantages of 2D PHMM but to exclude its disadvantages. First, to reduce computation time, a color quantization is proposed to reduce the computation load as required by true color processing. The log-polar mapping is then employed to reduce the spatial resolution. More important, the log-polar mapping [14–16] can also be used to achieve the rotation, scale and translation invariant requirement. The invariant property together with the flexibility of 2D PHMM lead to the result that similar trademarks can be retrieved effectively, even those with different numbers of components or non-rigid deformation.

More specifically, the proposed method includes two stages: database creation and query comparison. The former is concerned with construction of 2D PHMM for each image in the database. The latter deals with matching the query image to each of the 2D PHMMs in the database.

The database creation stage consists of two major phases: feature extraction and construction of 2D PHMM. The feature extraction phase is further composed of two steps: color quantization and log-polar mapping. A color quantization method based on the YIQ color model is proposed to reduce the number of colors. The quantized colors are defined as cellular decomposition of chromaticity terms followed by luminance decomposition. Accordingly, the number of colors can be reduced from 256^3 true colors to 36 colors. After color quantization, connected components can be labeled [17] and foreground and background components can be found out. The centroid of all foreground objects is considered as the origin of the polar coordinate system. The log-polar mapping can then be performed on the polar coordinate system to resample the image. The sizes of resampled images can be reduced 18–300 times. More important, the resampled images are rotation, scale and translation invariant which in turn can be used to construct geometric invariant 2D PHMMs.

In the query comparison step, it also consists of two major phases: feature extraction as well as matching between the query image and 2D PHMMs in the database. The first step is the same as that in the database creation step. To match the query image, a modified 2D Viterbi algorithm [12,13] is used to estimate the probability values between the query image and 2D PHMMs in the database. The probability values can be considered matching scores to retrieve similar images. In other words, the images of which 2D PHMMs best match the query can be retrieved.

The remainder of this study is organized as follows. Feature extraction and retrieval method are described in