Improving the Matching of Graphs Generated from Shapes by the Use of Procrustes Distances into a Clique-based MAP Formulation

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Abstract

Structural graph matching methods often fail when trying to match graphs which are small and present low structural constraints. An extra source of information is needed in order to eliminate the ambiguities produced by the lack of structural information. In this paper we introduce positional information into the cliques model in order to enhance the matching criterion. Procrustes methods provide a proper framework to do statistics with coordinate positions. Results show that our model significantly improves the matching capability in graphs generated from shapes (handwritten capital letters).

Acknowledgements

This research was partially supported by Consolider Ingenio 2010, project CSD2007-00018, by the CICYT project DPI 2007-61452 and by the Universitat Rovira i Virgili (URV) through a predoctoral research grant.

1. Introduction

Structural graph matching techniques exploit structural constraints provided by graphs, in order to find an optimum matching [2] [3] [4].

The model presented in [4] (Section 3) provides a good means of matching graphs with high or even moderate structural constraints. It has demonstrated to be powerful when applied to the matching of large graphs of road maps and also Delaunay graphs.

Almost any object can be represented by a graph. In the case of shapes, we can obtain a graph representation via the *skeletonization* of an input image and by placing the nodes at the end points, junction points and high curvature points of the skeleton. Graphs generated from shapes are typically small and they present low structural constraints. In these cases, a purely structural criterion often leads to ambiguities and therefore, an extra source of information is needed. Information of point positions is traditionally used in Statistical Shape Analysis [1]. With the use of Procrustes methods (Section 2), we are able to make the comparisons of such point-sets invariant to Euclidean similarity transformations. Our aim here is to use such techniques to enhance the matching criterion.

In Section 2 Procrustes distance is described. In Section 3 the cliques model by Wilson and Hancock [4] is introduced. In Section 4 our contribution to the cliques model is defined in order to improve the matching of graphs generated from shapes. In Section 5 results are presented. Finally, in Section 6 some conclusions are given.

2. Procrustes distance

Consider two point-sets X_1 and X_2 arranged in $k \times m$ matrices of cartesian coordinates of k points in m dimensions. The *Procrustes distance* $d(X_1, X_2)$ is the closest Euclidean distance between X_1 and X_2 over the Euclidean similarity transformations of X_1.

Given the above definition, the Procrustes distance between X_1 and X_2 is defined as:

$$d(X_1, X_2) = \inf_{\Gamma,\beta,\gamma} \parallel X_2 - \beta X_1 \Gamma - 1_k \gamma^T \parallel , \quad (1)$$

where $\parallel X \parallel = \mathrm{trace}\left(X^T X\right)^{\frac{1}{2}}$ is the Euclidean norm, $\beta \in \Re^+$ is a positive scaling factor, $\Gamma \in SO(m)$ is a $m \times m$ rotation matrix and $\gamma \in \Re^m$ is a translation m-vector.

Following Dryden and Mardia [1] we obtain the Procrustes distance first by substituting X_1, X_2 into (1) by their centered versions normalized to unit size $Z_1 = \frac{CX_1}{\|CX_1\|}$ and $Z_2 = \frac{CX_2}{\|CX_2\|}$, where $C = I_k - \frac{1}{k} 1_k 1_k^T$ is the centring matrix which applies a translation that brings the centroids of X_1 and X_2 to the origin.

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Afterwards, the minimizing parameters are found at $\hat{\gamma} = 0$, $\hat{\beta} = \frac{\mathrm{trace}\left(Z_2^T Z_1\right)}{\mathrm{trace}\left(Z_1^T Z_1\right)}$ and $\hat{\Gamma} = UV^T$, where $V\Lambda U^T = \mathrm{svd}\left(Z_2^T Z_1\right)$ is the *singular value decomposition* of $Z_2^T Z_1$.

3. Clique-based MAP formulation

The aim of graph matching is to associate nodes in a data-graph $G_1 = (V_1, E_1, A_1)$, where V_1 is a set of nodes, E_1 is a set of arcs and $A_1 = \left\{x_u^{(1)}, \forall u \in V_1\right\}$ is a set of symbols associated with the nodes, against those in a model-graph $G_2 = (V_2, E_2, A_2)$, where $A_2 = \left\{x_v^{(2)}, \forall v \in V_2\right\}$. The matching is represented by a function $f : V_1 \rightarrow V_2 \cup \phi$ for the nodes in the data graph G_1 to those in the model graph G_2 augmented with a null-label.

In [4] the graphs are matched using *cliques*. For a given node indexed $\jmath$ from G_1, the clique $C_\jmath = \left\{u_1, \ldots, u_{|C_\jmath|}\right\}$ is defined as $C_\jmath = \jmath \cup \{\imath | \, (\imath, \jmath) \in E_1\}$. The matched realization of the clique $C_\jmath \subseteq V_1$ is denoted as

$$\Gamma_\jmath = \left\{f(u_1), \ldots, f(u_{|C_\jmath|})\right\} \ . \tag{2}$$

For each clique on the model graph $S_\imath$, a set of *structure-preserving mappings* (SPMs) are generated in order to obtain a dictionary $\Theta_\jmath = \left\{S_\imath^k\right\}$ where to evaluate each data graph clique $C_\jmath$.

The final decision rule to update the matching configuration according with the MAP criterion [4] is:

$$f(u) = \underset{v^{(2)} \in V_2 \cup \phi}{\arg\max} P\left(f(u^{(1)}) = v^{(2)} | x_u, x_v\right) P(f) \ , \tag{3}$$

where $P\left(f(u^{(1)}) = v^{(2)} | x_u, x_v\right)$ is the probability of match between nodes $u^{(1)} \in V_1$ and $v^{(2)} \in V_2$ given measurements only relative to the nodes under match, and $P(f)$ is the joint *prior* which gauges the overall consistency of the matching configuration. Next, the developement of this structural consistency measure is described.

Commencing by modelling the consistency of match of an individual clique as demanded by the Bayes rule:

$$P(\Gamma_\jmath) = \sum_{S_\imath^k \in \Theta_\jmath} P\left(\Gamma_\jmath | S_\imath^k\right) P\left(S_\imath^k\right) \ . \tag{4}$$

Assuming independence in the matching errors between adjacent nodes of the same clique, the conditional probabilities become

$$P\left(\Gamma_\jmath | S_\imath^k\right) = \prod_{r=1}^{|S_\imath^k|} P\left(f(u_r) | v_r\right) \ . \tag{5}$$

Matching errors and structural errors are assumed to occur with uniform probabilities P_e and P_ϕ respectively. Under these assumptions, the distribution rule under the product of (5) is

$$P\left(f(u_r)|v_r\right) = \begin{cases} P_\phi & \text{if } f(u_r) = \phi \vee v_r = \text{dummy} \\ (1 - P_e)(1 - P_\phi) & \text{if } f(u_r) = v_r \\ P_e (1 - P_\phi) & \text{if } f(u_r) \neq v_r \end{cases} \tag{6}$$

Combining (6) and (5) and assuming that each of the SPMs is equi-probable, i.e. $P\left(S_\imath^k\right) = \frac{1}{|\Theta_\jmath|}$, the final model for the clique matching probabilities expressed in the natural exponential form is

$$\begin{aligned} P(\Gamma_\jmath) = \tfrac{1}{|\Theta_\jmath|} \sum_{S_\imath^k \in \Theta_\jmath} \exp\left[-k_{er} H\left(\Gamma_\jmath, S_\imath^k\right) - \right. \\ \left. - k_{eq} E\left(\Gamma_\jmath, S_\imath^k\right) - k_\phi N\left(\Gamma_\jmath, S_\imath^k\right)\right] \ , \end{aligned} \tag{7}$$

where $N\left(\Gamma_\jmath, S_\imath^k\right)$ is the number of dummy nodes in $S_\imath^k$ plus the number of nodes assigned to the null label in $\Gamma_\jmath$, $H\left(\Gamma_\jmath, S_\imath^k\right)$ is the Hamming distance between non-null elements of $\Gamma_\jmath$ and non-dummy nodes of $S_\imath^k$, and $E\left(\Gamma_\jmath, S_\imath^k\right)$ is the number of coincidences between non-null elements of $\Gamma_\jmath$ and non-dummy nodes of $S_\imath^k$, $k_\phi = \log\left[\frac{1}{P_\phi}\right]$, $k_{er} = \log\left[\frac{1}{(1-P_\phi)P_e}\right]$ and $k_{eq} = \log\left[\frac{1}{(1-P_\phi)(1-P_e)}\right]$.

Finally, the joint prior is computed by averaging the clique matching probabilities over the nodes of the data graph, i.e.

$$P(f) = \frac{1}{|V_1|} \sum_{\jmath \in V_1} P(\Gamma_\jmath) \ . \tag{8}$$

The matching configuration is updated using the MAP decision rule given in (3) and according to a Discrete Relaxation scheme [4]. The strategy is to set P_e to an initial high value to reflect a poor labelling, and reduce it through iterations.

In the next section we describe our contributions to the model above, aimed to improve the matching of graphs generated from shapes.

4. Introducing Procrustes distances into the cliques model

Graphs generated from shapes are typically small and they present low structural constraints. These two

facts together are a potential source of ambiguity for purely structural matching methods. Our aim is to apply Procrustes methods to the point-sets extracted from the shapes in order to enhance the matching criterion. Procrustes methods provide a proper framework to do statistics with point positions. To that end, we augment the set of unary measurements associated with the nodes with the coordinates of the feature points. Hence, $A = \{(x_i, \overrightarrow{\rho_i}), \forall i \in V\}$, where $\overrightarrow{\rho_i} = (p_1, \ldots, p_m)$ is an m-vector of cartesian coordinates in m dimensions, associated with each node.

The idea underpinning this work is to weight the contributions of the consistently mapped nodes (i.e, those such that $f(u) = v$) with a gaussian probability density of the Procrustes alignment error. By introducing the alignment errors, different cliques with the same cardinality on a given graph are no longer susceptible to contribute the same amount to the energy functional.

Hence, the marginal probabilities of (6) become

$$P\left(f(u_r)|v_r\right) = \begin{cases} P_\phi & \text{if } f(u_r) = \phi \vee v_r = \mathrm{d} \\ (1 - P_e)(1 - P_\phi) P_m & \text{if } f(u_r) = v_r \\ P_e (1 - P_\phi) & \text{if } f(u_r) \neq v_r \end{cases} . \tag{9}$$

In our model P_m is the probability of match between two consistently mapped nodes $u_r^{(1)}$ and $v_r^{(2)}$, taking into account the whole set of consistently mapped nodes on that clique. Thus,

$$P_m\left(\overrightarrow{\rho'_{u_r}}, \overrightarrow{\rho_{v_r}}\right) = \exp\left[-\tfrac{1}{2}\left(\overrightarrow{\rho_{v_r}} - \overrightarrow{\rho'_{u_r}}\right)^T \Sigma^{-1} \left(\overrightarrow{\rho_{v_r}} - \overrightarrow{\rho'_{u_r}}\right)\right] , \tag{10}$$

which is the probability of matching nodes $u_r^{(1)}$ with $v_r^{(2)}$ according with the Procrustes distances of the coordinates, and the expected variance-covariance Σ of the data-graph node positions around the model-graph.

In the computation of $P_{match}\left(\overrightarrow{\rho'_{u_r}}, \overrightarrow{\rho_{v_r}}\right)$, the transformed coordinates $\overrightarrow{\rho'_{u_r}}$ resulting from the alignment process are used. As said before, the whole set of correctly mapped nodes on a given clique are taken into account in order to do the alignment. Therefore, a point-set X_1 is built from the cartesian coordinates of the data graph nodes that have been correctly assigned in the current mapping S_i of the matching conditional $P(\Gamma_j|S_i)$ (i.e. the data graph nodes u_r under the circumstance $f(u_r) = v_r$). Thus, $X_1 = \{\overrightarrow{\rho_{u_r}}|f(u_r) = v_r, r = 1, \ldots, |S_i|, f(u_r) \in \Gamma_j\}$ is a $k \times m$ matrix of cartesian coordinates of k points in m dimensions. Equivalently, a point set X_2 is built from the cartesian coordinates of the model graph nodes on which the data graph nodes have been correctly mapped to. Thus, $X_2 = \{\overrightarrow{\rho_{v_r}}|f(u_r) = v_r, r = 1, \ldots, |S_i|, v_r \in S_i\}$ is a $k \times m$ matrix as well.

Finally, the new coordinates of the data graph $\overrightarrow{\rho'_{u_r}}$ are taken from the transformed matrix $X_1^P = \beta X_1 \Gamma - 1_k \gamma^T$, after being aligned with X_2 using the method in Section 2.

Collecting terms and using the natural exponential form, our model for the clique matching probabilities is

$$P(\Gamma_\jmath) = \tfrac{1}{|\Theta_\jmath|} \sum_{S_i \in \Theta_\jmath} \exp\left[-k_{er}H - k_{eq}E - k_\phi N - \right. \\ \left. -\tfrac{1}{2}\mathrm{trace}\left(\left(X_2 - X_1^P\right)\Sigma^{-1}\left(X_2 - X_1^P\right)\right)\right] , \tag{11}$$

where $k_\phi = \log\left[\frac{1}{P_\phi}\right]$, $k_{er} = \log\left[\frac{1}{(1-P_\phi)P_e}\right]$ and $k_{eq} = \log\left[\frac{1}{(1-P_\phi)(1-P_e)}\right]$.

The joint prior is computed as in Equation (8) by averaging the clique matching probabilities over the nodes of the data graph.

A relaxation scheme similar than the one in Section 3, is implemented in order to iteratively update the matching configuration.

5. Results

We have evaluated our model under two different sources of noise: initial matching errors and positional disturbance on the feature points. The methods implemented in the experiments are: Gold and Rangarajan's graduated assignment [2], Luo and Hancock's structural matching using the EM algorithm [3] and, Wilson and Hancock's structural matching by discrete relaxation [4] (Section 3).

We have used 84 graphs extracted from handwritten capital letters. The mean and s.d of the number of nodes of the graphs are 5.8 and 2.1, respectively. The mean and s.d of the number of arcs are 4.9 and 2.2, respectively. Samples present moderate levels of structural corruption consisting of a few added extra nodes and extra arcs (notice that we are not evaluating our model under severe structural corruption). The data graphs of each class are matched against a prototypical graph of that class.

In the first experiment (Figure 1) we have tested the ability of recovering from initial matching corruption. The degree of corruption ranges from zero (initial matching 100% correct) to 1 (initial matching completely corrupted). Since the graduated assignment method does not require any initialization, we have plotted the mean correct matching rate.

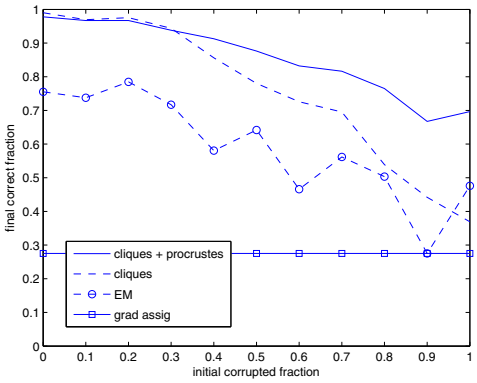

Figure 1. Final correct fraction versus initial corrupted fraction

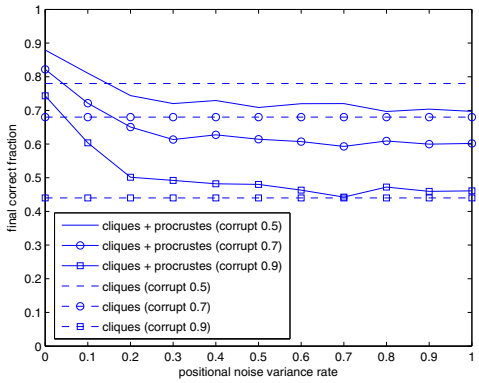

Figure 2. Final correct fraction rate versus positional disturbance

Results show a significant improvement of our model in the ability to recover from corrupted matching configurations, specifically under severe corruption conditions. The EM-based method and the graduated assignment present a poor performance. Although these methods usually obtain good results when aplied to more sophisticated graphs, their criteria has demonstrated to be too weak when applied to the type of graphs adressed here.

The second experiment (Figure 2) evaluates the tolerance of our method to severe noise in the coordinates of the nodes. We have applied gaussian white noise to the (x,y) coordinates of the point positions associated with the nodes. The variance of the noise ranges from zero to the total variance of the data. Hence, in the extreme case the variance due to noise is the same amount than the variance due to data. We have run three executions corresponding to three different fractions of initial corruption in the matching configuration. These are 0.5, 0.7 and 0.9 respectively. Since our method is the only one sensitive to this kind of noise, we have plotted comparative results of the cliques method [4] under the same levels of corruption.

Results show that our method improves cliques method while noise fraction is under 17% approximately, when corrupted fractions are 0.5 and 0.7. When corruption fraction is 0.9, our method is better for any noise value. It is interesting to note that positional noise degrades the effectiveness of our method just until a given threshold (approximately 25% of total variance). After that threshold, it stabilizes.

6. Conclusions

We have presented a method for improving the matching of graphs that are small and present low structural constraints, such as those obtained from shapes (e.g. letters). We enhance the matching criterion by the use of Procrustes methods on the coordinates of the nodes. Although we have evaluated our method with shapes it is applicable to any kind of object on which meaningful positional information can be extracted. The model presented integrates perfectly into the cliques framework and represents a negligible extra computational cost (for the graphs used in our experiments). Results show a significant improvement in recuperation ability of our model, specifically under severe corruption conditions where the recuperation rate is near 200% with respect to the cliques model. Positional disturbance does not degrade too much the performance of our model, getting results comparable to those obtained with the original cliques model.

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