POINT PATTERN MATCHING USING A GENETIC ALGORITHM AND VORONOI TESSELLATION

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ABSTRACT

Point pattern matching problem consists in identifying similar point patterns in two point sets which differ one each other in scale, orientation angle or position. A new objective function for the problem of point pattern matching is proposed here. The function scores not only the exact matching situations between patterns, but also the inexact ones. It has only one global maximum in the desired solution, and hence implosion cases which occur for very low scale factors are avoided. An efficient algorithm for the evaluation of the objective function is proposed. The algorithm requires a preprocessing stage to label the Voronoi regions of one of the point sets. Then, a genetic algorithm is used to maximize the proposed objective function.

1 INTRODUCTION

Point pattern matching problem consists in identifying corresponding points (control points) between two given sets. In other words, the problem is to find common patterns between two point sets which may differ one to another in scale, orientation angle and position.

Let $\mathcal{P}$ and $\mathcal{Q}$ be two given point sets. The problem of point pattern matching can be reformulated as determining the geometrical transformation (1) which applied to the set $\mathcal{P}$ superpose a maximum number of its points onto corresponding points in set $\mathcal{Q}$

$$\begin{pmatrix} p_x^T \\ p_y^T \end{pmatrix} = s \begin{pmatrix} cos\theta & -sin\theta \\ sin\theta & cos\theta \end{pmatrix} \begin{pmatrix} p_x \\ p_y \end{pmatrix} + \begin{pmatrix} t_x \\ t_y \end{pmatrix}. \quad (1)$$

In (1), (p_x, p_y) and (p_x^T, p_y^T) denote the coordinates of a point $p \in \mathcal{P}$ before and after applying the geometrical transformation. The four parameters that uniquely define the geometrical transformation (1) are: the scale factor s, the orientation angle θ and the translation values t_x, t_y.

Several algorithms have been already proposed for solving the point pattern matching problem. However, most practical methods provide only approximate solutions. In the context of fingerprint image registration a generalized Hough transform has been used in [1] to estimate the scale factor, orientation angle and translation parameters between two fingerprint images. The fingerprint registration reduces to point pattern matching as long as each fingerprint is represented as a set of feature points called minutiae. The method has a complexity of $\mathcal{O}(N^2)$ and requires a large amount of memory space to store the accumulator which is a four dimensional array. In [2], the case when the scale factor is unitary is considered. The matching problem is thereby reformulated as a 0-1 integer programming problem and an artificial neural network is proposed to solve it. A genetic algorithm for point pattern matching with application in two-dimensional shapes extraction has been proposed in [3]. There the scale range is limited to a very small interval around 1.

This paper is organized as follows. An objective function which allows a very large scale range between point patterns is derived in Section 2. A genetic algorithm is then proposed in Section 3 for the maximization of the objective function. Section 4 shows several simulation results for different point pattern matching situations.

2 THE OBJECTIVE FUNCTION

The objective function associates a real value (named *objective value*) to each geometrical transformation $T = (s, \theta, t_x, t_y)$. A valid objective function has to be chosen such a way to have a global extremum for the geometrical transformation T^* which represents the solution of the problem.

Denote by $\mathcal{P}^T$ the set of points obtained from $\mathcal{P}$ by applying the geometrical transformation T. The more points overlap in $\mathcal{P}^T$ and $\mathcal{Q}$, the better the geometrical transformation T is. Thus, a very simple objective function is obtained by associating to each transformation T, an objective value equal to the number of points from $\mathcal{P}^T$ which match the corresponding points of $\mathcal{Q}$. The solution of the problem is the transformation T^* which maximizes this objective function. However, the maximization of a such objective function is very difficult due

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to the very steep peaks that occur in the searching space. There is no information about how close the points in $\mathcal{P}^T$ are to the corresponding points in $\mathcal{Q}$. Therefore, the inexact matching situations are completely ignored and small differences between patterns are treated the same as higher ones. This objective function is rather discrete making any gradient based technique ineffective. Even genetic algorithms provide poor performance on such objective functions.

In order to obtain more continuous objective functions, the inexact matching situations has to be taken into account. A defocusing technique, which allows the points of $\mathcal{P}^T$ to contribute to the objective value even they are only in a neighborhood of the corresponding points of $\mathcal{Q}$ is described in [3].

In our work, the Euclidean distances between the points of $\mathcal{P}^T$ and their corresponding points of $\mathcal{Q}$, are used to compute the objective value. Let $r\left(p_i^T\right)$ denote the minimum Euclidean distance between the point $p_i^T \in \mathcal{P}^T$ and a point $q \in \mathcal{Q}$. That is:

$$r\left(p_i^T\right) = min\{d\left(p_i^T, q\right) | q \in \mathcal{Q}\}, \tag{2}$$

where $d\left(p_i^T, q\right)$ is the Euclidean distance between the points $p_i^T \in \mathcal{P}^T$ and $q \in \mathcal{Q}$.

The contribution of each point $p_i^T \in \mathcal{P}^T$ to the objective value is given by the function:

$$\lambda_i\left(T\right) = exp\left\{-\frac{r\left(p_i^T\right)}{\alpha}\right\}, \tag{3}$$

where α is a tuning parameter.

The objective function is then obtain by summing the contributions $\lambda_i\left(T\right)$ of all points $p_i^T \in \mathcal{P}^T$:

$$f\left(T\right) = \frac{\sum_{i=1}^{P} \lambda_i\left(T\right)}{P}, \tag{4}$$

where $P = |\mathcal{P}|$ is the cardinality of set $\mathcal{P}$.

The objective function $f\left(T\right)$ takes real values between 0 and 1. If all points $p_i^T \in \mathcal{P}^T$ are overlapped exactly with P points of $\mathcal{Q}$ then the objective function is 1.

If the transformation T^* is the desired solution of the point pattern matching problem, then it is a maximum of the objective function.

2.1 Implosion Cases

The function $f\left(T\right)$ could be used for solving the point pattern matching problem if the scale factor is fixed or restricted to a very small range. This function has more then one maxima, some of them even greater then the desired one. There are many transformations $\widetilde{T}$ which could be chosen such that $f(\widetilde{T}) > f(T^*)$. For a very low scale factor there is some translation values for which all the points of $\mathcal{P}^T$ are in a neighborhood of a single point $q_j \in \mathcal{Q}$. The contribution (3) of each point is quite large and hence the objective value is large. Here, such situations are called *implosion cases*.

Usually implosion cases are avoided either by imposing a unity scale factor [2], or by restricting the scale range [3].

In order to avoid implosion cases, we developed an objective function $F\left(T\right)$ which has only one global maximum in the desired solution T^*. The new function takes into consideration only the distance between each point $q_j \in \mathcal{Q}$ and its closest point $p_i^T \in \mathcal{P}^T$ among all $\mathcal{P}^T$ points which occur in the neighborhood of q_j.

Let R_j denote the set of all points $p_i^T \in \mathcal{P}^T$ which occur in the neighborhood of the point $q_j \in \mathcal{Q}$

$$R_j = \{p_i^T | r\left(p_i^T\right) = d\left(p_i^T, q_j\right)\}. \tag{5}$$

The minimum distance between a point q_j and its nearest neighborhood is defined as:

$$e\left(q_j\right) = \begin{cases} min\{r\left(p_i^T\right) | p_i^T \in R_j\}, & |R_j| > 0 \\ \infty, & |R_j| = 0 \end{cases}, \tag{6}$$

where $|R_j|$ denote the cardinality of set R_j. If there is no point p_i^T in the neighborhood of q_j ($|R_j| = 0$) the minimum distance $e\left(q_j\right)$ becomes infinity.

Using this notation, a contribution function similar with (3) is defined for each point $q_j \in \mathcal{Q}$:

$$\Lambda_j\left(T\right) = exp\left\{-\frac{e\left(q_j\right)}{\alpha}\right\}, \tag{7}$$

and the new objective function is:

$$F\left(T\right) = \frac{\sum_{j=1}^{Q} \Lambda_j\left(T\right)}{Q}, \tag{8}$$

where $Q = |\mathcal{Q}|$ denotes the cardinality of set $\mathcal{Q}$.

The function F has a unique global maximum in the desired solution T^*. Implosion cases are totally eliminated because only one point of $\mathcal{P}^T$ from the neighborhood R_j of each point $q_j \in \mathcal{Q}$ is taking into consideration for objective value computation. If, for a very low scale factor, almost all points of $\mathcal{P}^T$ are in the neighborhood of a single point of $\mathcal{Q}$, then the objective value approaches to $1/Q$. It does not have any more maxima for the transformations $\widetilde{T}$ with low scale factors.

2.2 The Evaluation of the Objective Function

The computation of (8) requires to identify the sets R_j and also to compute some Euclidean distances. These operations are time consuming and are avoided here by implementing a preprocessing stage. In this stage two integer matrixes R and E are constructed. Each matrix has the same dimensions as the image from which the set $\mathcal{Q}$ has been extracted.

The matrix R resembles the Voronoi cells of the $\mathcal{Q}$ points. Each entry in the matrix R has an integer value between 1 and Q. This value represents the label j associated with the central point $q_j \in \mathcal{Q}$ of the current Voronoi cell. The matrix E resembles an integer approximation of the Euclidean distance between each $\mathcal{Q}$ point and all the points that are in its Voronoi cell.

In other words, $R(x,y)$ is equal with the label j of the cell in which the point (x,y) occurs and $E(x,y)$ is an integer approximation of the Euclidean distance between the point (x,y) and the central point q_j of the cell.

The low computational complexity (of order $\mathcal{O}(1/N)$) method for Voronoi tessellation and the integer approximation of Euclidean distance in $\mathcal{Z}^2$, both proposed in [4] are used here to compute the matrixes E and R in the preprocessing stage. An example of these matrixes for a set of 30 points is shown in Fig. 1.

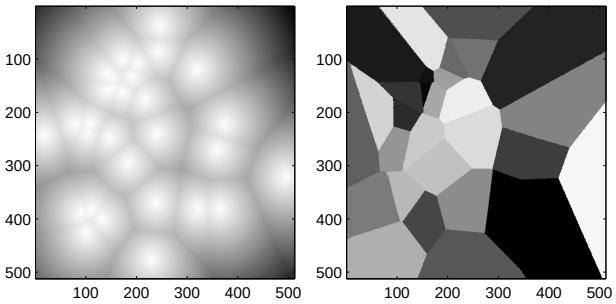

Figure 1: An example of E (left) and R (right) matrixes for a set of 30 points. The integer values are represented by gray levels from white (minimum value) to black (maximum value).

The algorithm for the evaluation of the objective function is shown in Fig.2. By using the matrixes E and R, already created in the preprocessing stage, the algorithm achieves low computational complexity (of order $\mathcal{O}(N)$).

PROCEDURE ObjectiveFunction
INPUT: $T=(s,\theta,t_x,t_y)$ - geometrical transformation
OUTPUT: F - objective value $F(T)$
$e[j] \leftarrow$MAXINT for all $j=1,\ldots,Q$
$F \leftarrow 0$
$\mathcal{P}^T \leftarrow T(\mathcal{P})$ - apply the transformation T onto set $\mathcal{P}$
FOR each point $p^T=(p_x^T,p_y^T) \in \mathcal{P}^T$ **DO**
  IF $e\left[R(p_x^T,p_y^T)\right] > E(p_x^T,p_y^T)$ **THEN**
    $e\left[R(p_x^T,p_y^T)\right] \leftarrow E(p_x^T,p_y^T)$
  END IF
END FOR
FOR $j=1,\ldots,Q$ **DO**
  $F \leftarrow F+exp(-e[j]/\alpha)$
END FOR
$F \leftarrow F/Q$
END PROCEDURE

Figure 2: The algorithm for objective function evaluation.

3 THE GENETIC ALGORITHM

3.1 Encoding Scheme

Each chromosome represents a unique geometrical transformation in an encoding form. The chromosome encoding scheme used in our work is similar with that described in [3]. Each chromosome has a bit string representation (9) which resembles in a quantized fashion the four parameters of the geometrical transformation.

$$C=\left(\underbrace{\overbrace{110\cdots01}^{s}}_{N_s bits}\underbrace{\overbrace{100\cdots11}^{\theta}}_{N_\theta bits}\underbrace{\overbrace{011\cdots10}^{t_x}}_{N_{t_x} bits}\underbrace{\overbrace{101\cdots00}^{t_y}}_{N_{t_y} bits}\right). \quad (9)$$

The range of each parameter is uniformly quantized and the Gray code is used in (9) for binary representation. The use of Gray codes avoid those situations when close values differ in almost every position of their binary representation.

The fitness of a chromosome is equal with the objective value $F(T)$ of the geometrical transformation T encoded by it.

3.2 Selection and Replacement Strategies

The algorithm maintains the size of the population constant during all iterations. At each iteration (generation) a number of parent chromosomes are selected from the population. The higher the fitness value of a chromosome the higher the probability to be selected. The Roulette Wheel Selection procedure [5] is used here.

The subpopulation (offspring), generated by performing genetic operations (crossover and mutation) onto the parents, replaces the entire old population. This replacement strategy called Generational Replacement [6] is combined here with an *elitist* strategy were the best chromosome always survives intact from one generation to the other.

4 EXPERIMENTAL RESULTS

Several point pattern matching experiments using the proposed algorithm has been performed. About 200 iterations are sufficient in almost all cases to obtain a relatively close approximation of the real transformation. The encoding scheme information of the geometrical transformation parameters, used in all experiments, are shown in Tab.1. Using this encoding scheme each chromosome has a length of 42 bits.

Parameter	Range	Number of bits
s	$0\ldots.10.23$	10
θ	$0\ldots.2\pi$	10
t_x and t_y	$-1024\ldots.1023$	11

Table 1: The ranges and the bit numbers used to encode the geometrical transformation parameters.

$No.$	P	Q	k	Iterations	s	$\hat{s}$	θ	$\hat{\theta}$	t_x	$\hat{t}_x$	t_y	$\hat{t}_y$
1	30	30	30	190	2.00	2.00	0.25π	0.25π	297	297	-484	-484
2	110	100	50	154	3.50	3.55	0.33π	0.34π	578	592	-975	-987
3	110	100	50	196	0.50	0.51	0.25π	0.25π	256	253	90	84
4	110	100	40	185	0.50	0.50	0.25π	0.31π	262	293	78	83
5	110	100	30	199	0.25	0.27	0.50π	0.51π	319	328	192	191
6	110	100	20	190	0.75	0.77	0.66π	0.66π	510	511	183	171

Table 2: Some experimental results for different geometrical transformations and different numbers k of common points.

The experimental point sets were constructed as in [2]. The set $\mathcal{P}$ is constructed by randomly selecting P points in a 512x512 image. An intermediate set of points is then constructed by randomly deleting $P-k$ points from $\mathcal{P}$ and randomly inserting other $Q-k$ points. Finally the set $\mathcal{Q}$ is obtained by applying a geometrical transformation T onto the intermediate set. In this way, a common pattern of k points occurs in both final sets $\mathcal{P}$ and $\mathcal{Q}$.

The results of different simulations, for different values of k, are shown in Tab.2. The real geometrical transformation is denoted by T and the estimated one is denoted by $\hat{T}$. For all experiments, the population size is 50, the crossover rate is 0.95, the mutation rate is 0.3 and the parameter α is 100. In all cases, the algorithm was stopped after 200 iterations. The best chromosome (geometrical transformation) and the iteration where it was found are specified in the table.

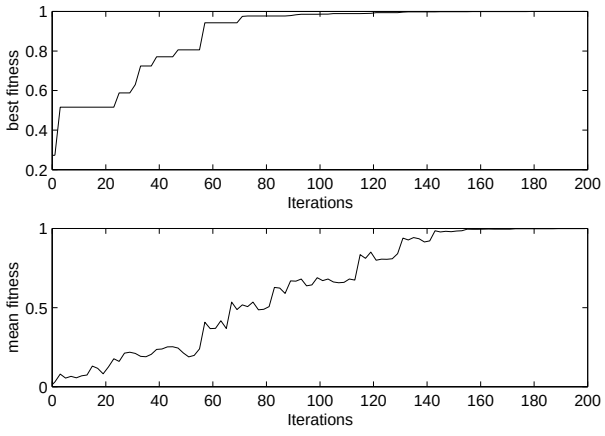

Figure 3: The best and mean fitness variations for the first experiment shown in Tab.2.

5 CONCLUSIONS

A new objective function for the problem of point pattern matching has been proposed. The function has a unique global maximum in the desired solution and hence implosion cases which occur for very low scale factors are avoided. Two integer matrixes E and R (Fig.1) are constructed in a preprocessing stage. Using these matrixes a fast algorithm for objective value computation (Fig.2) can be used.

Some simulation examples for different point pattern matching situations have been as well presented. A genetic algorithm has been used here to maximize the proposed objective function.

ACKNOWLEDGMENT

The authors would like to thank Prof. Pauli Kuosmanen for many valuable hints and fruitful discussions on the topic of this paper.

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