Relational Matching by Discrete Relaxation

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Abstract

This paper describes a symbolic approach to relational matching. The novelty of the method lies in its Bayesian modelling of relational consistency through the use of an explicit constraint corruption process. Unlike many alternatives in the literature, the method is not limited to the use of binary constraints; it can accommodate N-ary relations of varying order. In consequence of this assumed model the consistency of match is gauged by a compound exponential function of a higher-order Hamming distance between symbolic relations; there is a single exponential associated with each potential relational mapping. These exponential functions naturally soften the symbolic constraints represented by the relational mappings, The method may be operated without the need for an explicit null matching process. Unmatchable entities are identified by a constraint filtering operation once the relaxation scheme has converged. The utility of the method is illustrated on the matching of hedge structures in SAR images against their cartographic representation in a digital map.

1 Introduction

Relational matching is a task that pervades computer vision at both high and intermediate levels [1, 7, 9, 10, 11]. For instance, at intermediate levels it is basic to stereopsis [1, 7] where image pairs must be registered prior to the computation of depth estimates and also to sensor fusion where images from a number of different sources must be integrated together [11]. It is also a critical ingredient at higher levels when relational models are to be matched against segmental image entities [9]. The matching process is frequently abstracted in terms of relational graphs [1, 7, 9]; the critical ingredient being an efficient and robust way of searching a large space of matching possibilities when the data under study is corrupt or the model uncertain [1]. It is invariably poor initial image segmentation that limits the effectiveness of classical graph matching methods [10]. The main difficulties stem from the loss of image entities due to undersegmentation and the presence of spurious entities due to noise or oversegmentation [11]. Since these effects corrupt the topologies of the relational graphs, the matching process must therefore be accomplished by inexact means.

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Because of their intrinsically parallel nature and their capacity to locate consistent interpretations from incomplete or uncertain input, relaxation processes provide an attractive means of inexact matching [2, 5, 9]. The relaxation algorithms available for relational matching may be divided into two distinct categories [2, 3, 5]. The discrete method locates optimal globally consistent labellings via iterative symbol swapping operations [5] and is to be contrasted with the probabilistic relaxation method in which optimal matches are located via the updating of continuous matching probabilities [9]. Despite drawing on very different computational processes, the two relaxation schemes share the common goal of locating matches that optimise a global consistency measure [8]. It is the difficulties associated with defining a sufficiently fine global measure of relational consistency that have provided the main obstacle to the realisation of effective discrete relaxation processes for practical matching applications. Most of the alternatives reported in the literature confine their attention to counting consistently matched relations [10]. Under conditions in which there are few initially correct matches and very few, if any, consistent relations, this can lead to a deadlocked update process [5]. It is for this reason that matching has proved to be more computationally tractable when either abstracted in terms of attribute relations [1] or approached in a probabilistic relaxation framework [9]. Our aim in this paper is to demonstrate not only that the rejection of discrete relaxation as a means of matching is premature, but that it offers certain advantages in terms of both interpretation and ease of control.

In order to meet these aims, we present the development of a Bayesian criterion that objectively quantifies the global consistency of match. The critical representational ingredient in this devlopment is a set of mappings between relational subunits of the graphs under match [10]. It is the size of these subunits that determines the effectiveness of the matching process to draw upon relational constraints. Rather than limiting our attention to binary or low-order relations we use subunits that consist of entire object-neighbourhoods. Detailed development of the Bayesian criterion requires the specification of a set of probability distributions which model the processes at play in corrupting the consistent patterns of match represented by the relational mappings. Under the assumption of a uniform and memoryless distribution of matching errors, consistency is gauged by compounding a series of exponential functions of the Hamming distances between the relations in the matched-graph and those in the model graph.

It is this mathematical structure of our matching criterion that is both unique and endows it with greater robustness to error than the alternatives reported in the literature. Each potential relational mapping is represented by an individual exponential function of Hamming distance. Partially matched relational units have an increasing contribution to the consistency measure according to their decreasing Hamming distance. Our Bayesian approach therefore provides a natural way of softening relational constraints, which both overcomes the problems of deadlock and renders the matching process tractable by conventional optimisation methods. In the work reported here the updating to locate the optimal matching is achieved using a deterministic MAP estimation process [5]. Although our matching criterion has a single parameter, namely the uniform probability of matching errors, this is used in the spirit of a control variable rather than a static quantity of fixed physical meaning; it is gradually reduced during the relaxation scheme to impose consistency through a graded hardening of constraints, much like the temperature of an annealing schedule [2]. Because our discrete relaxation method naturally accommodates partially matched relations, there is no imperative requirement for an explicit null-matching model.

The basic philosophy in constructing the Bayesian matching criterion is to pool the two sources of error together. Nodes are discarded to the null category on the basis of an arc consistency test applied as a postprocessing step.

The outline of this paper is as follows. In Section 2 we describe the formal ingredients of our graph matching process, including details of how the potential relational mappings are constructed. Section 3 illustrates how this set of mappings may be exploited in constructing a Bayesian model of matching errors and gives details of the MAP estimation scheme used to locate the optimal matching. In Section 4 we describe the constraint filtering technique used to assign matches to the null category. Experiments relating to a matching application involving synthetic aperture radar data are described in Section 5. Finally, Section 6 offers some conclusions.

2 Relational Graphs

We abstract the matching process in terms of relational graphs [1, 9, 10]. According to this representation the nodes represent entities to be matched. The arcs represent binary relations operating between the nodes. In the experimental study reported in Section 4 we will be interested in matching hedge structures segmented from SAR images against their digital map representation. Here the nodes represent linear segments. Arcs denote the existence of a geometrically meaningful relation between two such line-segments; since hedge structures in the data are largely associated with quadrilateral field boundaries, the relations that most interest are those in which pairs of linear segments are orthogonal or nearly orthogonal to one another. We have adopted this representation purely on the basis of convenience and it does not impose a limitation on the utility of our matching method. The framework presented in this paper is applicable to a variety of relational abstractions; for instance we have also successfully matched Delaunay graphs representing a Voronoi tesselation generated by the line segments. We use the notation $G = (V, E)$ to denote the graphs under match, where V is the set of nodes and E is the set of arcs. Our aim in matching is to associate nodes in two such graphs $G_1 = (V_1, E_1)$ and $G_2 = (V_2, E_2)$ using constraints provided by suitable relational subunits. Formally, the matching is represented by a function from the nodes in graph G_1 to those in graph G_2. With these ingredients, the match is represented by the function $f : V_1 \rightarrow V_2$. The function f consists of a set of Cartesian pairs drawn from the space of possible matches between the two graphs, i.e. $f \subseteq V_1 \times V_2$; it provides a convenient device for indexing the nodes in the graph G_1 against their matched counterparts in the graph G_2. We use the notation $(u, v) \in f$ to denote the match of node $u \in V_1$ against node $v \in V_2$.

In performing the matches of the nodes in graph G_1 we will be interested in exploiting structural constraints provided by the graph G_2. There are two issues at play in selecting structures appropriate to this task. If the structural units are too small then the matching process is impoverished in terms of the contextual information upon which it can draw in locating a consistent match. This limits the effectiveness of the relaxation scheme, rendering it susceptible to noise or error. If, on the other hand, the structural units are too large, then the matching process becomes excessively burdensome in terms of its computational requirements; the limitation stems from the need to explore the space of relational mappings between representational subunits. We will strike a compromise by using subgraphs that consist of neighbourhoods of nodes interconnected by arcs; for

convenience we refer to these structural subunits or N-ary relations as supercliques.

The superclique of the node indexed j in the graph with arc-set E is denoted by the set of nodes $C_j = j \cup \{i|(i,j) \in E\}$. We use the notation $R_j = (u_1, u_2, ..., u_{|C_j|})$ to denote the N-ary symbolic relation represented by the nodes of the superclique $C_j \subset V_1$ in the data graph G_1. The matched realisation of this superclique is therefore denoted by the relation $\Gamma_j = (f(u_1), f(u_2), ..., f(u_{|C_j|}))$. Our aim in performing discrete relaxation operations is to modify the match to optimise a measure of global consistency with the constraints provided by the model graph G_2. The constraints available to us are provided by the N-ary symbol relations on the supercliques of the model graph G_2. The critical ingredient in developing our relaxation scheme is therefore the set of feasible mappings between each superclique of graph G_1 and those of graph G_2. The set of feasible mappings, or dictionary, for the superclique C_j is denoted by $\Theta(C_j) = \{S_i|S_i \in V_2^{|C_j|}\}$. Each element S_i of $\Theta(C_j)$, is therefore a relation formed on the nodes of the model graph; we denote such consistent relations by $S_i = (v_1, v_2, ..., v_{|C_j|})$. The dictionary of feasible mappings for the superclique C_j therefore consists of all the consistent relations of cardinality $|C_j|$ that may be elicited from the graph G_2. In practice these relations are formed by performing cyclic permutation of the non-centre nodes for each superclique of the requisite size; this process effectively preserves the adjacency structure of the model graph while leaving dictionary invariant to potential scene rotations.

3 Discrete Relaxation

Our strategy in developing the graph-matching criterion is to sum the matching probabilities over the supercliques in graph G_1 and to use this in the spirit of the average consistency measure of Hummel and Zucker [8]. In order to proceed, we require a means of computing the probability of each superclique matching as specified by the function f. In other words, we are interested in computing the probability of the matched relation Γ_j assigned to the superclique C_j of graph G_1. As we noted in the previous section, the consistent labellings available for gauging the quality of match are represented by the set of relational mappings from C_j onto G_2, i.e. $\Theta(C_j)$. As demanded by the Bayes rule, we compute the probability of the required superclique matching by expanding over the basis configurations belonging to $\Theta(C_j)$

$$P(\Gamma_j) = \sum_{S_i \in \Theta(C_j)} P(\Gamma_j|S_i).P(S_i) \tag{1}$$

The development of a useful graph-mapping measure from this expression requires models of the processes at play in matching and of their roles in producing errors. These models are represented in terms of the conditional matching probabilities $P(\Gamma_j|S_i)$ and of the joint priors $P(S_i)$ for the consistent relations in the dictionary. In developing the required models we will limit our assumptions to the case of matching errors which are memoryless and occur with uniform probability distribution.

To commence our modelling of the conditional probabilities, we assume that the various types of matching error for nodes belonging to the same superclique are memoryless. In direct consequence of this assumption, we may factorise the required probability distribution over the constituents of the relational mapping under consideration. As a result the conditional probabilities may be expressed in terms of a product over label confusion

probabilities

$$P(\Gamma_j|S_i) = \prod_{k=1}^{|S_i|} P(f(u_k)|v_k) \tag{2}$$

Our next step is to propose a model of the processes which give rise to erroneous matches. We assume that matching errors occur with a uniform and memoryless probability distribution. If the probability of matching error is P_e, then the confusion probabilities appearing under the product of equation 2 are therefore assigned according to the following distribution rule

$$P(f(u_k)|v_k) = \begin{cases} 1 - P_e & \text{if } f(u_k) = v_k \\ P_e & \text{if } f(u_k) \neq v_k \end{cases} \tag{3}$$

As a natural consequence of this distribution rule the joint conditional probability is a function of a single physically meaningful variable. This variable is the Hamming distance $H(\Gamma_j, S_i)$ between the assigned matching and the feasible relational mapping S_i. This quantity counts the number of conflicts between the current matching assignment Γ_j residing on the superclique C_j and those assignments demanded be the relational mapping S_i. With these ingredients, the resulting expression for the joint conditional probability acquires an exponential character

$$P(\Gamma_j|S_i) = K_{C_j} \exp[-k_e H(\Gamma_j, S_i)] \tag{4}$$

where $K_{C_j} = (1 - P_e)^{|C_j|}$. The exponential constant appearing in the above expression is related to the matching-error probability, i.e. $k_e = \ln \frac{(1-P_e)}{P_e}$. The expression may be regarded as providing a natural way of softening the hard relational constraints operating in the model graph. Having developed an exponential expression for the joint conditional matching probabilities, it only remains to specify the distribution of the prior probabilities for consistent relations in the dictionary. Here we adopt a uniform distribution of the available unit probability mass over the set of possibilities $\Theta(C_j)$, i.e. $P(S_i \in \Theta(C_j)) = \frac{1}{|\Theta(C_j)|}$. The final expression for the superclique matching probability is therefore

$$P(\Gamma_j) = \frac{K_{C_j}}{|\Theta(C_j)|} \sum_{S_i \in \Theta(C_j)} \exp[-k_e H(\Gamma_j, S_i)] \tag{5}$$

Before proceeding, it is important to comment on the structure of the above expression. The most striking and critical feature is that the consistency of match is gauged by a series of exponentials that are compounded over the dictionary of consistently mapped relations. It is this feature that distinguishes it from alternatives reported in the literature [1, 9]. Each relational mapping contributes a single exponential to the probability of match. It is this feature that allows our method to operate in a robust manner when the space of relational mappings is large. Recent theoretical studies suggest that compound exponentials of the type defined above offer tangible benefits over linear or quadratic measures in terms of the number of relational mappings accommodated and the label-error probability of the resulting match [6]. Moreover, the importance of the different relational constraints is naturally graded by Hamming distance; relational mappings of large Hamming distance contribute insignificantly while those of small Hamming distance dominate. By gradually reducing P_e, the exponentials appearing in equation (5) approach their delta-function limits. This

effectively corresponds to subjecting the softened relational constraints operating in the matching problem to a graded hardening. In the limit of vanishingly small error probability the matching probabilities become binary in nature; their role is to effectively count the number of consistently matched relational units. Under these conditions our matching criterion becomes similar in function to the relational distance measure of Shapiro and Haralick [10]. It is also worth noting that had we adopted a confusion probability model based on multivariate Gaussian attribute relations rather than the purely symbolic specification of equation (3), then our criterion would be equivalent to that of Boyer and Kak [1] under conditions of small attribute deviations between the two graphs.

With the superclique mapping probabilities to hand, we can define a global criterion of match between the two graphs. In doing this we would like to remain close in spirit to the average consistency measure widely employed in relaxation schemes [5, 9]. For this reason, we base our criterion on the average superclique matching probability. The functional associated with the matching $f : V_1 \rightarrow V_2$ is

$$F(f) = \frac{1}{|V_1|} \sum_{C_j \subset V_1} P(\Gamma_j) \tag{6}$$

With the average consistency criterion to hand we can iteratively update the mapping function $f : V_1 \rightarrow V_2$ on a node-by-node basis to locate an an optimal match. This updating process is effected by replacing one of the Cartesian pairs belonging to f by a node-to-node match that results in the greatest improvement in the value of the global functional. The location of an optimal global match can be accomplished in a number of ways [2, 3, 5]; these alternatives include simulated annealing [2] and deterministic annealing [3]. Rather then adopting one of these more elaborate optimisation schemes, we will adopt a very simple deterministic MAP estimation approach to locate the best match. This optimisation strategy has the dual advantages of accommodating the persistence of observational information and being realisable by simple gradient ascent. The aim of this decision scheme is to locate the matching configuration that has optimal *a posteriori* probability (MAP) with respect to the available observations. In [5] we showed how a criterion similar to that developed here but tailored to low-level labelling problems could be used to model the joint prior in such a scheme. According to the MAP philosophy, $F(f)$ is used in the spirit of the joint prior. Observational evidence for matching affinity between data node $u \in V_1$ and model node $v \in V_2$ is captured by the single probability of the relevant measurements, i.e. $P(f(u_k)|\underline{x}_k)$. The initial configuration of the relaxation scheme is seeded on the basis of the maximum value of $P(f(u_k)|\underline{x}_k)$. Updated matches are selected to optimise the following quantity which is proportional to the *a posteriori* probability of the global matching configuration

$$P(f(u_k)|\underline{x}_k)F(f) \tag{7}$$

In order to ensure consistency of the final match we must exert control over the parameter of the global criterion. This parameter is the probability of matching errors. Since we expect the relaxation scheme to improve the accuracy of the labelling, one control strategy is to reduce the matching-error probability to a small terminal value according to some deterministic iteration dependant schedule. The error probability P_e may therefore be regarded as a control variable, much in the spirit of the temperature in an annealing schedule.

4 Constraint Filtering

With these ingredients, the deterministic relaxation scheme iteratively improves the labelling and reduces the value of label error probability to locate the match of maximum achievable consistency. However the final match may still retain a substantial number of residual inconsistencies. As we mentioned before there are two sources of error hindering the graph matching process. The matching errors modelled in Section 3 are eliminated by optimisation, but residual inconsistencies persist in the form of the erroneous matching of segments for which no feasible match exists. These are clearly undesirable in the final match.

These mis-matched entities are the result of a matching model which does not incorporate a null match category, nor any of the modelling components associated with the inclusion of unmatchable elements. This approach does however have certain tangible benefits; we need not include the possibility of null-matched elements in the superclique probabilities, nor do we require prior knowledge of the number of unmatchable elements expected to be present in the data. The softening of relational constraints implied in equation 5 enables the matching process to accommodate these erroneously matched segments while still locating the most consistent match. We therefore require a postprocessing step which discards unmatchable elements to a null category. Formally, these unmatchable nodes in graph G_1 are accommodated by augmenting the node-set for model graph G_2 by the null-match label ϕ.

Our philosophy throughout this paper has been to use a measure of consistency to gauge the correctness of a match. We therefore propose a post-processing step to filter out unmatchable elements which is based on a consistency measure. Clearly if the graphs under match are uncorrupted, we would anticipate a final match which is completely consistent over the whole graph. When data corruption and model uncertainty are present, this potential area of consistency is broken up into smaller patches, the size of which is limited by the process of constraint corruption. Unmatchable elements, on the other hand, have no consistent interpretation and are therefore are unlikely to form patches of consistency.

We commence by forming a new graph $G'_1 = (V'_1, E'_1)$ which contains the consistently labelled portions of G_1. To form G'_1 we first eliminate arcs whose mapping does not appear in G_2

$$E_1{}' = \{(u_1, u_2) | (f(u_1), f(u_2)) \in E_2\} \tag{8}$$

We then remove disjoint nodes which are no longer connected by an arc; these nodes have no support and are therefore considered to be unmatchable

$$V_1{}' = \{u | (u, v) \in E_1{}', v \in V_1\} \tag{9}$$

with the disjoint node being consigned to the null category, i.e.

$$u \notin V_1{}' \Rightarrow f(u) = \phi \tag{10}$$

The graph $G_1{}'$ now consists of a number of internally connected yet potentially disjoint patches, in which all the nodes satisfy the arc consistency constraint. Suppose that Λ_i denotes the index-set of one of these disjoint graph partitions. If there are p such partitions, then $V'_1 = \bigcup_{i=1}^{p} \Lambda_i$ and there are $\subseteq\subseteq$ rconnecting edges, i.e if $i \neq j$

then $(\Lambda_i \times \Lambda_j) \cap E_1' = \emptyset$. If correct matching were the only process which generated consistency, then G_1' would contain only the correctly labelled portion of the graph. However, a small amount of spurious consistency is generated from local isomorphism between unmatchable segments and regions of G_2. Since the probability of accidentally forming a partition of size $|\Lambda_i|$ in the initial labelling is equal to $V_2^{-|\Lambda_i|}$ we gauge the overall consistency of each partition by the number of nodes contained within it. In practical matching applications the regions of spurious consistency are small, typically much smaller than correctly labelled regions, and in this case it is sufficient to reject those regions whose size falls below some threshold value T

$$|\Lambda_i| < T \Rightarrow \forall u \in \Lambda_i [f(u) = \phi] \tag{11}$$

For example if we set the threshold level at $T = 2$, then we effectively assign all nodes interconnected by a disjoint edge to the null category. For the experimental study reported in section 5, it is this physically intuitive value that has been used. However, in other applications it may be desirable to set the threshold so as to ensure that the probability of accidental local isomorphism does not become unacceptably large.

5 Experiments

For the experimental aspects of this study we are interested in matching hedge structures detected in SAR images of rural scenes against their representation in the form of digital map data. An example image is shown in Figure 1 and the corresponding map data is shown in the righthand image of Figure 3. As we mentioned in the introduction, this is a complex task due to the segmentation problems posed by the raw data and the unreliable nature of the ground-truth map information. Hedge structures present themselves as intensity ridges of variable width in the SAR image. The raw intensity data is both noisy and exhibits anisotropies associated with the directionality of the radar used to sense the scene; the anticipated fidelity of feature detection may be expected to be subject to orientation dependent systematics. For instance, inspection of Figure 1 reveals shadowing associated with the directionality of the radar. At the cartographic level there are discrepancies between map and data. Many of the linear hedge structures recorded in the map data are absent from the SAR image while some genuine hedges are not mapped. These problems are compounded by the fact that hedgerows are not recorded as a distinct cartographic class in the digital map.

We commence the processing of the SAR data by applying a relaxation operator to the raw image data to extract intensity ridges of good connectivity. The ridge extraction process relies on refining the output of a pair of directional line detection filters using a dictionary-based relaxation scheme [4]. Example ridge contours are shown in Figure 2. The lefthand image of Figure 3 shows the linear segments extracted from the line contours.

The initial matches between the linear segments extracted from the SAR data and their map representation are established on the basis of the angular affinity. The matching probabilities are computed by considering the orientation difference between linear segments in data and model, $\theta_{u,f(u)}$, using the known rotation needed to transform between the scenes, Φ

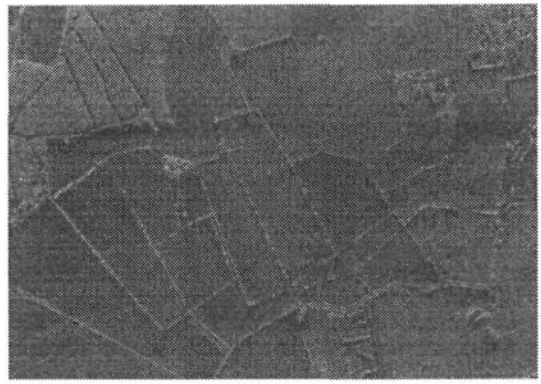

Figure 1: Raw SAR Image

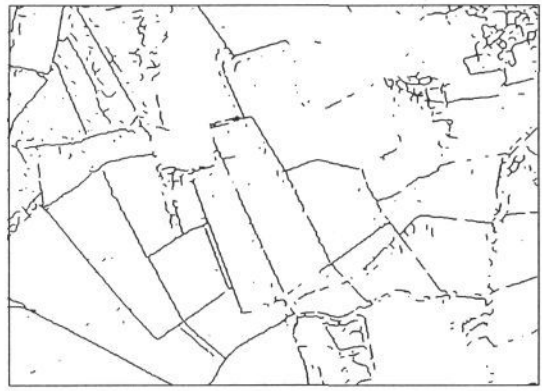

Figure 2: Result of line detection

$$P(f(u_k)|\underline{x}_k) = \frac{\exp[-\frac{(\theta_{u,f(u)}-\Phi)^2}{2\sigma^2}]}{\sum_{w\in V_2}\exp[-\frac{(\theta_{u,w}-\Phi)^2}{2\sigma^2}]} \tag{12}$$

The mean rotation parameter may be adaptively determined to minimise a global error criterion along the lines suggested in [11]. The angle variance σ may be chosen to reflect anticipated systematics in the estimation of line-orientation. Although there is clearly a considerable body of information remaining untapped by our matching affinity model, it must be stressed that this aspect of the matching process is not our prime concern in this paper. Rather, our aim is to demonstrate how the discrete relaxation method can improve the consistency of a very poor initial match using softened symbolic constraints. In any case, since linear segments are invariably subject to fragmentation, the ability to recover an acceptable match based purely upon orientation information may provide certain operational advantages in terms of ease of control.

The experimental matching study is based on 90 linear segments in the SAR data and 34 segments contained in the map. However only 18 of the SAR segments have feasible matches within the map representation. Figure 3 illustrates the initial matching

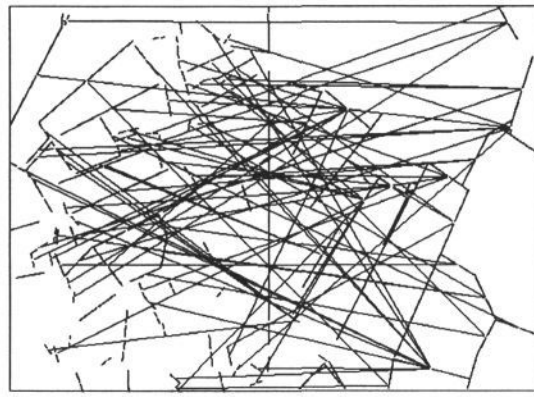

Figure 3: Initial unfiltered match

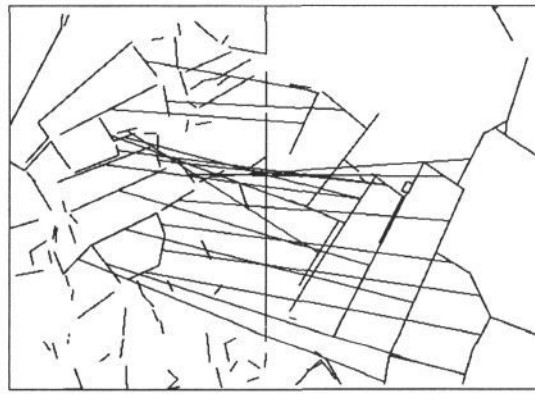

Figure 4: Final filtered match

configuration; the lines between the left and right halfs of the figure indicate matches between the midpoints of the lines. The spatial pattern of matches displays a high degree of randomness. In addition, certain linear segments in the map which are subject have multiple matches in the SAR data. This second feature is largely a result of orientation ambiguities among the line-segments. When the constraint filtering step is applied to this initial configuration, only 3 correct matches are recoverable.

Application of the discrete relaxation method increases the number of correct matches to 16 with 74 errors after 10 iterations. Beyond this point there is no further iterative change in the matching configuration, in other words, the discrete relaxation process has reached stable convergence. The number of matching errors is still substantial but by using the constraint filtering technique described in Section 5, inconsistent matches are removed producing the result shown in Figure 4. The final result contains all 16 correct matches and only 3 residual errors. Moreover, the number of multiple matches is signficantly reduced; only one of the errors falls into this category. In addition to improving the fidelity of match the discrete relaxation scheme has also increased the level of relational consistency.

6 Conclusions

We have described a symbolic approach to relational matching in machine vision. The novelty of the method stems from its Bayesian modelling of relational consistency through the use of an explicit constraint corruption process. Unlike many alternatives in the literature, the method is not limited to the use of binary constraints; it can accommodate N-ary relations of differing or varying order. In consequence of this assumed model the consistency of match is gauged by a compound exponential function of the Hamming distances between symbolic relations; there is a single exponential associated with each potential relational mapping. It is this feature of our consistency measure that bestows tangible performance benefits, rendering it more robust to errors and allowing it to operate effectively in a large space of relational mappings. This robustness to inconsistency means that the method may be operated without the need for an explicit null matching process. Unmatchable entities are identified by a constraint filtering operation once the relaxation scheme has converged.

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