Graph-Based Feature Matching Using Descriptive and Relational Parameters

Olaf Hellwich and Wolfgang Faig

Abstract
A graph-based matching algorithm for edge features was developed. It conducts a breadth-first search in two next-neighbor graphs starting at hypothetically matched feature pairs. A match is established by comparing feature properties using a match function. Main advantage of the matching algorithm is its applicability to various domains, such as stereo vision or matching images and GIS data. Digitized stereo image pairs for the investigation of automobile accidents are used to illustrate the method. For objects with distinctive edges, 80 to 90 percent of the resultant feature pairs were found to be correct.

Introduction
The fundamental idea of the proposed matching method for edge features is that any property of the edge features can be compared with the help of a match function. In this way, the properties contribute to a measure of similarity of the candidate features. As no constraints have to be fulfilled, one or several properties that differ for candidate feature pairs do not prevent the algorithm from identifying a correct match, as long as the correspondence can be proven with a high similarity value resulting from the match function.

This simplicity is seen as the main advantage of the approach, because it results in a high flexibility and a wide range of possible applications. It also provides a robust matching when noisy imagery or unusual object arrangements are encountered.

The search strategy for the matching of feature pairs is straightforward. Initially, particularly significant edges are extracted from two edge-neighborhood graphs. The two sets of significant edges are compared in all combinations. Candidate feature pairs which acquire a high similarity value are accepted as initial hypothetic matches. They are taken as start nodes for a further search for corresponding nodes in the graphs, i.e., for each hypothetical match, the generation of a connected component of matched feature pairs is tried. During the breadth-first search in the graph, a best first choice selection of matching pairs is performed.

This means that both the relational information of the graph as well as the similarity identified by the match function support the establishment of correctly matched features.

Previous Work
McIntosh and Mutch (1988) used a match function in order to compare straight lines. The match function computes a weighted mean of edge parameter similarities. Edge parameters compared are, for instance, length, direction, and contrast. McIntosh and Mutch's (1988) approach was extended towards a comparison of relational edge parameters.

Ayache and Faverjon (1987) proposed a method of prediction and propagation of hypotheses applied to a graph-based description of images. The images are first reduced to neighborhood graphs of edge segments. Linear segments are generated by a polygonal approximation of edge elements in the images. The neighborhood relations between the edge segments are established with the help of a bucketing technique. An image is subdivided into rectangular grid meshes. All edges which belong partially or completely to the same grid mesh are considered neighbors. The constraints used by the stereo matching algorithm are epipolar constraint, geometric similarity constraint, continuity constraint, and uniqueness constraint.

A graph-based matching approach more elaborate than Ayache and Faverjon's technique was presented by Horaud and Skordas (1989). An image is described in form of a relational graph. In the matching process not only the features and their attributes are evaluated, but also the relationships between nearby features are considered. In order to find a mapping function between the images which considers relations between features in the left and in the right image, a correspondence graph is built. The stereo correspondence problem is therefore formulated in form of a search for maximum cliques in a graph. Horaud and Skordas perform an exhaustive as well as a simplified heuristic search in the correspondence graph.

Comparison of Edge Features
For the formulation of a matching algorithm for edge features, some definitions are made. An edge is defined as a one-dimensional discontinuity-like irregularity in the brightness function that has a comparatively homogeneous brightness and steepness. When average brightness, contrast, and steepness of such an irregularity changes considerably, this continuation of the irregularity is regarded to be another edge. A chain of pixels along an edge is called an edge streak.

Corner points, i.e., discontinuities in the direction of an edge streak subdivide edge streaks into edge segments. The task to be solved here is the generation of matches of edge segments from two corresponding edge neighborhood graphs

Department of Surveying Engineering, University of New Brunswick, Fredericton, N.B. E3B 5A3, Canada.

O. Hellwich is presently at the Technische Universität München, Germany.

Photogrammetric Engineering & Remote Sensing,
Vol. 60, No. 4, April 1994, pp. 443–450.

0099-1112/94/6004–443$03.00/0
©1994 American Society for Photogrammetry and Remote Sensing

that describe neighborhood relations between the edge segments.

Matches are established by comparing various candidate edge segment pairs. A correct match of two edge segments is assumed when the similarity of the edges for both segments is (1) higher than for other candidate segment combinations (i.e., the edge pair is a mutually best match) and (2) higher than a threshold. The similarity of a candidate pair is derived from parameters describing the edge segments and the relations between neighboring edge segments. The set of parameters supplied to the match function is easily adjustable to specific matching tasks.

Edge Parameters

The parameters used in the implemented stereo matching method can be subdivided into descriptive and relational parameters.

Descriptive parameters describe the properties of an edge segment and, hence, make them distinctive from other segments. The descriptive parameters are derived by an analysis of edge-support regions which include the edge segments and their vicinity. The parameters used in the implemented version of the matching algorithm are maximum and minimum brightness, contrast, width, steepness, average brightness in the edge-support region, length, direction, and curvature.

Relational parameters give information about the neighborhood relations between an edge and adjacent edges. They have either topologic or geometric content. The relational parameters used in the implemented version of the algorithm are closest distance between the edge segments, direction to the neighboring edge, perpendicularity, parallelity, collinearity, and the side on which the neighboring edge is situated.

The Match Function

The match function for the comparison of candidates for matching evaluates the edge parameters (McIntosh and Mutch, 1988):

$$s = \frac{\sum_i (w_i \cdot v_i)}{\sum_i w_i} \tag{1}$$

where v_i is the similarity value for a parameter pair, and w_i is the weight of parameter i. The result of the match function is a similarity value s of the features compared. The weights w_i are defined according to the image or object type.

The similarity values v_i of the parameters are computed according to the nature of the specific parameters. Generally, the computation is conducted as follows (after McIntosh and Mutch, 1988):

$$v_i = \frac{\min(|p_{jL}|,|p_{kR}|)}{\max(|p_{jL}|,|p_{kR}|)} \tag{2}$$

where p_{jL} and p_{kR} are the instantiations of the compared parameters, e.g., the lengths of segment j in the left image L and segment k in the right image R.

For some parameters, Equation 2 is not suitable.

The similarity value for segment directions t_L, t_R is computed as (McIntosh and Mutch, 1988):

$$v_t = \frac{\delta - |t_L - t_R|}{\delta} \tag{3}$$

where t_L, t_R are the directions of the left and right segment in rad/100.

The value δ is interpreted as the maximum allowable difference between the directions compared. If the magnitude of the difference $|t_L - t_R|$ is larger than δ, then the similarity value v_t will be negative. δ is computed according to

$$\delta = \delta_{\max} \cdot \frac{50}{\min(50, l_L + l_R)} \tag{4}$$

where $\delta_{\max}$ is set to 80 rad/100, and l_L, l_R are the lengths of the left and the right segments. This means that δ is generally 80 rad/100; a value that has been determined empirically. δ is increased when the sum of the segment lengths is less than 50 pixels, as directions of short segments agree considerably less than directions of longer segments.

For the propagation step, i.e., the generation of connected components using the graph description, for both the left and the right edge segments L and R, "parent" nodes in the edge-neighborhood graphs are known. This provides the possibility to compare relational parameters. The similarity value of two relations r_L, r_R between parent and neighbor nodes is computed according to

$$v_r = \frac{1}{5}\left(\frac{\delta - |t_{rL} - t_{rR}|}{\delta} + \frac{\min(d_{rL},d_{rR})}{\max(d_{rL},d_{rR})} + C + P + S\right) \tag{5}$$

where t_{rL} = direction between related edge segments in the left graph,
t_{rR} = direction between related edge segments in the right graph,
d_{rL} = distance between related edge segments in the left graph,
d_{rR} = distance between related edge segments in the right graph,
δ = computed value according to Equation 4,

$$C = \begin{Bmatrix} \text{100 if both left and right relation are referring} \\ \text{to edges belonging to the same edge streak.} \\ \text{50 if both left and right relation are referring} \\ \text{to edges not belonging to the same edge streak.} \\ \text{0 otherwise} \end{Bmatrix},$$

$$P = \begin{Bmatrix} 100, \text{ if } r_L, r_R \in \boldsymbol{P} \\ 100, \text{ if } r_L, r_R \in \boldsymbol{N} \\ 100, \text{ if } (r_L, r_R \notin \boldsymbol{P} \wedge r_L r_R \notin \mathrm{N}) \\ 0, \text{ if } ((r_L \in \boldsymbol{P} \wedge r_R \in \boldsymbol{N}) \vee (r_L \in \boldsymbol{N} \wedge r_R \in \boldsymbol{P})) \\ 50 \text{ otherwise} \end{Bmatrix},$$

and

$$S = \begin{Bmatrix} 100, \text{ if } r_L, r_R \in \boldsymbol{L} \\ 100, \text{ if } r_L, r_R \in \boldsymbol{R} \\ 0 \text{ otherwise} \end{Bmatrix}.$$

Here $\boldsymbol{P} = \{r|r$ is a relation of parallel edge segments$\}$,
$\boldsymbol{N} = \{r|r$ is a relation of perpendicular edge segments$\}$,
$\boldsymbol{L} = \{r|r$ is a relation between a parent node and child node on its left side$\}$, and
$\boldsymbol{R} = \{r|r$ is a relation between a parent node and child node on its right side$\}$.

(For parent and child nodes in the propagation tree, see section on the Propagation Algorithm.)

Thus, the similarity of two relations depends on the direction and the distance between the related segments, edge-streak membership, and topology.

The parameters compared by the match function are determined by the application domain stereo vision. For other domains, such as matching of digitized maps, the parameters

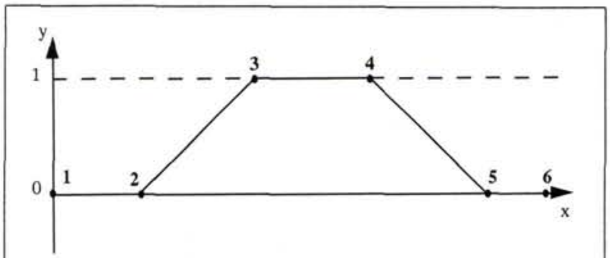

Figure 1. General shape of the weight function of a parameter.

p and, if necessary, the parameter similarity functions $v_p(p)$ have to be adapted to the specific problems. Image geometry can also be taken into account as a parameter of the match function. It would, however, be impossible to rigorously observe geometrical constraints such as epipolar geometry, as this would contradict the basic principle not to enforce any constraints. The geometry parameter could only be evaluated using a moderately high weight w that does not prevent other important parameters from influencing the match function value.

The Matching Procedure

The matching process consists of three steps: (1) the prediction of hypotheses, (2) the propagation of the predicted hypotheses based on the edge neighborhood graph, and (3) the solution of conflicts between concurrent connected components. Ayache and Faverjon (1987) used a similar algorithm.

The Prediction of Hypotheses

In the prediction step a set of particularly obvious matches is attempted. First, sets of comparatively distinctive edge segments are extracted from the edge neighborhood graphs using a selection function that weights the segment parameters. Then, the match function (Equation 1) is applied to the sets of distinctive edges exhaustively.

The selection function derives a measure of distinctiveness d for each edge segment. It computes the averages of weight function values for specified parameters:

$$d = \frac{\sum_{i=1}^{n} w_i(p_i)}{n} \qquad (6)$$

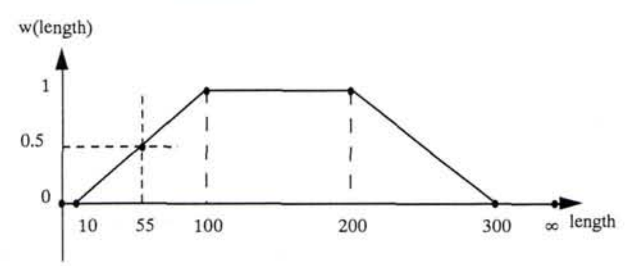

Figure 2. Weight function of the parameter length.

where p_i = argument of parameter i, $w_i()$ = weight function for parameters p_i, and n = number of parameters evaluated.

A weight function w_i is given in digitized form as a set of x-values defining a standard function curve. The general shape of the graph of a weight function is shown in Figure 1. The x-values of the points 1 to 6 are defined for each parameter. Figure 2 gives an example for the derivation of a weight function value for the specific parameter length (in pixels). The graph indicates that lines of a length $l < 10$ pixels have a weight of 0. Lines of a length $100 < l < 200$ have a weight of 1. This implicitly means that these lines are regarded as most significant for matching purposes. Lines with a length $l > 300$ have a weight of 0. This is taking into account that very long lines probably are split up in the other image and, therefore, cannot be matched reliably. For lines with $10 < l < 100$ and $200 < l < 300$, a linear interpolation is conducted; e.g., a line with $l = 55$ has a weight of 0.5.

When the measures of distinctiveness d have been derived for all edge segments, a histogram for d-values is computed. With a known percentage p of edge segments to be selected, a threshold value d_t is derived from the histogram. All edge segments i with $d_i > d_t$ are elements of the set of selected significant segments S. This evaluation is conducted for both edge neighborhood graphs.

Then all possible combinations of significant edge segments (s_{iL}, s_{jR}) from the left and right edge neighborhood graphs are compared using the match function (Equation 1); i.e., the cross product $S_L \times S_R$ is computed. The set of mutually best matches $\boldsymbol{M}$, i.e.,

$$\begin{aligned} \boldsymbol{M} = \{(s_{iL}, s_{jR}) | m(s_{iL}, s_{jR}) &= \max\{m(s_{iL}, s_{jR})_{j=0}^{n_R}\} \wedge \\ m(s_{iL}, s_{iR}) &= \max\{m(s_{jL}, s_{iR})_{j=0}^{n_L}\}\} \end{aligned} \qquad (7)$$

where $m()$ = match function, and n_L, n_R = number of edge segments in the left and right edge neighbourhood graphs, is considered for further processing. As can be seen in Equation 7, "mutually" best means that both the assignment of the best matching right segment to the left segment as well as the assignment of the best matching left segment to the right segment result in the same pair of edge segments. When the similarity measure $m(s_{iL}, s_{iR})$ is greater than a threshold, the match is accepted as an initial match of a hypothesis, i.e., of a connected component to be generated.

In the prediction step, the parameters compared by the match function are all the descriptive edge parameters that have been assigned a weight factor w_i.

The Propagation Algorithm

In the propagation step, connected components or cliques are generated by searching the edge neighborhood graphs for further potential matches, starting with the initial hypothetic matches. The neighboring edges of the initial match (p_L, p_R) are compared in all combinations. This means that they are assignments among the cross product of neighboring edges, i.e., elements of

$$\{m(s_L, s_R) | s_L \in \boldsymbol{N}_L \wedge s_R \in \boldsymbol{N}_R \wedge (s_L, s_R) \in \boldsymbol{N}_L \times \boldsymbol{N}_R\}$$

where $\quad \boldsymbol{N} = \{s | s \text{ is neighbor of } p\}$

Two classes for the acceptance of a detected match are defined as follows:

(I) Matched edge segment pairs which
  (A) are elements of the set of mutually best matches $\boldsymbol{M}$ (according to Equation 7) or matches where one segment s_i is matched to a segment s_j which is

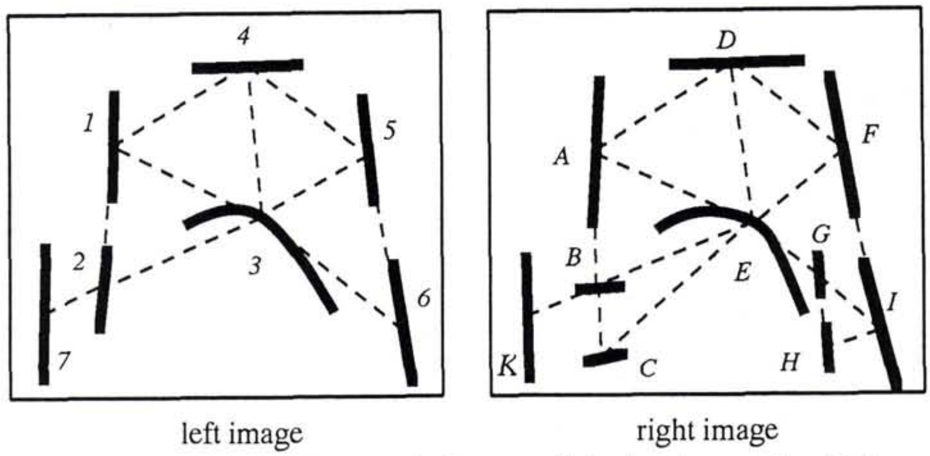

Figure 3. Two edge-neighborhood graphs. The most distinctive edges are 3 and E. An initial match of a hypothesis could be the match (3, E).

matched to a segment s_k belonging to the edge streak to which s_i also belongs, i.e., elements of the set

$$
\begin{aligned}
\tilde{M} = \{(s_{iL}, s_{iR}) \text{ such that} \\
&[m(s_{iL}, s_{iR}) = \max\{m(s_{iL}, s_{jR})\}_{j=0}^{n_R} \wedge \\
&m(t_{iL}, s_{iR}) = \max\{m(t_{iL}, s_{jR})\}_{j=0}^{n_L} \wedge \\
&s_{iL}, t_{iL} \in \text{edge streak } k] \vee \\
&[m(s_{iL}, s_{iR}) = \max\{m(s_{jL}, s_{iR})\}_{j=0}^{n_R} \wedge \\
&m(s_{iL}, q_{iR}) = \max\{m(s_{jL}, q_{jR})\}_{j=0}^{n_L} \wedge \\
&s_{iR}, q_{iR} \in \text{edge streak } l]\}
\end{aligned}
\tag{8}
$$

and which
(B) have a match function value greater than a threshold t_1:

$$m(s_L, s_R) > t_1$$

These matches are regarded as valid matches of a connected component.

(II) matches which fulfill condition A as before and (B) have a match function value greater than a threshold t_2, and less than the threshold t_1:

$$t_1 > m(s_L, s_R) > t_2$$

These matches are not considered being members of the set of connected components, but they are used for further propagation of matches in order to find more matches of class I.

The search algorithm for matches between the edge neighborhood graphs is now explained.

The propagation strategy is based on a breadth-first search in a tree. The search starts by comparing neighbors of the segments of an initial hypothetical match. Thus, the initial match is the root node of a tree. Its child nodes are the matches of classes I and II among the neighbors of the initial segments. As a breadth-first search is conducted in the graph, the first generation child nodes are established in direct sequence. Then, the second generation child nodes are searched by comparing all neighbors of a first generation match. This means that the breadth-first tree degenerates to a linear list with generation indices.

In every generation, all matches of classes I and II become further tree nodes of the next generation, if they are not already part of the tree as a node of an earlier or of the same generation. The propagation is ended as soon as no further tree nodes can be generated, or if there are more than three generations of class II nodes in sequence.

Figure 3 shows two neighborhood graphs to be matched, Figure 4 gives an example for the generation of the propagation tree, and Table 1 shows the class I and class II matches established during the propagation.

During the build-up of the propagation tree, the potential matches of class I are considered to belong to a connected component. Ambiguous assignments are solved at the end of the processing of a hypothesis. If multiple matches occur between different edge streaks, the match with the greater similarity value is preferred.

When a match which is found during the propagation of a hypothesis is the initial match of another hypothesis, the other hypothesis is discarded. This saves computation time as the second hypothesis would result in a connected component similar or even equal to the one generated.

According to the details and features described before, the propagation algorithm was implemented as shown in Figures 5 and 6. The procedure Match_Neighbors_of does

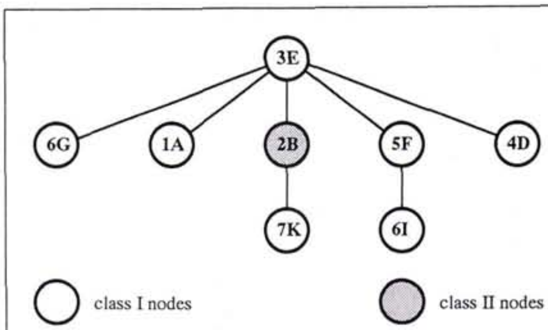

Figure 4. The propagation tree. Even though the edge segments 2 and B do not seem to match very well (see difference in direction), match (7,K) was found.

TABLE 1. MATCHES FROM HYPOTHESIS PROPAGATION. MATCH (6, G) WAS OVERWRITTEN BY MATCH (6, I).

parent node	class I matches	class II matches	discarded matches
(3,E)	(6,G) (1,A) (5,F) (4,D)	(2,B)	
(2,B)	(7,K)		
(5,F)	(6,I)		
			(6,G)

```
for all hypotheses {
    treat initial match ( pL, pR) as root node;
    while tree not completely processed {
        get tree node (tL, tR);
        Match_Neighbours_of (tL, tR);
    }
    for both edge neighbourhood graphs {
        for all segments {
            discard ambiguous matches;
        }
    }
}
```

Figure 5. Propagation algorithm.

```
Procedure Match_Neighbours_of (pL, pR) {
    compute match function values for NL x NR;
    for all left neighbours {
        if mutually matched {
            if ( m(sL, sR) > t1) {
                if (sL, sR)∉tree, Make_Tree_Node;
                Make_Match;
                check for not yet processed hypothesis;
            } else if (m(nL, nR) > t2) {
                if (sL, sR)∉tree, Make_Tree_Node;
            }
        } else if sL is matched to a right segment sR which is
        matched to another segment tL of the edge streak of sL {
            if ( m(sL, sR) > t1) {
                if (sL, sR)∉tree, Make_Tree_Node;
                Make_Match;
                check for not yet processed hypothesis;
            }
        } else if sR is matched to a left segment sL which is
        matched to another segment qR of the edge streak of sR{
            if ( m(sL, sR) > t1) {
                if (sL, sR)∉tree, Make_Tree_Node;
                Make_Match;
                check for not yet processed hypothesis;
            }
        }
    }
}
```

Figure 6. Algorithm for the procedure Match_Neighbors_of.

the comparison of neighboring nodes of an established match. The procedure Make_Tree_Node adds a node to the propagation tree. The procedure Make_Match adds a match to the connected component. During the tree generation, several entries per edge segment can occur. Afterwards, the main procedure discards the ambiguous matches in the connected component.

Solution of Conflicts Between Different Connected Components

After all hypotheses are processed, the resulting connected components have to be combined. Generally, this contributes to covering the area of image overlap with matched segments. However, conflicts between concurring hypotheses arise as well. The decision as to which of the conflicting hypotheses is preferred is based on the strength of prediction of a hypothesis. The connected component with the largest number of matched segment pairs is considered to be the correct one.

When two matches are conflicting, the match belonging to the stronger hypothesis is always preferred. Then the strength of the weaker hypothesis is reduced by one. During the process of solving contradictions, only the original strengths of prediction are compared. This avoids that the order in which the hypotheses are evaluated for ambiguous matches influences the result of the process.

After the solution of conflicts between concurring connected components, the remaining strengths of prediction are compared with a threshold. The threshold should be set according to the image type and the number as well as reliability of the matches needed. Hypotheses weaker than the thresholding strength are discarded completely, as those hypotheses often are not based on correct matches (Ayache and Faverjon, 1987).

Experimental Results

The developed feature-based matching method was implemented on Sun workstations as part of a stereo vision software package using the X-Window user interface (Hellwich, 1992). The program system was applied to imagery taken for car accident investigation. The final goal of the digital stereo measurements was the determination of the depths of dents in the car bodies.

Images of cars are characterized by well-determined curved edges of various shapes as well as by specular reflections in some parts. All images were taken outdoors under common conditions for close-range photogrammetry. No special measures were observed. The images were taken with a 24- by 36-mm camera on color slide film. They were digitized with an Apple McIntosh slide scanner using the DeskScan software for the FrameGrabber card. Then a reduction from color to greyscale was conducted. The images have a resolution of about 600 by 400 pixels.

The first picture shows the image pair of a grey 1987 Skoda (Figure 7). The damaged door of the car is used as the object of demonstration. The matches generated are displayed in Figure 8. The match numbers enable the alert eye to identify matched edge segments. The unlabeled edge segments are unmatched. Another image pair is presented in Figure 9 while Figure 10 shows the resulting matches on the object of interest.

Intensive tests of the matching method resulted in about 80 to 90 percent correct matches among the matches found on the objects of interest.

Figure 11, an image pair of an oil tank, demonstrates the limitations of the match function in the proposed form. The welding seams are well-defined edges. In spite of that, only a few correct matches are found, as the edges are not sufficiently distinctive. An evaluation of disparity gradients in the match function would solve the problem. Disparity gradients can be obtained from the disparities of parent and child nodes in the propagation tree.

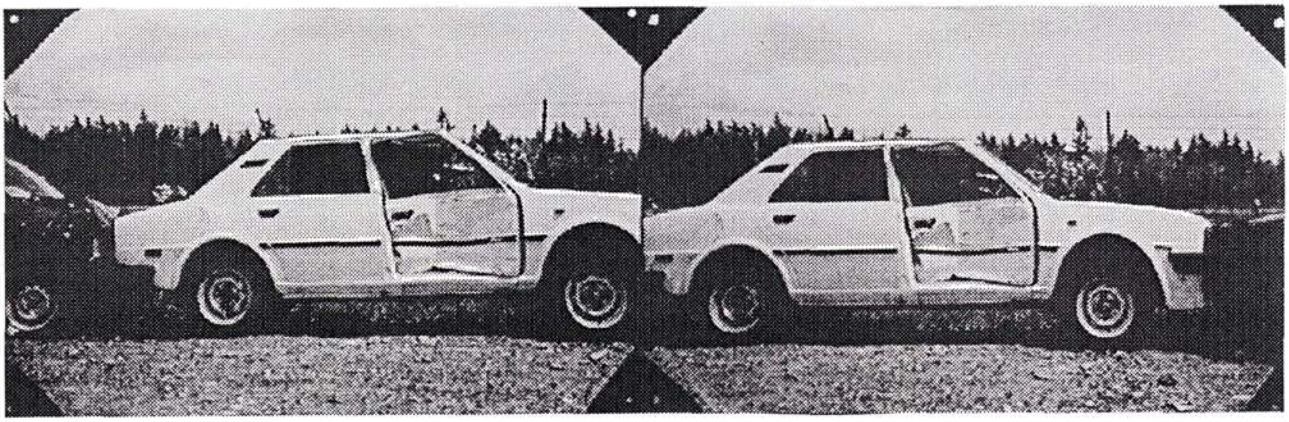

Figure 7. Image pair of a grey 1987 Skoda.

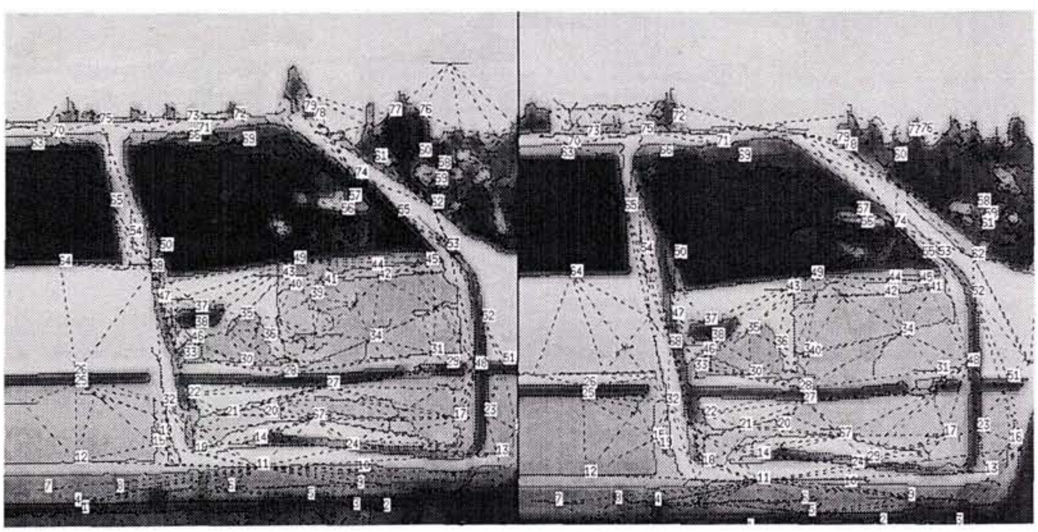

Figure 8. Matched segments superimposed to the Gaussian convolved image.

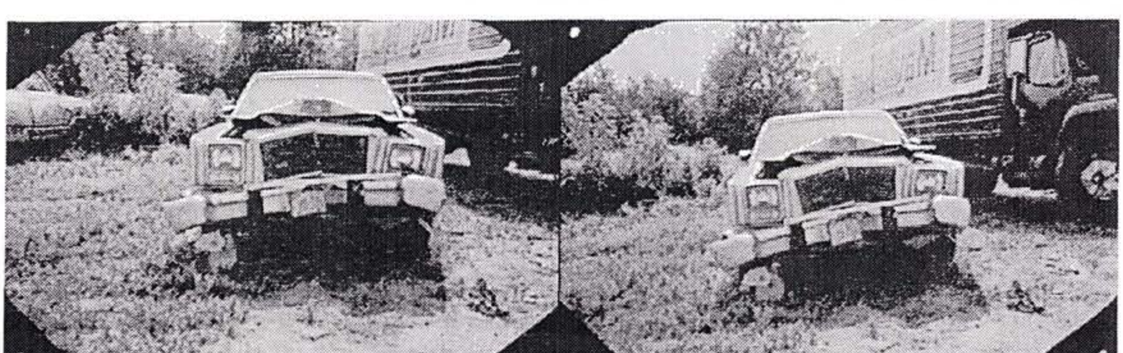

Figure 9. Image pair of a white Mercury Grand Marquis.

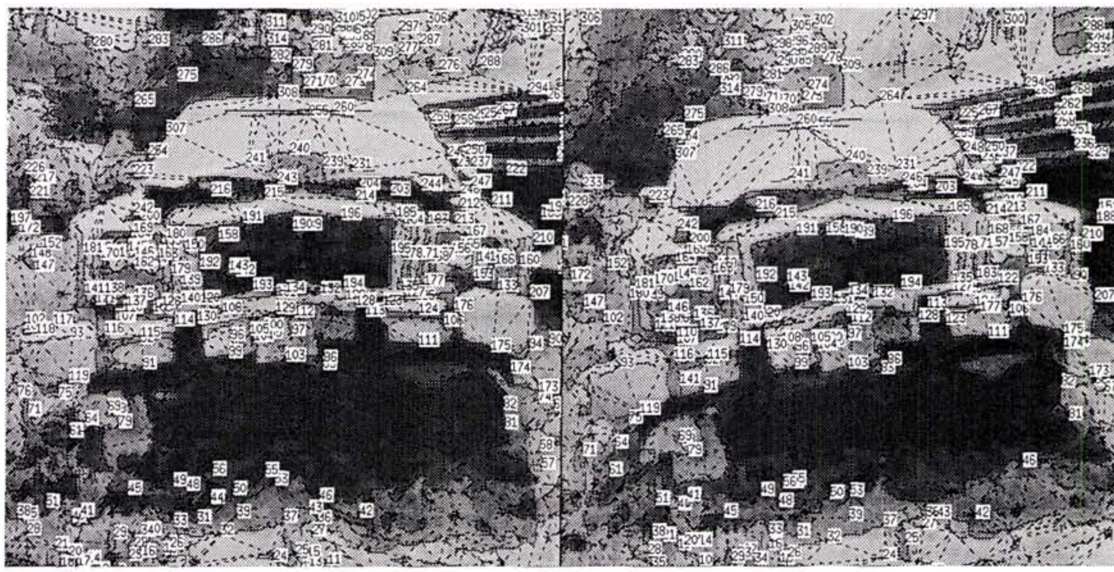

Figure 10. Matched segments of the white Mercury Grand Marquis image pair.

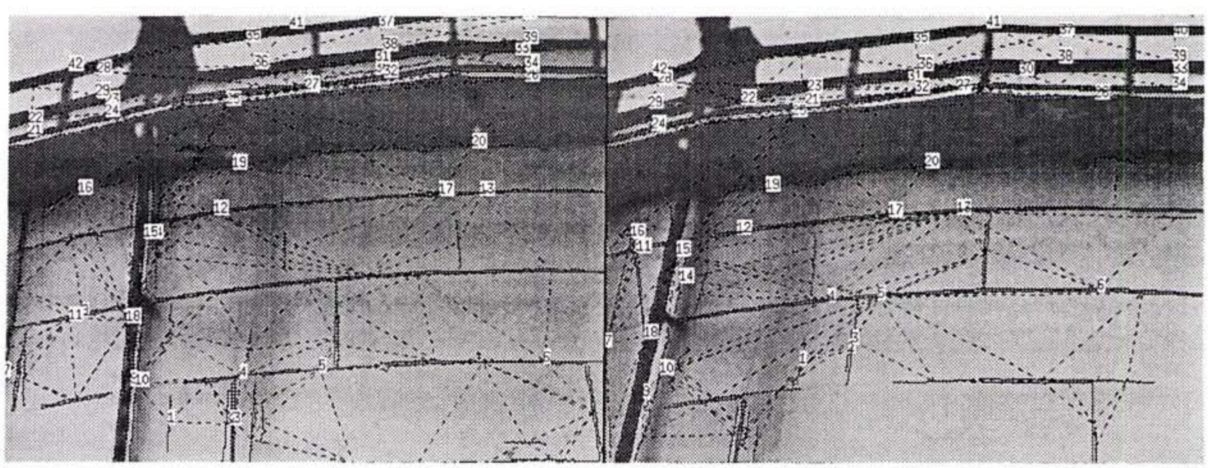

Figure 11. Matched segments of an image pair of an oil tank.

Conclusions

A matching algorithm was developed using a graph structure to control the search for matches and to exploit relational properties for the identification of matches.

The main advantages of the matching algorithm are

- its applicability to various domains, such as stereo vision or the matching of images and GIS data;
- its independence from epipolar geometry which makes the algorithm applicable to images taken with different imaging devices; and
- the availability of reliability information in form of the similarity values of established matches and the numbers of matches (strength) of a connected component.

Experimental results indicated difficulties of the matching method for images of objects with well-defined but indistinctive edges. The problem is expected to be solved by an evaluation of disparity gradients in the match function.

References

Ayache N., and B. Faverjon, 1987. Efficient Registration of Stereo Images by Matching Graph Descriptions of Edge Segments, *International Jounal of Computer Vision*, pp. 107-131.

Hellwich, O., 1992. *Graph-Based Edge Matching in Stereo Vision*, M.Sc.E. Thesis, Dept. of Surveying Engineering, Univ. of New Brunswick, Fredericton, 113 p.

Horaud, R., and T. Skordas, 1989. Stereo Correspondence Through Feature Grouping and Maximal Cliques, *IEEE Transactions on Pattern Analysis and Machine Intelligence*, Vol. 11, No. 11, pp. 1168-1180.

McIntosh, J. H., and K. M. Mutch, 1988. Matching Straight Lines, *Computer Vision Graphics and Image Processing*, Vol. 43, No. 3, pp. 386-408.

(Received 7 August 1992; accepted 15 December 1992; revised 26 January 1993)

Meeting Announcement

ISPRS Commission II
Systems for Data Processing, Analysis, and Presentation

held in conjunction with

The 6th Canadian Conference on GIS

June 6-10, 1994
Ottawa, Ontario

ISPRS Commission II, "Systems for Data Processing, Analysis, and Presentation" will offer a large exhibit area, as well as a strong technical program of paper and poster sessions. The Technical program will provide a vast opportunity to showcase the leading technologies and the latest research projects from around the globe. This Symposium, since accompanied by the 6th Canadian Conference on GIS, will not only provide an informative program on Photogrammetry and Remote Sensing, but also on GIS, management, education, and research, as well as the latest in systems technology.

Delegates to either the ISPRS Commission II Symposium or the 6th Canadian Conference on GIS will be free to explore and access sessions of the other.

As a special guest speaker, Her Royal Highness Princess Maha Chakri Sirindhorn of the Royal Family of Thailand will be opening the Symposium. The Princess holds a great interest in GIS and remote sensing and their environmental applications.

An Accompanying Persons Program as been designed to explore the National Capital Area, its world class museums, and monuments of national significance.

For more information, please contact:

Dr. Mosaad Allam
Chairman
ISPRS Commission Symposium
615 Booth Street, Room 700
Ottawa, Ontario
Canada K1A 0E9