

# Feature-based correspondence: an eigenvector approach

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*We propose a novel method for performing point-feature correspondence based on a modal shape description. Introducing shape information into a low-level matching process allows our algorithm to cope easily with rotations and translations in the image plane, yet still give a dense correspondence. We also show positive results for scale changes and small skews, and demonstrate how reflectional symmetries can be detected.*

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The correspondence problem is a generic one in computer vision, arising whenever a match must be found between the features of two related patterns. It emerges in paradigms as diverse as stereo fusion, structure-from-motion, model-based recognition and navigation. In this paper we propose a novel token-based technique for matching two sets of point features, using a modal shape description.

Our starting point is the work of Scott and Longuet-Higgins. After identifying two shortcomings of their algorithm, we outline our modal approach and give some experimental results. We conclude with a set of open problems and directions for future research.

## PREVIOUS WORK

The correspondence problem has long intrigued computer vision researchers, and a vast literature is testimony to the numerous techniques proposed to solve it. There are two main classes of algorithm, *intensity-based* and *feature-based*. The former operate directly on the raw grey-level data in images, while the latter employ pre-processing stages to extract *features*

(or *tokens*) such as corners, edges or blobs. We adopt the feature-based approach for various reasons, among them the undesirability of dense temporal sampling (which intensity-based techniques demand) in our application (mobile robot navigation).

In a recent paper<sup>1</sup>, Scott and Longuet-Higgins proposed an algorithm to match 2D point-features across a pair of images. Consonant with the 'minimal mapping' philosophy of Ullman<sup>2</sup>, they incorporated an affinity measure between features (based on inter-element distances) and a competition scheme allowing candidate features to contest matches. These criteria were formulated as a *principle of proximity* (favouring matches across shorter distances), and a *principle of exclusion* (favouring one-to-one matches). The resulting mapping then effectively minimized the overall sum of the squared distances travelled by the features, subject to the uniqueness constraint.

A remarkable feature of the algorithm was its elegant implementation, founded on a well-conditioned eigenvector solution which involved no iteration. As input, the algorithm received a set of  $m$  features ( $\mathbf{x}_{i,1}$ ) in image  $I_1$  and  $n$  features ( $\mathbf{x}_{j,2}$ ) in image  $I_2$ . The computation then consisted of three stages. The first step was to enumerate all possible pairwise matches and store their affinities in a *proximity matrix*  $\mathbf{G}$ . Each element  $G_{ij}$  recorded the attraction between the  $i^{\text{th}}$  feature in  $I_1$  and the  $j^{\text{th}}$  feature in  $I_2$  via a Gaussian-weighted distance metric:

$$G_{ij} = e^{-d_{ij}^2/2\sigma^2}, \quad i = 1 \dots m, \quad j = 1 \dots n$$

where  $d_{ij}^2 = \|\mathbf{x}_{i,1} - \mathbf{x}_{j,2}\|^2$  was the squared Euclidean distance between the two features. Thus  $G_{ij}$  ranged from 0 for widely-separated features ( $d_{ij} = \infty$ ) to 1 for coincident features ( $d_{ij} = 0$ ). The parameter  $\sigma$  controlled the degree of interaction between the two sets of features. This was roughly like placing a small circle around a feature in  $I_1$  and only allowing it to interact with those features in  $I_2$  lying within the circumference. Hence, a small value of  $\sigma$  enforced

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local interactions, while a larger value permitted more global interactions.

The second step was to perform a *singular value decomposition* (SVD) of  $\mathbf{G}$ , i.e. express  $\mathbf{G}$  as:

$$\mathbf{G} = \mathbf{T}\mathbf{D}\mathbf{U}$$

The  $\mathbf{T}$  and  $\mathbf{U}$  matrices were orthogonal, i.e. their rows (and columns) were mutually perpendicular and had unit length. The  $\mathbf{D}$  matrix contained the (positive) singular values along its diagonal in descending numerical order.

The final step was to compute the correlation (in a scalar-product sense) between  $\mathbf{T}$ 's rows and  $\mathbf{U}$ 's columns, giving an *association matrix*  $\mathbf{P}$ :

$$\mathbf{P} = \mathbf{T}\mathbf{E}\mathbf{U}$$

where  $\mathbf{E}$  was obtained by replacing each diagonal element in  $\mathbf{D}$  by a 1. The element  $P_{ij}$  then indicated the strength of attraction between features  $\mathbf{x}_{i,1}$  and  $\mathbf{x}_{j,2}$ , where 1 indicated a perfect match and 0, no match at all. The correspondence between the two features was 'strong' only if  $P_{ij}$  was largest in both its row and its column, implying a mutual consent to the match. When  $P_{ij}$  was largest in its column but not its row (or *vice versa*), a 'weak' correspondence was implied, with multiple features competing for the match.

This algorithm was shown<sup>1</sup> to maximize the trace of  $\mathbf{P}'\mathbf{G}$ . In other words, the  $\mathbf{P}$  matrix was effectively a 'mask' which slotted over  $\mathbf{G}$  and selected the biggest elements. Since  $G_{ij}$  was large precisely when  $d_{ij}^2$  was small, an overall minimum squared distance mapping was ensured. This can be understood intuitively by imagining pieces of string tied between matching features with the aim of minimizing the total amount of string used. At the same time, however,  $\mathbf{P}$  was orthogonal, so there could only be *one* large element per row or column. Hence, no feature in  $I_1$  could be strongly coupled with more than one feature in  $I_2$ , neatly giving the exclusion principle.

Empirical results<sup>1</sup> showed that the algorithm successfully matched random scatter diagrams undergoing 2D translations, expansions and shears. A theoretical proof confirmed that the algorithm would always recover these mappings, provided that  $\sigma$  was sufficiently large. Our investigation of the algorithm's performance on real-world objects confirmed this claim, but we draw attention to two weaknesses.

Firstly, the algorithm does not cope with large rotations in the image plane. An example is given in Figure 1a, where features on the outline of a bottle have been rotated about the optic axis by 80°. Clearly, the algorithm fails to generate the correct correspondence; the correct matches (obtained using our algorithm) appear in Figure 1b. This failure is a consequence of treating all features as equal, with no regard for the structure *within* the image. For instance, Figure 1a contains violations of the continuity constraint (whereby neighbouring features in  $I_1$  should remain neighbours in  $I_2$ ).

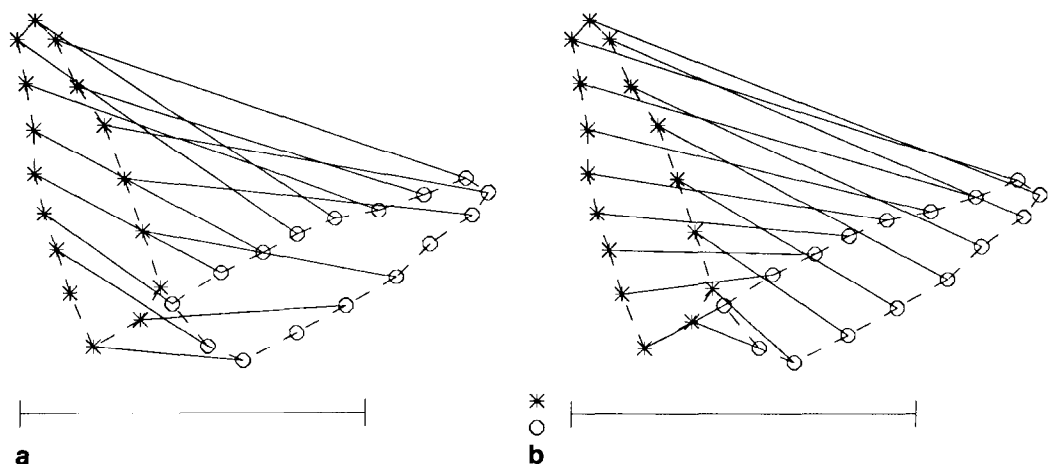
Secondly, implementation considerations can make the assumption of large  $\sigma$  unreasonable, since this forces the smaller singular values towards zero. Consequently some columns in  $\mathbf{T}$  (and rows in  $\mathbf{U}$ ) become unstable, and the association matrix becomes incorrect. This phenomenon is so marked that sometimes even a simple 1D translation cannot be properly matched<sup>3</sup>, although the exact effect obviously varies from computer to computer (depending on the maths processor).

## EIGENVECTOR APPROACH

In devising our solution, we sought to retain the clear strengths of the above algorithm while overcoming its weaknesses. It was apparent that in order to deal with rotations, the structure inherent within the individual images would have to be accounted for, requiring a *shape representation*. The algorithm presented here first analyses each image separately to extract its *modes*, and then uses these modes to establish correspondence. The modes essentially encode the 'shape' of the scene based on the inter-feature distances, and so constitute a shape description.

To gain an intuitive understanding of the approach, consider an image with  $m$  features, and suppose that we define a set of  $m$  axes to act as a coordinate system in an  $m$ -dimensional space. Each image-feature is then assigned a coordinate in this higher space, i.e. each feature is mapped from its 2D image-plane into a hyperspace with  $m$  axes. We perform such a mapping independently for each image, and when the 'shapes' of the images are similar, features which belong together will coincide in the hyperspace. We outline the algorithm below and then demonstrate its operation with a worked example.

Figure 1. Bottle rotated about the optic axis by 80°: \* : image  $I_1$ ; ○ : image  $I_2$ ; — :  $\sigma$  (a) Output of algorithm (only strong attractions are shown, which is why certain features remain unmatched); (b) output of our algorithm (correct solution)



## The algorithm

Consider first how to form the modes of a single image having  $m$  features  $\mathbf{x}_i$ . A square *proximity matrix*  $\mathbf{H}$  is created, recording the distances between features *within* the image. In other words, here we use *intra-image* distances, rather than *inter-image* distances. (Taylor and Cooper<sup>4</sup> employed a similar matrix of all possible point-to-point distances in their Chord Length Distribution (CLD) model of 2D shape; however, they adopted a more statistical approach, finding correlations between the inter-point distances.)

We employ the same Gaussian-weighted metric as before:

$$H_{ij} = e^{-r_{ij}^2/2\sigma_x^2}$$

where  $r_{ij}^2 = \|\mathbf{x}_i - \mathbf{x}_j\|^2$ . Evidently  $\mathbf{H}$  is symmetric ( $r_{ij} = r_{ji}$ ), and its diagonal elements are unity ( $r_{ii} = 0$ ). The parameter  $\sigma_x$  again controls the interaction between features, with the subscript  $x$  emphasizing that interaction occurs between features in the *same* image rather than features in two different images. For small  $\sigma$ , then, each feature only has knowledge of its local surround, while for large  $\sigma_x$ , each feature is more globally aware. Since the two analyses proceed independently, the value of  $\sigma$  can be different for the two images, say  $\sigma_1$  and  $\sigma_2$  respectively.

Next, we compute the eigenvalues  $\lambda_i$  and eigenvectors  $E_i$  of  $\mathbf{H}$ , i.e. solve:

$$\mathbf{H}E_i = \lambda_i E_i, \quad i = 1 \dots m$$

The eigenvectors are of unit length and are mutually orthogonal, and hence form an orthonormal basis. They are termed *modes* by analogy with mechanical oscillating systems, whose eigenvectors describe the modes of vibration. (The mechanism for generating these modes was described in Scott and Longuet-Higgins<sup>5</sup>, where the modes were used to group image features into 'natural clusters'. We have employed these modes as a shape description and have extended them to allow matching between images.)

In matrix form:

$$\mathbf{H} = \mathbf{V}\mathbf{D}\mathbf{V}^T$$

The diagonal matrix  $\mathbf{D}$  contains the (positive) eigenvalues along its diagonal in decreasing size. The *modal matrix*  $\mathbf{V}$  is orthogonal, and has the eigenvectors as its column vectors (i.e.  $\mathbf{V} = [E_1 | \dots | E_m]$ ). Each row of  $\mathbf{V}$  can then be thought of as a *feature vector*  $F_i$ , containing the  $m$  modal coordinates of feature  $i$ , i.e. the expansion of the  $i$ th image feature along the  $m$  modal axes:

$$\mathbf{V} = \begin{bmatrix} F_1 \\ \vdots \\ F_m \end{bmatrix}$$

This computation proceeds simultaneously for the two images. That is, for image  $I_1$  ( $m$  features) we obtain  $\mathbf{H}_1 = \mathbf{V}_1\mathbf{D}_1\mathbf{V}_1^T$  while for image  $I_2$  ( $n$  features) we obtain  $\mathbf{H}_2 = \mathbf{V}_2\mathbf{D}_2\mathbf{V}_2^T$ . The associated feature vectors

are written  $F_{i,1}$  and  $F_{j,2}$ . The final stage is to correlate the two sets of feature vectors, yielding the association matrix  $\mathbf{Z}$ . As before,  $Z_{ij}$  reflects the confidence in the match between  $\mathbf{x}_{i,1}$  and  $\mathbf{x}_{j,2}$ . Here, four points should be noted. Firstly, because the images have different numbers of features, their number of modes will differ. We therefore truncate the  $|m-n|$  least significant modes from the image with more features, where 'least significant' is indicated by smallest eigenvalues. Thus both modal matrices will have  $k$  columns (or modes), where  $k = \min\{m,n\}$  (in fact, fewer than  $k$  modes can also be used). Effectively, we have discarded components of the feature vectors along the least important axes. This truncation naturally affects the orthogonality of the truncated matrix (either  $\mathbf{V}_1$  or  $\mathbf{V}_2$ ); we will discuss this further in the section on our experiments.

Secondly, the sign of each eigenvector is not unique, since switching its direction does not violate the orthonormality of the basis. However, it is vital that both sets of axes have *consistent* directions, since we wish to directly compare the feature vectors. A sign correction stage is thus necessary. Briefly, we treat  $\mathbf{V}_1$  as the reference basis and proceed to orient the axes in  $\mathbf{V}_2$  one at a time, choosing for each that direction which maximally aligns the two sets of feature vectors (expanded only along the axes which have already been untangled). Further details are given in Shapiro<sup>3</sup>.

Thirdly, the association matrix  $\mathbf{Z}$  differs from  $\mathbf{O}$  in that a perfect match is now indicated by the value 0, while a value of 2 indicates no match at all. Best matches are thus given by elements in  $\mathbf{Z}$  which are *smallest* in their row and column. The values  $Z_{ij}$  are obtained by taking the Euclidean distance between feature vectors:

$$Z_{ij} = \|F_{i,1} - F_{j,2}\|^2$$

rather than their scalar product. The advantages of this approach are robustness to truncation of inessential modes, improved sensitivity (due to an increased range of values) and a convenient interface to the sign correction algorithm.

Finally, we consider the feasibility of scaling the eigenvectors in  $\mathbf{V}$  by their corresponding eigenvalues, essentially giving more weight to the dominant modes. This weighting is already implicit in the ordering of the modes, which aligns the components of the feature

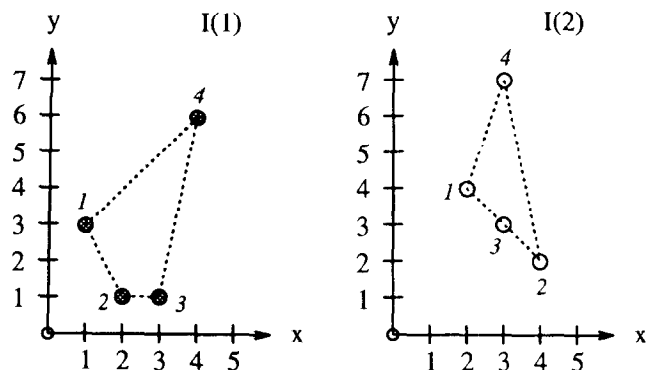


Figure 2. Two images to be matched, each having four features. Image  $I_2$  (open dots) is a distorted version of  $I_1$  (solid dots), and has moved upwards and to the right. The features have been labelled arbitrarily, and the correct solution is 1-1, 2-3, 3-2 and 4-4

vectors ('sorts the axes'), and dictates the sequence of processing in the sign correction stage. More importantly, though, retaining the normalization of the modes allows a fixed range (and hence interpretation) of values in the association matrix (e.g.  $Z_{ij}=2$  always implies a perfect match). Without this, assessing the relative merits of alternative pairings would be tricky.

### Example

Two sets of features are shown in Figure 2, and the aim is to discover the correct correspondence. For the first image, we choose  $\sigma_1=4$  and obtain:

$$\mathbf{H}_1 = \begin{bmatrix} 1.00 & 0.86 & 0.78 & 0.57 \\ 0.86 & 1.00 & 0.97 & 0.40 \\ 0.78 & 0.97 & 1.00 & 0.44 \\ 0.57 & 0.40 & 0.44 & 1.00 \end{bmatrix}, \mathbf{V}_1 = \begin{bmatrix} 0.53 & 0.02 & 0.81 & -0.24 \\ 0.54 & -0.34 & -0.12 & 0.76 \\ 0.54 & -0.29 & -0.52 & -0.60 \\ 0.37 & 0.90 & -0.23 & 0.10 \end{bmatrix}$$

Similarly, for the second image we set  $\sigma_2=4$  and obtain (after sign correction):

$$\mathbf{H}_2 = \begin{bmatrix} 1.00 & 0.78 & 0.94 & 0.73 \\ 0.78 & 1.00 & 0.94 & 0.44 \\ 0.94 & 0.94 & 1.00 & 0.61 \\ 0.73 & 0.44 & 0.61 & 1.00 \end{bmatrix}, \mathbf{V}_2 = \begin{bmatrix} 0.53 & 0.09 & 0.71 & -0.45 \\ 0.49 & -0.51 & -0.57 & -0.41 \\ 0.54 & -0.25 & 0.12 & 0.79 \\ 0.42 & 0.82 & -0.39 & 0.03 \end{bmatrix}$$

Each row in  $\mathbf{V}_1$  and  $\mathbf{V}_2$  refers to an image feature, and thus if the (arbitrary) numbering of two features in an image is changed, their feature vectors simply change positions in  $\mathbf{V}$ . The feature vectors for our example are plotted in Figure 3. The left column contains the feature vectors of  $I_1$  (the rows of  $\mathbf{V}_1$ ), while the right column contains the  $I_2$  counterparts. Each graph represents a 4/vector, with the magnitude of the components shown. The abscissa therefore indexes the position of the component in the vector, while the ordinate gives its value (between  $-1$  and  $+1$ ). It is clear, by comparing the 'shapes' of these vectors, that feature 1 in  $I_1$  pairs with feature 1 in  $I_2$ , that feature 2 in  $I_1$  pairs with feature 3 in  $I_2$ , and so on.

The relative similarities between these two sets of features are finally summarized in the association matrix  $\mathbf{Z}$ :

$$\mathbf{Z} = \begin{bmatrix} \mathbf{0.06} & 2.22 & 1.62 & 2.18 \\ 2.33 & \mathbf{1.60} & 0.07 & 1.96 \\ 1.68 & 0.09 & \mathbf{2.35} & 1.65 \\ 1.87 & 2.37 & 1.94 & \mathbf{0.04} \end{bmatrix}$$

The rows in  $\mathbf{Z}$  index features in  $I_1$ , while the columns index features in  $I_2$ . The fourth row, for instance, derives from comparing the fourth row in  $\mathbf{V}_1$  (feature vector  $F_{4,1}$ ) with the four rows in  $\mathbf{V}_2$  (feature vectors

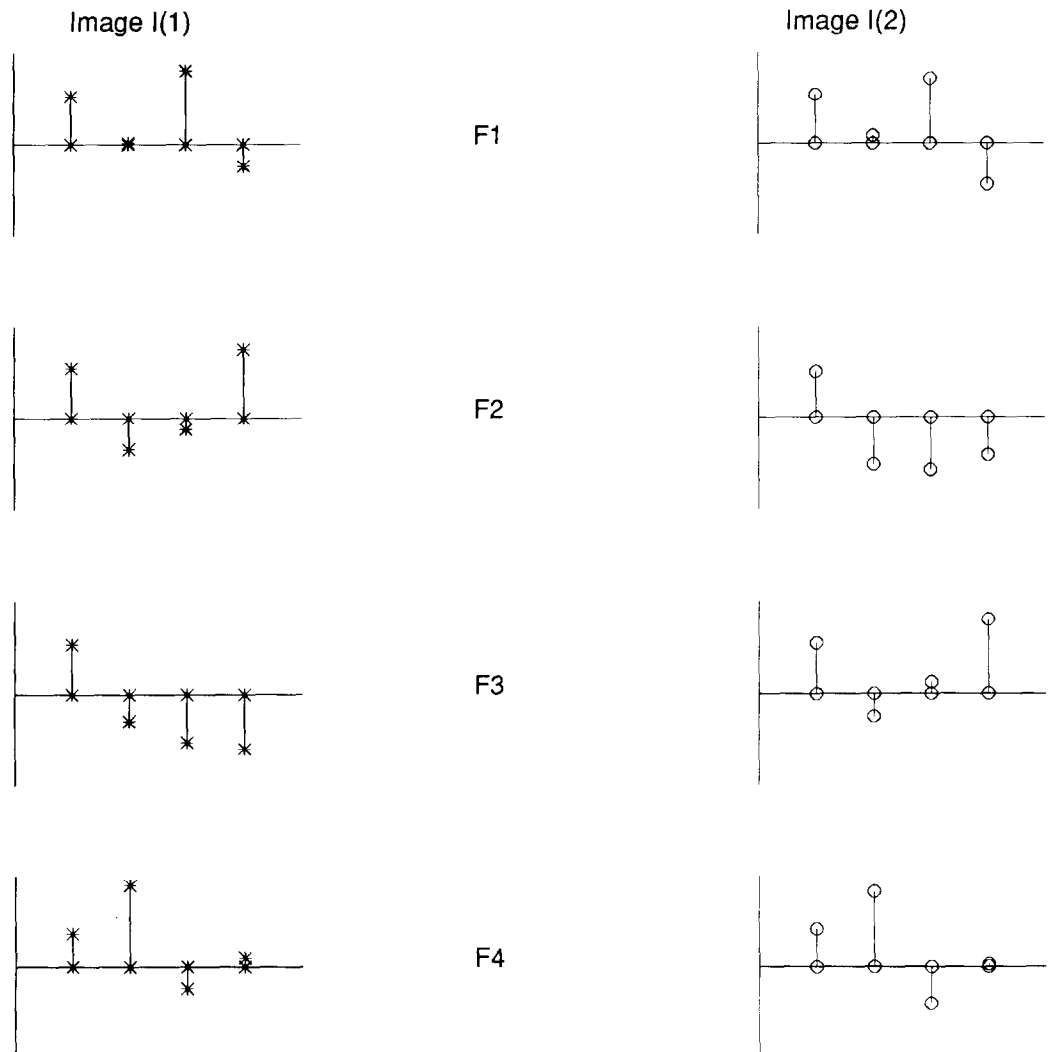


Figure 3. Plots of the eigenvectors in the worked example (see text)

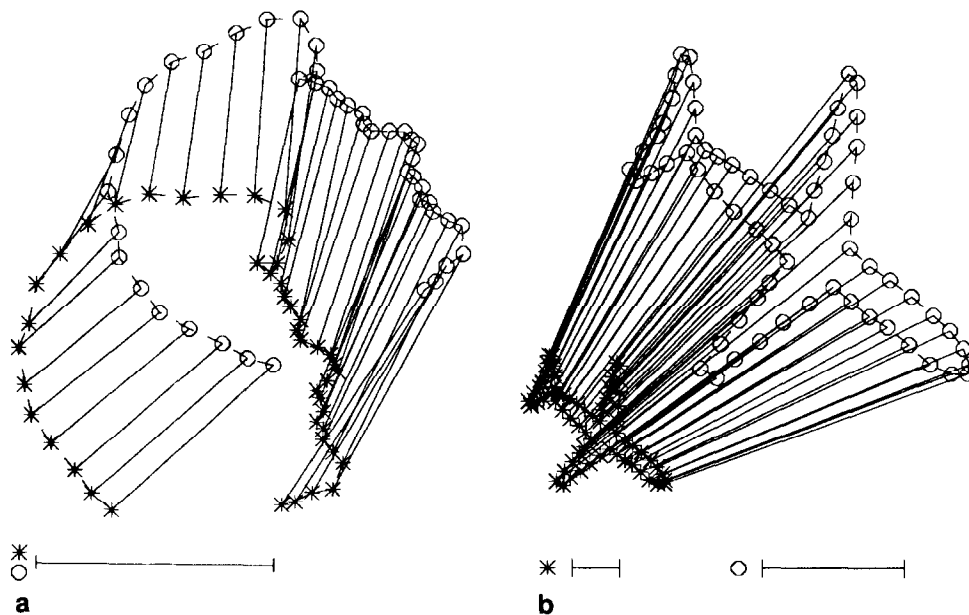


Figure 4. Modal algorithm copes with rotation, translation and scale. (a) Outline of a head translated and rotated in the image plane ( $\Delta x = 5$ ,  $\Delta y = 3$ ,  $\theta = 25^\circ$ ); (b) aero-plane scaled by a factor of  $2\frac{1}{2}$ . Here,  $\sigma_1$  and  $\sigma_2$  are unequal ( $\sigma_2 = 3\sigma_1$ )

$F_{j,2}$ ). The smallest elements are shown in bold and give the correct answer (see Figure 2 caption). Thus, the second feature in  $I_1$  matches the third feature in  $I_2$  (element  $Z_{23}$ ), and so on.

## RESULTS

Because the modes are based solely on the distances between features, the shape description is unaffected by transformations which preserve these distances (such as rotations, translations and reflections in the image plane). This is demonstrated clearly in Figures 1b and 4a ( $\sigma_1 = \sigma_2$  in both cases). The program also

handles uniform scale well (Figure 4b), since scaling the image by  $S$  is equivalent to replacing  $\sigma$  by  $\sigma/S$ . Information about the relative sizes of  $\sigma_1$  and  $\sigma_2$  is contained in the eigenvalues of  $\mathbf{H}_1$  and  $\mathbf{H}_2$ .

Furthermore, our shape description provides information about reflectional symmetries by identifying all possible matches (Figure 5a–d). The symmetries are detected when switching the sign of the axis has no detrimental effect on the match. In such cases, the number of arbitrary sign choices equals the number of (orthogonal) reflectional symmetries. The modes have also proven to be fairly robust to distortions in the image, so long as the global shape doesn't change substantially. Figure 5e shows the performance of the

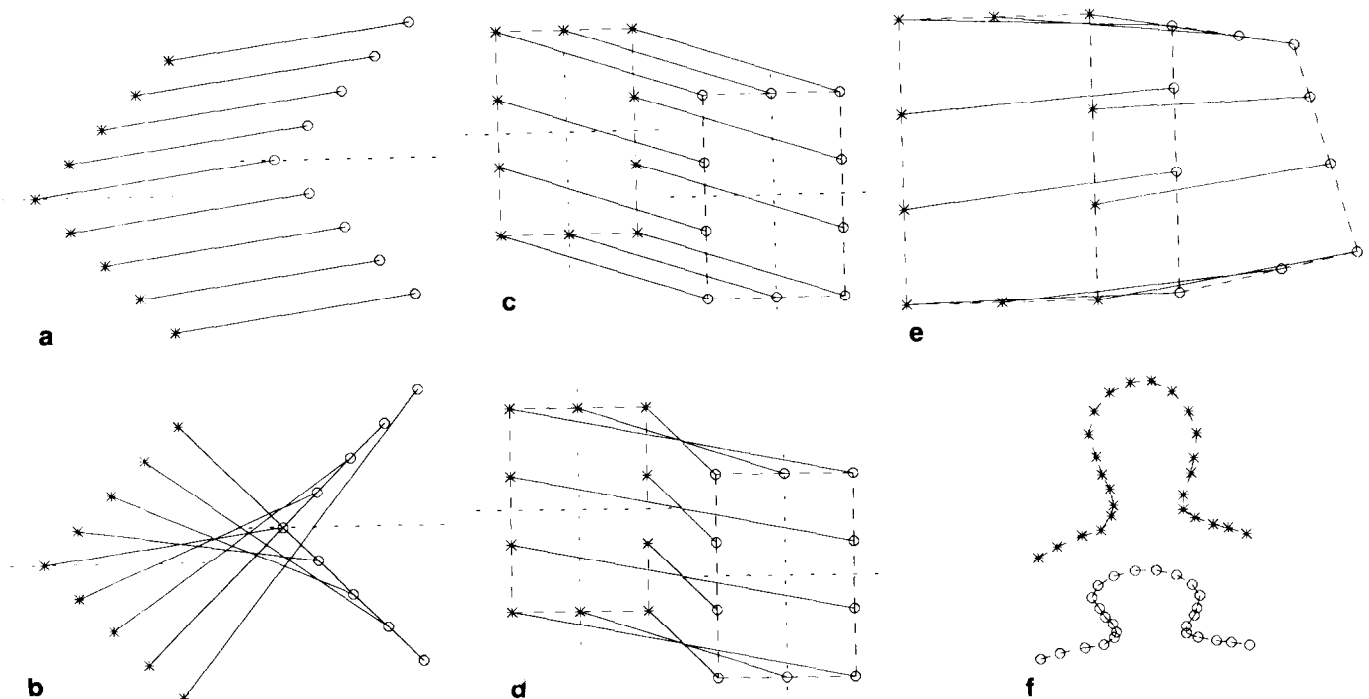


Figure 5. Modal algorithm (dotted lines show symmetry axes). (a) (b) Two possible mappings for a roof-like shape (one reflectional symmetry); (c) (d) two of four possible mappings for a rectangle (two reflectional symmetries); (e) rectangle skewed by small perspective distortion; (f) two skewed shapes whose modes are too dissimilar to match

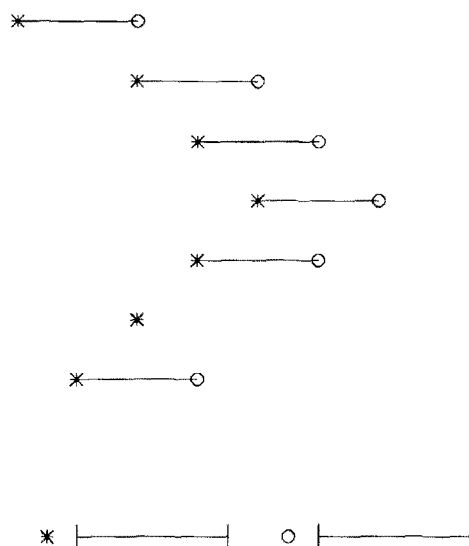


Figure 6.  
Example with  
different  
numbers of  
features in  
each image  
( $m = 7, n = 6$ )

algorithm when faced with small perspective distortion. However, for large slant (Figure 5f), the 'shape' of the figure changes too much and the match is unsuccessful.

Finally, we present an example where the number of features in the images differs (see Figure 6). However, because this requires truncation of the extra modes in one image, the algorithm cannot tolerate too many missing points, a consequence of the global nature of the algorithm. No reliable upper bounds for such cases have yet emerged from our tests, and this is the subject of ongoing investigation.

## CONCLUSION

We have presented a novel correspondence algorithm which generates a modal description of an image based on the spatial distribution of its features. This shape representation allows rotations and translations in the image plane to be handled trivially. The algorithm also copes with uniform scaling and small skews, and moreover detects multiple valid matches arising from reflectional symmetries. From an implementation viewpoint,

the algorithm is well-conditioned, linear in the number of features, and potentially parallelizable; moreover, it gives a one-shot solution. However, as with any global shape representation, the presence of occlusion and multiple moving objects present difficulties which have not yet been resolved.

Future research will address the feasibility of incorporating inter-image feature distances ( $d_{ij}$ ) into the algorithm; at present, only intra-image distances ( $r_{ij}$ ) are used. Rigorous tests on noise tolerance have still to be conducted, and we also intend to investigate rotational symmetries and automatic selection of the  $\sigma$ 's. Finally, many of the applications mentioned in the introduction (such as data and model matching) involve sets of point-features not necessarily related by the transformations we have examined; this important problem remains to be tackled.

## ACKNOWLEDGEMENTS

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