Tree Representation for Image Matching and Object Recognition

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Abstract. The problem of matching two images of the same objects but after movements or slight deformations arises in medical imaging, but also in the microscopic analysis of physical or biological structures. We present a new matching strategy consisting of two steps. We consider the grev level function (modulo a normalization) as a probability density function. First, we apply a density based clustering method in order to obtain a tree which classifies the points on which the grey level function is defined. Secondly, we use the identification of the hierarchical representations of the two images to guide the image matching or to define a distance between the images for object recognition. The transformation invariance properties of the representations allow to extract invariant image points. Using the identification of the trees, they allow, in addition, to find the correspondence between invariant points even if these have moved locally. Then, we obtain the transformation function as the thin plate interpolation of the corresponding point pairs. On the other hand, if we use tree identification, this enables us to propose several criterias to distinguish between real deformations and noise effects. In practice, we treat, for instance, first coarse trees (with few leaves) and pass to ever refining trees, after. The method's results on real images will be discussed.

1 Introduction

The use of structural information in images for recognition tasks has been realized since the inception of machine vision ([22], [23], [1]). A graph structure allows us to represent the extracted information. This structure is useful to represent information about topology and shape of and between the extracted features and therefore to compare two images, but also to guide the process of matching corresponding features coming from two different images. In [10] for instance, an algorithm for matching Delaunay graphs obtained from selected points of segmented lines has been proposed for matching satellite images. If we want to match images in which *local* movements appear (e.g., rigid transformations of *individual* objects in the image or images of deformable objects) a structural representation can also, as will be shown, be used to follow real deformations or

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movements of objects and to distinguish them from noise effects. For this, we have to construct the graph (a tree in our case) in such a way that its structure is kept even if deformations appear or features have moved.

A grey level function $g: \mathbb{R}^n \to \mathbb{R}_{\geq 0}$, n=2 or n=3, with compact support I, associates to each physical point in the image scene (represented by \mathbb{R}^n) a value ($\in \mathbb{N}$ in the technical realization) corresponding to its physical properties and will be considered as being given by the acquisition device. g is eventually smoothed and normalized, in order to have a continuous (or even derivable) density function.

The presented approaches apply density based classification methods ([29], [14], [15],[26]) to the grey level function in order to construct trees. These methods confine points in clusters at several levels if the points are in regions of (respective to the level) high density. We will call the resulting tree (section 2) a confinement (or density) tree representation of the image. If we choose the classification method proposed in [29] and [15] the resulting tree corresponds to the component tree defined in [13]. Under reasonable conditions, we will demonstrate that the presented representation is invariant with respect to an arbitrary topological transformation (section 2).

Matching is done now by identification of the two density trees corresponding to the two images. The method given therefore tries to associate the leaves of the trees and is based on the (intra-) tree distance (defined in section 4), which is robust with respect to instabilities in the trees. The instabilities arise as we transform a continuous function (the grey level function) into a discrete structure. Little noise can result in different tree structures (section 3).

The idea behind this tree representation matching strategy is that the density tree will adapt itself to global and local movements in the image (Figure 1). This allows us to define *characteristic* points (*candidates* for landmarks [4]) and to find corresponding point (i.e., landmark) pairs, associated to nodes in the tree, even if local movements appear. Moreover it allows us to detect if in one of the images a cluster – intermediary node or leave in the tree – has been changed by noise effects (section 4). All this has a series of applications as detailed in section 5.

The main originality of our research work lies in two points:

- To apply hierarchical classification of the points on which the grey level function is defined for image matching, to found this strategy on a topological basis, and to define a distance between two images based on their density tree representation for object recognition.
- To propose a tree identification algorithm which respects local instabilities
 of the tree at all levels. The tree identification problem arises also in other
 domains (Shasha et al. [25]).

In [21] we have already described these principles of the strategy, here we will detail the algorithm and show how to obtain practical results. We will remark that Leu and Huang [18] used a comparison of ordered trees to define a distance between objects for object recognition. However, a tree identification method

able to handle instabilities in the tree is not proposed and the algorithm's suitability to match images where non-affine deformations appear is not investigated. Moreover, the tree construction approach does not use statistical methods, but is of geometrical nature based on the closed¹ contour in a segmented image. A tree matching approach for signal processing has been investigated in [7]. Independently from our work, Kok-Wiles et al. presented in [16] a multi-scale matching approach integrating a hierarchical representation of the image.

A recent general overview of matching algorithms can be found in [20].

The remainder of the paper is organized as follows. In section 2, we detail the construction of the confinement tree and the invariance theorem associated to it. Using the confinement trees of two images we define a distance between them in section 3. In section 4, we show how to apply the hierarchical representations for image matching and present some results on real images in section 5 before concluding in section 6.

2 Construction and Invariance Properties of a Density Tree

Confronted with the classification task based on a density function we were led to a mathematical entity denoted confiner, appearing in a natural way when we look for stochastic equivalents of attractors in [8]. Given a density function $g: \mathbb{R}^n \to \mathbb{R}_{>0}, n \in \mathbb{N}$, the *confiners* are defined as the maximal connected subsets (or components, Gaal [11], p. 105) C_l of the level sets $L_l = \{x \in \mathbb{R}^n | g(x) \geq 1\}$ $l\}, l \in \mathbb{R}_{>0}$. In the classification domain we found these components first in a contribution by Wishart [29] and further investigations by Hartigan [14,15], where they are called high density clusters. Considering them taken on several levels $l_k, k = 1, ..., r$ (r from resolution) including the 0 level, they define obviously a tree (by "set inclusion") as illustrated in Figure 1. The tree is finite if ghas a finite number of extremas. We call this tree confinement (or density) tree and if g is a grey level function (n = 2, 3) of an Image I_g we use the term confinement tree representation of I_q . The confiners taken at level l_k are the nodes (intermediary nodes and leaves) of the tree at level k. We have chosen this classification method because of the invariance theorem and its consequences shown below. Curiously, in the case of point distributions, a corresponding property has already been mentioned in the contributions of Wishart [29] and Hartigan [14,15] (without assuming the paradigm to hold and only in the case of an affine transformation) even if they did not address a matching problem.

In practice, we take all grey levels of the image into account and we delete confiners with a mass (which we calculate as the sum of all normalized grey values associated to the pixels in the confiner) less than a factor λ of the mass of all confiners at this level. We call λ the lop-parameter of the tree representation. We choose the discrete d4-distance for defining the connectivity between pixels.

¹ Simply edge detection [6] is not sufficient.

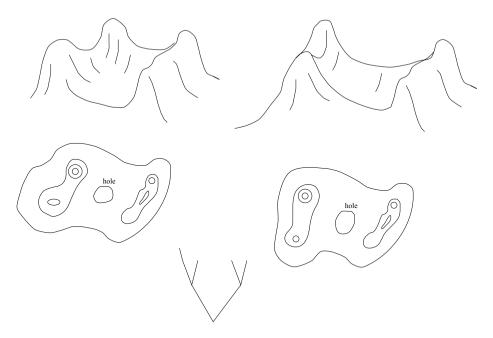


Fig. 1. Illustration of the main advantage and the corresponding tree representation.

The time to calculate the tree is O(rn), where n is the number of pixels and r is the number of levels.

The following hypothesis, which we formulate first in a strong version, is the foundation of the transformation invariance property of our method. In a less rigorous framework we can find similar hypotheses in Optical Flow research [3].

Medical Imaging Paradigm. Let $\phi: A \to B$ be the transformation expressing movements and deformations of objects in the images A and B which appear when passing from A to B, f_A the density associated to image A, f_B that associated to image B, and X an image point of the image A. Then we can assume $f_A(X) = f_B(\phi(X))$ (apart from local noise effects).

Let us remark that: (1) for the paradigma to hold we should consider images covering the whole space in which movements appear (thus, 3D images in general) and that the paradigma is a realistic assumption in a larger context than in medical imaging but not in general; (2) if for two images A and B the acquisition device (or its location) has changed we have to assume $f_A(X) = \alpha f_B(\phi(X)) + \beta$, where α and β can be calculated a priori. The following theorem still holds under this assuption.

Invariance Theorem. Let A, B, f_A, f_B , and ϕ be defined as in the Paradigma. Then: if ϕ is a topological application, then, apart from noise effects, the density trees (constructed as proposed above) of images A and B are identical, moreover, the confiners of A are transformed into the confiners of B.

According to the definition (Gaal [11], pp. 186, 187) a topological transformation is bijective and bicontinuous (i.e., ϕ and ϕ^{-1} are both continuous). As the image of a maximal connex set under a topological application stays a maximal connex set, ϕ induces, using the paradigm, a bijection between the nodes of the two trees; this proves the theorem (see [21]).

The importance of the property lies on the fact that the tree is invariant referred to local movements. The effect of noise will be detailed below.

We will remark that an octree [24], for instance, would not have this invariance property. However, in the next section we will be confronted with a problem associated to this approach.

3 Image Distance and Noise Sensitivity

Algorithms used to compare trees have been developed according to their domain of application. In hierarchical clustering and taxonomy Boorman and Olivier [5] and Farris [9] compared the shapes of two taxonomic trees. These trees have labeled leaves called OTUs which are the same in both trees. Boorman and Olivier decomposed the trees in terms of simpler structures for which adequate metrics are available. These simpler metrics are then used to induce a distance on trees. Farris referred to the number of nodes on the path between the OTUs as the *cladistic difference* between the OTUs and compared the differences corresponding to the same OTUs. Using the idea of language transformation Lu [19] derived one tree from the other by a series of elementary transformations, with applications in pattern recognition. The distance between the two ordered trees is the minimum-cost sequence of transformations. Zhang et al. [30] extended this distance definition to unordered trees, this makes its calculation a NP-complete problem (Zhang et al. [30]). Shasha et al. [25] proposed an enumerative algorithm and some heuristics for the distance calculation. Restricting the allowed tree transformations Tanaka [27] achieved a polynomial matching algorithm. Our inter-tree distance is an extension of Farris's comparison of the cladistic differences.

Let us denote the two trees to compare by A and B. Our distance definition is based on the *(intra-) tree distance dT* associated to a tree T (T = A or T = B), which is defined for each couple of nodes (L1, L2) by the sum of the weights (for the definition of the weights see section 5) associated to the edges in the path which relates the nodes in the tree (Barthélemy and Guénoche [2]). Let Nodes(A) (resp. Leaves(A)) denote the set of nodes (resp. leaves) of the tree A. A mapping a from Leaves(A) into Nodes(B) is represented by a set of couples $a = \{(A_i^L, B_i)_{1 \le i \le M}, A_i^L \in \text{Leaves}(A), B_i \in \text{Nodes}(B)\},$

(M denotes the number of leaves in A; $B_i = B_j$ for $i \neq j$ is allowed). The cost C(a) of such a mapping is

 $C(a) = \sum_{1 \le i \le j \le M} |dB(B_i, B_j) - dA(A_i^L, A_j^L)|.$

Let $\mathcal{M}(A, \overline{B})$ denote the set of all possible mappings from Leaves(A) into Nodes(B). The *inter-tree distance* is defined by:

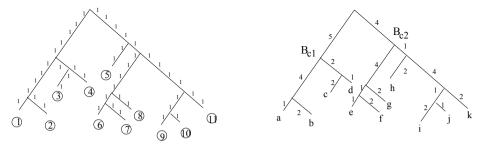
$$d(A,B) = \frac{1}{M^{2}-M} \min_{a \in \mathcal{M}(A,B)} C(a) + \frac{1}{(M')^{2}-M'} \min_{b \in \mathcal{M}(B,A)} C(b), \tag{1}$$

where M (resp. M') denotes the number of leaves in A (resp. B).

A problem concerning the invariance of the trees occurs, if more than two confiners merge together at the same level approximately (see Figure 2). If, due to noise, the order of fusion changes, we will have an exchange between the confiner subtrees. Our approach to deal with this is the use of the (intra) tree distance in the definition of the inter-tree distance above. We call this problem the problem of simultaneous fusion. Figure 3 illustrates the robustness of the use of our inter-tree distance d(A, B).



Fig. 2. Illustration of the problem of simultaneous fusion.



Tree A (total weight = 44, weight constant = 1)

Tree B (total weight = 44, weight constant = 1)

Fig. 3. Example for weighted trees A and B (each edge is weighted by a certain number of 1's) with a subtree exchange and illustration of the robustness of the intra-tree distance: for instance |dA(1,5) - dB(a,h)| = |16 - 18| < |dA(1,5) - dB(a,e)| = 4. If $A_k^L = A_{k_0}^L = 5$ and $B_{k_0} = r(B)$, we have $A_{k_r} = A$, $A_{k_1}^L = 2$, $A_{k_2}^L = 9$ and we get $bestfit(B_{c_2}) = 3$ for the leaves h, b, i and $bestfit(B_{c_1}) = 7$ for the leaves d, f, b.

4 Matching Algorithm

Here we present an algorithm that we have designed to identify the two resulting trees. Its interest lies in its efficiency in computation time and in its robustness with respect to small differences between the two trees due to noise. The central theme behind our algorithm can be seen as the association of the leaves of A to the nodes of B such that the minimum $\min_{a \in \mathcal{M}(A,B)} C(a)$ in (1) is achieved, or reciprocally for $\min_{b \in \mathcal{M}(B,A)} C(b)$. In order to minimize the cost function we could apply a nonlinear optimization method as graduated assignement [12]. This is currently under research. The here presented algorithm makes use of the special characteristics of the problem such as the possibility to integrate geometrical information. First, let us introduce some notations.

With subtree(N), where N is a node, we denote the subtree rooted in N. We will also use the notations father(N), confiner(N), and r(T) = root(T) in the evident sense, child(N) for the set of all children of node N. mass(N) as the sum over all weights in subtree(N), and q_T (T=A or T=B) for the grey level function associated to T.

In the following algorithm we try to associate each leaf (or a certain number of selected leaves, see section 5) A_k^L of A to a node B_k of B by moving the leaf A_h^L downwords in the tree B.

Initialization:

We initialize the leaves of A on the root of B.

Bifurcation:

If A_k^L is associated to node B_{k_0} we are looking for the child of B_{k_0} which minimizes the best fit value which we are defining now:

 $A_{k_0} := \text{root of the subtree containing } A_k^L \text{ and minimizing } |mass(B_{k_0}) - mass(A_i)|,$ $1 \leq i \leq M$;

 $A_{k_0}^L := A_k^L;$

 $A_{k_1}^{L^U} := \text{leaf in } subtree(A_{k_0}) \text{ with largest distance from } A_k^L;$ $A_{k_2}^L := \text{leaf in } subtree(A_{k_0}) \text{ which maximizes the sum of its distances to } A_k^L \text{ and } A_{k_1}^L.$ For each $B_{k_c} \in child(B_{k_0})$ do:

 $bestfit(B_{k_c}) := minimum of the sum below while minimizing over all triplets$ $(B_{k_0}^L, B_{k_1}^L, B_{k_2}^L)$, with leaf $B_{k_0}^L$ in $subtree(B_{k_c})$ and leaves $B_{k_1}^L, B_{k_2}^L$ in B:

$$\sum_{0 \le i < j \le 2} |dA(A_{k_i}^L, A_{k_j}^L) - dB(B_{k_i}^L, B_{k_j}^L)| + \sum_{i=0}^2 |dA(A_{k_i}^L, r(A)) - dB(B_{k_i}^L, r(B))|.$$
 (2)

Return the child $B_{k_{best}} \in child(B_{k_0})$ realizing the min of the best fit among all those childs.

If the bifurcation corresponds to a subtree with just two leaves, we use a geometrical criterion easy to define (based on the barycenters of the concerned confiners).

We will remark, as we are minimizing over all leaves $B_{k_1}^L, B_{k_2}^L$ in the whole tree B to define best fit, that it does not care if $subtree(A_{k_0})$ does not correspond exactly to $subtree(B_{k_0})$

If we fall short of a certain level of resolution the influence of noise can become important. In our practical applications this was only the case at the last bifurcations of some of the branches (section 5). Therefore we could use the geometrical criterion based on the barycenters of the concerned confiners for the decision at the last bifurcation (see Figure 5,6). For instance, we impose a limit for the distortion of the transformation function (visualized by the grid in Figure 6). Or we set bounds for the values $relPos(N_1, N_2, \phi)$ (eventually normalized by $min(relPos(N_1, N_1, id), relPos(N_2, N_2, id))$), where we define $relPos(N_1, N_2, \phi)$, the relative position between N_1 of A and N_2 of B, as the normalized sum

$$\sum_{P_1 \in C_1, P_2 \in C_2} \frac{(g_A(P_1) + g_B(\phi(P_2)))d(P_1, \phi(P_2))}{mass(N_1) + mass(N_2)},$$

where $C_1 = confiner(N_1)$, $C_2 = confiner(N_2)$, and where $d(P_1, P_2)$ is the euclidian distance between the points (pixels) P_1 and P_2 . Another way to define a stop criterion is to demand that, if $B_{i_{best2}}$ is the second best choice after $B_{i_{best}}$, that: $bestfit(B_{i_{best2}}) > 2bestfit$. A third way consist in taking the leaves B_0^L, B_1^L, B_2^L for which the minimum for bestfit (in equation (2)) is achieved and search for them the leafs in $subtree(A_{k_0})$ realizing the minimum in equation (2) written for B_0^L, B_1^L , and B_2^L as initial leaves. If the leaf corresponding to B_0^L is not in the same subtree of $subtree(A_{k_0})$ as $A_{k_0}^L$ we stop and remove it if other selected leaves $A_{k_0}^L$ are in $subtree(A_{k_0})$. If not, we associate A_{k_0} and B_{k_0} .

Another way to identify the two trees is based on the lop parameter λ (section 2). We lop A and B with lop parameter $\lambda 1$ such that just 5 leaves rest in A and and we associate the leaves in A with the nodes in B minimizing the cost function. We remove outliers from the mapping. After, we choose $\lambda 2$ such that 6 leaves appear in A and associate the new leaf, minimizing the cost function, where we fix the previous mapping, and so on (Figure 7).

5 Applications

Applications of our method include the study of the relative movement of grains in microscopic metallurgical images or of cells in microscopic biological images. On the other hand, we can also employ our method to detect asymetries in breast or brain images, or to detect where in an image movements occur. In the first case this serves to detect a tumor and its location. In the second case the method helps us to apply watershed, optical flow or active contour techniques at the found place. If we just want to rediscover the affine transformation between two succesive 2D slides of a 3D image, we apply a least square minimization of the euclidean distance between the corresponding invariant characteristic points found by our identification algorithm. An alternative to this is to proceed as Thirion [28] for matching extremal points and just to define the characteristic points with the help of the trees.

A further interesting application of the proposed method is the comparison of two brain images resulting from functional MRI. Here occur small local deformations as well as global shifts. The aim is to locate positions where the brain activation (and therefore the intensity of the functional signal) changed.

The Figure 4 shows the tree representations of the images and the selected nodes of the trees. The selected nodes are the nodes in the middle of the subbranches presenting the largest number of tree levels between two bifurcations and having no subbranch with the same property as successor. Figure 5 shows the new position in the lower tree of Figure 4 of the selected nodes of the upper tree after the application of our matching algorithm which we simplified. We get the best results (Figure 5) when we weight each edge of the tree just by a constant such that both trees have the same total weight. This results from the fact that the changes in grey intensity are larger than those concerning the topological structure, especially in the upper right part of the brain, where a tumor is located. However, for detecting the tumor or its location after matching, weights constructed from the intensity values contain useful information.

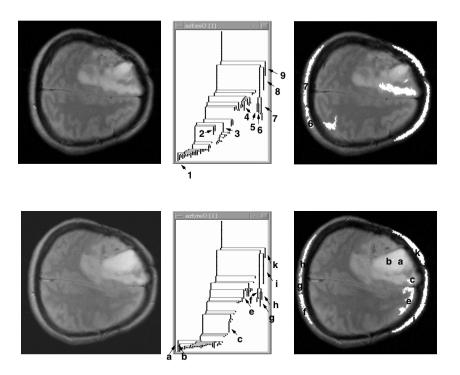
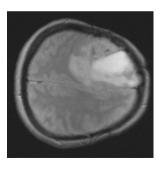


Fig. 4. Top left: Initial image of the upper slide of the brain image; middle: corresponding density tree; top right: highlighted confiners as marked by the arrows in the tree; bottom: the same as above for lower slide of the brain image.





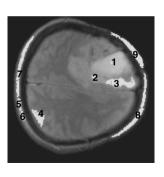
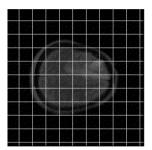
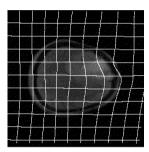


Fig. 5. Initial image of the lower slide of the brain image on the left, confiners found after tree identification marked by arrows in the corresponding density tree in the middle, and highlighted confiners as marked by the arrows in the tree on the right. Outlier 2 can be removed with one of the stop criteria.





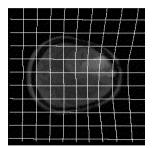
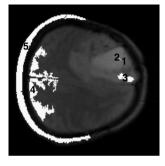
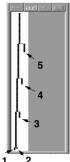
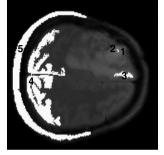


Fig. 6. Initial image of the upper slide of the brain image with initial grid on the left, image of the lower slide and transformed grid after thin plate spline interpolation based on the confiners in the figure before except confiner 2 in the middle, and transformed grid based on the same confiners except confiner 2 and confiner 3 on the right.







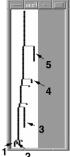


Fig. 7. From left to right: (1) Image of the lower slide of the brain image and highlighted confiners as marked by the arrows in the tree next to it, (2) tree A loped such that just 5 leaves occur, image of the upper slide with highlighted confiners as marked by the arrows in the tree on its right, (4) tree B loped with the same lop parameter as tree A.

6 Conclusion

We showed the usefulness of a tree representation of a density or grey level function known in statistics (density or confinement tree) and in image analysis (component tree). We based this on a topological invariance theorem we could establish under reasonable (in practice) hypothesis, which justifies the use of this tree for image matching and object recognition. In order to get practical results we have presented a tree identification algorithm and several criteria for detecting automatically the level at which the resolution becomes noise sensitive.

References

- Barrow, H.G., Poppelestone, R.J.: Relational Descriptions in Picture Processing. Machine Intelligence 6 (1971) 377–396
- Barthélemy, J.-P., Guénoche, A.: Les arbres et les représentations des proximités. Masson, Paris, (1988)
- 3. Black, M. Jepson, A.D.: Estimating optical flow in segmented images using variable-order parametric models with local deformations. IEEE Trans. PAMI 18 (1996)
- Bookstein, F.: Principal wraps: Thin-plate splines and the decomposition of deformations. IEEE Trans. PAMI 11 (1989) 567–585
- 5. Boorman, S.A., Olivier, D.C.:Metrics on spaces of finite trees. J. Math. Psych. 10 (1973)
- 6. J. Canny: A computional approach to edge detection. IEEE Trans. PAMI 8 (1986) 679--698
- Cheng, Y.C., Lu, S.Y.: Waveform correlation by tree matching. IEEE Trans. PAMI 7 (1985) 299–305
- Demongeot, J., Cosnard, M., Jacob, C.: Attractors and confiners: Deterministic and stochastic approaches. In: Diner, S., Fargue, D., Lochak, G. (eds.): Dynamical systems

 A renewal of mechanism. Centennial of Gorge David Birkhoff. World Scientific, Singapore (1986)
- Farris, J.S.: A successive approximations approach to character weighting. J. Syst. Zool. 18 (1969) 374–385
- Finch, A.M., Wilson R.C., Hancock, E.R.: Matching Delaunay graphs. Pattern Recognition 30 (1997) 123–140
- 11. Gaal, S.A.: Point set topology. Academic Press, New York, (1964)
- Gold, S., Rangarajan, A.: A graduated assignment algorithm for graph matching. IEEE Trans. PAMI 18 (1996) 377–388
- Hanusse, P., Guillataud, P.: Sémantique des images par analyse dendronique. In: AFECT, 8th Conf. Reconnaissance des Formes et Intelligence Artificielle, Vol. 2. Lyon (1992) 577–588
- 14. Hartigan, J.A.: Clustering algorithms. Wiley, New York, (1975)
- 15. Hartigan, J.A.: Statistical theory in clustering. J. of Classification 2 (1985) 63–76
- Kok-Wiles, S.L., Brady, J.M., Highnam, R.: Comparing mammogram pairs for the detection of lesions. In: Karssemeijer, N. (ed.): 4th International Workshop of Digital Mammography, Nijmegen, Netherlands, June 1998. Kluwer (1998)
- Lavallée, S., Szeliski, R.: Recovering the position and orientation of free-form objects from image contours using 3D distance maps. IEEE Trans. PAMI 17 (1995) 378–390

- Leu, J.G., Huang, I.N.: Planar shape matching based on binary tree shape representation. Pattern Recognition 21 (1988) 607–622
- Lu, S.-Y.: A tree-to-tree distance and its application to cluster analysis. IEEE Trans. PAMI 1 (1979) 210–224
- Maintz, J.B.A., Viergever, M.A.: A survey of medical image registration. Medical Image Analysis 2 (1998) 1–36
- 21. Mattes, J., Demongeot, J.: Dynamic Quantization, Classification, and Imaging. In: 22nd Annual Conference of the Gesellschaft für Klassifikation e.V., Dresden, Germany, March 1998. Studies in Classification, Data Analysis, and Knowledge Organization. Springer-Verlag, Berlin Heidelberg New York (to appear)
- 22. Pavlidis, T.: Analysis of set patterns. Pattern Recognition 1 (1968)
- 23. Rastal, J.S.: Graph family matching. Research Memorandum, MIP-R-62. Departement of Machine Intelligence and Perception Edinburgh (1969)
- 24. Samet, H.: The design and analysis of spatial data structures. Addison Wesley Publishing Company, Reading, Massachusetts (1990)
- Shasha, D., Wang, J.T.-L., Zhang, K., Shih, F.Y.: Exact and approximate algorithms for unordered tree matching. IEEE Trans. Syst., Man, Cybern. 24 (1994) 668–678
- Silverman, B.W.: Density estimation for statistics and data analysis. Chapman and Hall, London (1986)
- Tanaka, E.: A metric between unroted adn unordered trees and its bottom-up computing method. IEEE Trans. PAMI 16 (1994) 1233–1238
- 28. Thirion, J.-P.: New feature points based on geometric invariants for 3D image registration. International Journal of Computer Vision 18 (1996) 121–137
- Wishart, D.: Mode analysis: A generalization of the nearest neighbor which reduces chaining effects. In: Cole, A. J. (Ed.): Numerical Taxonomy. Academic Press, London (1969) 282–319
- Zhang, K., Statman, R., Shasha, D.: On the editing distance between unordered labeled trees. Information Processing Letters 42 (1992) 133–139