# Hierarchical Matching of Panoramic Images *

Roland Glantz and Marcello Pelillo
Dipartimento di Informatica, Università Ca' Foscari di Venezia
30172 Venezia Mestre, Italy
{glantz,pelillo}@dsi.unive.it

Walter G. Kropatsch
Pattern Recognition and Image Processing Group
Institute of Computer Aided Automation 183/2, Vienna University of Technology
A-1040 Vienna, Austria
krw@prip.tuwien.ac.at

## Abstract

*When matching regions from "similar" images, one typically has the problem of missing counterparts due to local or even global variations of segmentation fineness. Matching segmentation hierarchies, however, not only increases the chances of finding counterparts, but also allows us to exploit the manifold constraints coming from the topological relations between the regions in a hierarchy. In this paper we match hierarchies from panoramic images by constructing an association graph $G_A$ whose vertices represent potential matches and whose edges indicate topological consistency. Specifically, a maximal [maximum] weight clique of $G_A$ corresponds to a topologically consistent mapping with maximal [maximum] total similarity. To find "heavy" cliques, we adapt a greedy pivoting-based heuristic to the weighted case. Experiments on pairs of panoramic images demonstrate the reliability of the results.*

## 1. Introduction

Vision tasks such as detection, recognition, and tracking usually involve segmentation. Although, in general, the segmentation method must be chosen according to the application (segmentation itself is an ill-defined problem), the following situation is quite common.

- The segmentation method allows for various levels of fineness.
- For selected levels of fineness the corresponding segmentations form a hierarchy in the sense that a region from a coarser segmentation is the union of regions from a finer segmentation.
- The optimal level of fineness, if any, is a local property.
- One-to-one correspondences between regions and real world objects are rare. Often a region merely contains or is contained in a region corresponding to a real world object.

Hence, it is often a good idea to consider hierarchies of segmentations instead of single segmentations determined by a fixed level of fineness.

For recognition tasks, another reason to employ hierarchies is that the objects are often also hierarchical. In the following, our perspective is purely two-dimensional, i.e. we do not address problems (like occlusion) coming from the fact that three-dimensional objects in a three-dimensional world are represented by two-dimensional regions of two-dimensional images. Recognizing the same hierarchical object in two segmentation hierarchies thus means to find a one-to-one hierarchy-preserving mapping between regions of one hierarchy and regions of the other hierarchy. Besides preservation of the hierarchy, it is natural to require that topological relations as the (non-) neighborhood relation and the (non-) enclosure relation are also preserved. For an example see Figure 1.

To define all relations in a consistent way, we employ a framework for hierarchical segmentation [5] in terms of topological minors [4]. Specifically, a segmentation step corresponds to taking a topological minor of a plane graph, which, in turn, corresponds to coarsening a finite topology [13]. In the experiments we employ a new hierarchical segmentation method motivated by the intuitive notion of watersheds [5]. It avoids many problems associated

*This work is supported by the Austrian Science Foundation (FWF) under grant P14445-MAT and by MURST under grant MM09308497.

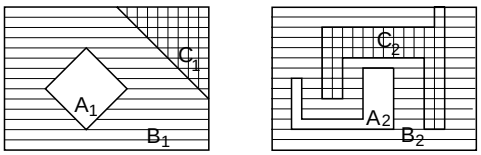


**Figure 1. The mapping $A_1 \rightarrow A_2$, $B_1 \rightarrow B_2$, $C_1 \rightarrow C_2$ is topologically consistent.**

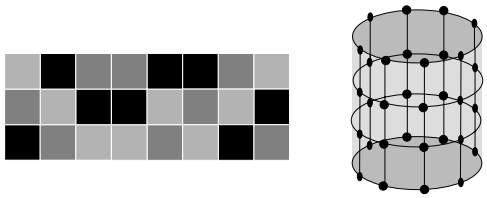

**Figure 2. A panoramic image (left) and the corresponding spherical graph (right) with 26 regions.**

with classical watershed approaches [11]. In particular, the basins are now separated by one-dimensional elements instead of (two-dimensional) pixels and the topological relations between the basins are well-defined. Technically, segmentation is done by dual graph contraction [8].

To find topologically consistent mappings with high total similarity between the matched regions, we propose to construct an association graph whose vertices represent potential matches and whose edges indicate topological consistency. In particular, a consistent mapping with maximal [maximum] total similarity between the matched regions corresponds to a clique with maximal [maximum] total weight in the association graph. To find "heavy" cliques we employ a variant of the pivoting-based heuristic presented in [10].

The paper is organized as follows: In Section 2 we explain our hierarchical segmentation method for the special case of panoramic images. The definitions of the topological relations and the association graph are given in Section 3. The heuristic to find consistent matches with a high total similarity is sketched in Section 4 and experimental results are presented in Section 5.

## 2. Segmentation of Panoramic Images

### 2.1. Graph-based representations

In our approach an image takes the form of an embedded graph, the vertices, edges and regions of which play the roles of the zero-, one-, and two-dimensional cells of a cellular complex [7]. The cylindric nature of panoramic images suggests to construct a graph $G$ which is embedded on a cylinder as illustrated in Figure 2. Specifically, the pixel corners and pixel borders of the panoramic image are represented by the vertices and edges of $G$, respectively. Thus, each pixel corresponds to exactly one region of $G$ on the mantle of a cylinder in $\mathbb{R}^3$. However, we also consider the bottom and the top disk of the cylinder as regions of $G$. A a consequence, $G$ allows a spherical embedding and, by stereographic projection [13], an embedding on $\mathbb{R}^2$. In particular, we may encode panoramic images by plane graphs as defined below.

Throughout the paper a *graph* $G = (V, E, \iota)$ is given by a finite set $V$ of elements called vertices, a finite set $E$ of elements called edges with $E \cap V = \emptyset$, and an incidence relation $\iota$ which associates with each edge $e \in E$ a subset of $V$ with one or two elements. The vertices in $\iota(e)$ are called the end vertices of $e$. Note that the definition includes graphs with self-loops (i.e. edges with only one end vertex) and multiple edges (i.e. several edges with identical sets of end vertices). A graph is called *simple*, if it has neither self-loops nor multiple edges.

In the following, we restrict ourselves to a special class of plane graphs, i.e. plane graphs defined in terms of *arcs* and *closed polygons*. Arcs and closed polygons are concatenations of finitely many straight line segments in $\mathbb{R}^2$. While an arc is homeomorphic to the closed unit interval $[0, 1]$, a closed polygon is homeomorphic to the unit circle in $\mathbb{R}^2$ [4]. On one hand, the restriction to this special class of plane graphs allows us to adopt the approach towards the definition of plane graphs chosen in [4]. On the other hand, the special class is general enough to deal with pixel-based images, Voronoi- and Delaunay-diagrams. In this paper a *plane* graph is a graph $G = (V, E, \iota)$ such that

- $V \subset \mathbb{R}^2$.
- For all $e \in E$ the set $e \cup \iota(e)$ is either an arc or a closed polygon. The set $e \cup \iota(e)$ is a closed polygon, if and only if $e$ is a self-loop.
- For each $e \in E$ such that the set $e \cup \iota(e)$ is an arc and for each homeomorphism $h_e : [0, 1] \mapsto e \cup \iota(e)$ it holds that $h_e\{0, 1\} = \iota(e)$.
- $e_1 \cap e_2 = \emptyset$ for all $e_1 \neq e_2 \in E$.

In contrast to [4] the end vertices of an edge do not belong to the edge. Thus, $G$ partitions $\mathbb{R}^2$ into points from $V$, piecewise linear elements from $E$, and *regions*, i.e. the connected components of $\mathbb{R}^2 \setminus (V \cup E)$. The set of all regions is denoted by $\overline{V}$. If $g$ is a mapping from $\overline{V}$ to $\mathbb{R}_0^+$, the triple $(G, \overline{V}, g)$ is called *plane image* (with gray values $g(\cdot)$). Note that the "gray values" may also reflect geometric region properties.

## 2.2. Segmentation hierarchies

Intuitively speaking, an edge from $E$ always separates at most two elements from $\overline{V}$. Formally, the elements separated by $e$ are the unique (and possibly identical) elements $\overline{v}, \overline{w} \in \overline{V}$ such that $\overline{v} \cup e \cup \overline{w}$ is an open subset of $\mathbb{R}^2$. This defines a mapping $\overline{\iota}(\cdot)$ from $E$ to the one- or two-element subsets of $\overline{V}$ and thus a graph $\overline{G} = (\overline{V}, E, \overline{\iota})$. The graph $\overline{G}$ is the dual of the graph $G$ [4]. Note that the edge sets of $G$ and $\overline{G}$ are identical. Thus, a (one-dimensional) element of $E$ serves to relate a pair of zero-dimensional elements from $V$ and a pair of two-dimensional elements from $\overline{V}$. In terms of cellular complexes [7] the elements of $V$, $E$, and $\overline{V}$ play the roles of zero-, one-, and two-dimensional cells, respectively. Formally, set

$$\mathcal{C} := V \cup E \cup \overline{V} \quad \text{and} \quad dim(c) := \begin{cases} 0 & \text{if } c \in V, \\ 1 & \text{if } c \in E, \\ 2 & \text{if } c \in \overline{V}. \end{cases}$$

Special neighborhoods of cells, so called stars, serve (1) to equip $\mathcal{C}$ with a finite topology, the so called star-topology [1], and (2) to define the topological relations in Section 3.

The star of a cell $c$ is a set of cells containing $c$ and the *higher-dimensional cells adjacent to* $c$ [1].

$$star(c) := \begin{cases} \{c\} & \text{if } c \in \overline{V}, \\ \{c\} \cup \overline{\iota}(c)\} & \text{if } c \in E, \\ \bigcup (star(e) : c \in \iota(e)) & \text{if } c \in V. \end{cases}$$

As shown in [5], segmenting $(G, \overline{V}, g)$ corresponds to coarsening the star topology derived from $G$, which, in turn, corresponds to taking a topological minor $G_M$ of $G$ (i.e. $G_M$ has a subdivision which is a subgraph of $G$). Thus, any segmentation of $(G, \overline{V}, g)$ can be written as $(G_M, \overline{V_M}, g')$, where $G_M$ is a topological minor of $G$. Conversely, each $(G_M, \overline{V_M}, g')$, where $G_M$ is a topological minor of $G$, is a segmentation of $(G, \overline{V}, g)$. In particular, we may define hierarchies of segmentations in terms of topological minors.

**Definition 2.1 (Hierarchy of segmentations)** *Let $\mathcal{I}_{i=0}^m = (G_i, \overline{V_i}, g_i)_{i=0}^m$ be a sequence of plane images such that $G_{i-1}$ is a topological minor of $G_i$, $1 \leq i \leq m$. Then, the sequence $\mathcal{I}_{i=0}^m$ is called a hierarchy of segmentations.*

Technically, the generation of topological minors can be done by the iteratively parallel method *dual graph contraction* [8]. In particular, it suffices to specify the conditions for edge contractions in $G$ and in $\overline{G}$.

## 2.3. Morphological segmentation

Morphological segmentation methods rely on the intuitive idea of flooding a topographic surface in order to find the watersheds and to determine the catchment basins [11]. The topographic surface, in turn, is often derived from the original image by means of an edge filter [12]. Our graph-based concept allows to employ edge filters whose responses refer to (one-dimensional) edges instead of (two-dimensional) pixels. If $(G, \overline{V}, g)$ is a plane image and if $E$ is the edge set of $G$, an edge filter is a mapping $f : E \mapsto \mathbb{R}_0^+$. For the experiments in this paper we chose the absolute gray value difference

$$f(e) := |g(\overline{v}) - g(\overline{w})|\,, \text{ where } \overline{\iota}(e) = \{\overline{v}\} \cup \{\overline{w}\}, \quad (1)$$

if both $\{\overline{v}\}$ and $\{\overline{v}\}$ are not background regions. Otherwise, $f(e)$ is set to a value exceeding all responses that do not involve the background regions. The following is invariant to strictly monotonic variations of $f(\cdot)$. Merging regions in the classical watershed approach now corresponds to removing *weak* edges, i.e. edges $e \in E$ such that $f(e)$ is minimal with respect to all edges bounding the same region. Formally, $e$ is weak, if there exists $\overline{v} \in \overline{V}$, $\overline{v} \in \overline{\iota}(e)$ such that $f(e) \leq f(e')$ for all $e'$ with $\overline{v} \in star(e')$. Let $G_C$ denote the subgraph of $G$ induced by the non-weak non-bridges. Then the *morphological segmentation* of $(G, \overline{V}, g)$ is the plane image $(G_M, \overline{V_M}, g_M)$, where

- $G_M$ is the plane graph obtained from $G_C$ by concatenating all edges separated by vertices of degree 2,
- $\overline{V_M}$ are the regions of $G_M$, and
- $g_M(\overline{V_M})$ is the size-weighted mean gray value of the regions merged into $\overline{V_M}$.

Another application of the edge filter $f$, this time on $(G_M, \overline{V_M}, g_M)$, brings us back to the initial situation, and so on. The result of this procedure is a hierarchy of segmentations (see Definition 2.1).

Note that the number of regions from $G_M$ is at most half the number of regions from $G$. Thus, the topological minor obtained after at most $log_2(|\overline{V}|)$ steps (after each step $f(\cdot)$ is updated) will have but one bounded region. This not only guarantees to arrive at segmentations with a small number of regions, as is indispensable for the methods introduced in the next sections. It also guarantees that the whole hierarchy of segmentations can be computed in $O(log(|\overline{V}|))$ parallel steps [6].

In the experiments (see Section 5), however, we observed that merging via small regions may yield non-robust results. Specifically, let $\overline{v}_1$, $\overline{v}_2$, and $\overline{v}_3$ be three regions of $G$ such that $\overline{v}_1$, $\overline{v}_3$ are large, $\overline{v}_2$ is small, and the gray value of $\overline{v}_2$ lies in between those of $\overline{v}_1$ and $\overline{v}_3$. Then, it may happen that $\overline{v}_1$ and $\overline{v}_3$ are merged via $\overline{v}_2$. To prevent merging via small regions, we introduce directions of contractions in $\overline{G}$ and

1. set the attribute of a directed edge to the product of the $f$-value of the corresponding undirected edge and the size of the region at the source of $e$,
2. contracting an edge only if it points from a smaller to a larger region,
3. never contract two edges with the same source.

The result of this procedure is a segmentation hierarchy as defined at the end of Section 2. For an example see Figure 4.

## 3. A new association graph

The plan of the section is as follows. A subset relation, a neighborhood relation, an enclosure relation, and combinations thereof (see Figure 3) are defined for pairs of regions from possibly different topological minors in a segmentation hierarchy. Then, the topological association graph is defined via topological consistency of potential matches between regions from different hierarchies.

In the following, let $(G_i, \overline{V_i}, g_i)_{i=0}^m$ be a segmentation hierarchy with $G_i = (V_i, E_i, \iota_i)$ for all $i$. Furthermore, let $\overline{v} \in \overline{V_i}$ for some $i$ and let $\overline{w} \neq \overline{v}$, $\overline{w} \in \overline{V_j}$ for some $j$. Besides $\overline{v} \subset \overline{w}$ or $\overline{v} \supset \overline{w}$ the regions $\overline{v}$ and $\overline{w}$ potentially fulfill the relations defined below.

- The regions $\overline{v}$ and $\overline{w}$ are said to be neighbors: $\overline{v} \sim \overline{w}$, if there exists an edge $e_0 \in E_0$ such that $\overline{c_1} \cap \overline{v} \neq \emptyset$ for some $\overline{c_1}$ in $\overline{\iota_0}(e_0)$ and $\overline{c_2} \cap \overline{w} \neq \emptyset$ for some $\overline{c_2}$ in $\overline{\iota_0}(e_0)$.
- The region $\overline{v}$ is said to enclose $\overline{w}$: $\overline{v} \triangleright \overline{w}$, if there exists a closed polygon $e \in E_i$ for some $i$ such that $\overline{v}$ is contained in the exterior of $e$ and $\overline{w}$ is contained in the interior of $e$.
- The region $\overline{v}$ is said to be apart from the region $\overline{w}$: $\overline{v} \mid \overline{w}$, if

$$(\overline{v} \not\subset \overline{w}) \wedge (\overline{v} \not\supset \overline{w}) \wedge (\overline{v} \not\triangleright \overline{w}) \wedge (\overline{v} \not\triangleleft \overline{w}). \qquad (2)$$

From $\overline{v} \neq \overline{w}$ it follows that the five relations $v \subset w$, $v \supset w$, $v \triangleright w$, $v \triangleleft w$, and $v \mid w$ exclude each other and cover all possibilities. Moreover, each of the five relations may occur together with the neighborhood relation and together with the complement of the neighborhood relation. Thus, there are ten combinations of the (non-) neighborhood relation with the other five relations and these ten relations cover all possibilities (see Figure 3). In the following, a combination of the (non-) neighborhood relation with one of the other five relations is denoted by the symbol of the (non-) neighborhood-relation followed by the symbol for the other relation. Examples of the topological relations are given in Table 1. The following is a straight forward definition of an association graph, whose vertices represent potential matches and whose edges indicate topological consistency.

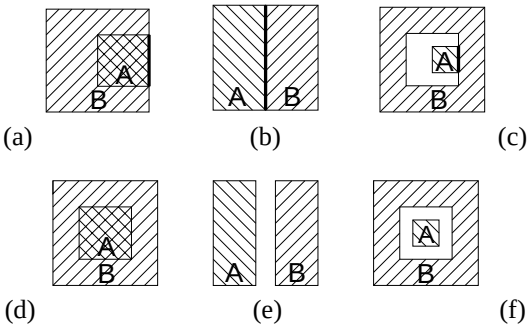


**Figure 3. The 10 topological relations. The thick lines indicate the edges defining the neighborhood relations. (a)** $A \sim\subset B$, $B \sim\supset A$. **(b)** $A \sim| B$. **(c)** $A \sim\triangleleft B$, $B \sim\triangleright A$. **(d)** $A \not\sim\subset B$, $B \not\sim\supset A$. **(e)** $A \not\sim| B$. **(f)** $A \not\sim\triangleleft B$, $B \not\sim\triangleright A$.

**Definition 3.1 (Topological association graph)** *Let $(G^1{}_i, \overline{V}^1_i, g^1{}_i)_{i=0}^{k_1}$ and $(G^2{}_i, \overline{V}^2_i, g^2{}_i)_{i=0}^{k_2}$ be two hierarchies of segmentations. Furthermore, let $\overline{v}^1 \in \overline{V}^1_i$ for some $i$, $\overline{w}^1 \in \overline{V}^1_j$ for some $j$, $\overline{v}^2 \in \overline{V^2}^2_k$ for some $k$, and $\overline{w}^2 \in \overline{V}^2_l$ for some $l$. The pair $(\overline{v}^1, \overline{v}^2)$ is said to be topologically consistent with the pair $(\overline{w}^1, \overline{w}^2)$, if the topological relation between $\overline{v}^1$ and $\overline{w}^1$ (one out of ten) is the same as the topological relation between $\overline{v}^2$ and $\overline{w}^2$. The topological association graph of $(G^1{}_i, \overline{V}^1_i, g^1{}_i)_{i=0}^{k_1}$ and $(G^2{}_i, \overline{V}^2_i, g^2{}_i)_{i=0}^{k_2}$ is the simple graph (see Section 2) $G_A = (V_A, E_A, \iota_A)$ defined by*

- $V_A = (\bigcup_{i=1}^{k_1} \overline{V}^1_i) \times (\bigcup_{i=1}^{k_2} \overline{V}^2_i)$,
- $E_A = \{\{v, w\} : v \neq w \in V_A,$ *$v$ is topologically consistent with $w$, and*
- $\iota_A(e) = e \quad \forall e \in E_A$.

**Table 1. Topological relations from Figure 3b. Merging $A$ with $B$ results in $D$.**

| | $A$ | $B$ | $C$ | $D$ | $\mathbb{R}^2$ |
|---|---|---|---|---|---|
| $A$ | $=$ | $\sim\triangleleft$ | $\not\sim\triangleleft$ | $\not\sim\subset$ | $\not\sim\subset$ |
| $B$ | $\sim\triangleright$ | $=$ | $\sim\triangleleft$ | $\sim\subset$ | $\not\sim\subset$ |
| $C$ | $\not\sim\triangleright$ | $\sim\triangleright$ | $=$ | $\sim\triangleright$ | $\not\sim\subset$ |
| $D$ | $\not\sim\supset$ | $\sim\supset$ | $\sim\triangleleft$ | $=$ | $\not\sim\subset$ |
| $\mathbb{R}^2$ | $\not\sim\supset$ | $\not\sim\supset$ | $\not\sim\supset$ | $\not\sim\supset$ | $=$ |

## 4. Heuristic for finding "heavy" cliques

Let $G$ be a simple graph (see Section 2) with vertex set $V$ and edge set $E$. A subset $V_c$ of $V$ is called a *clique* of $G$,

if for all $u \neq v \in V_c$ there exists $e \in E$ with $\iota(e) = \{u, v\}$. Furthermore, let $\mathcal{I}^m_{i=0}$ and $\mathcal{J}^n_{i=0}$ be two hierarchies of segmentations and let $G_A = (V_A, E_A, \iota_A)$ be the topological association graph of $\mathcal{I}^m_{i=0}$ and $\mathcal{J}^n_{i=0}$. By construction, a clique of $G_A$ corresponds to a topologically consistent one-to-one mapping between the regions of $\mathcal{I}^m_{i=0}$ and those of $\mathcal{J}^n_{i=0}$. In the following, let $\sigma : V_A \rightarrow \mathbb{R}^+$ be a similarity measure between regions, where one region is from $\mathcal{I}^m_{i=0}$ and the other is from $\mathcal{J}^n_{i=0}$. Finding a topologically consistent one-to-one mapping with a "high" total $\sigma$-value between the regions of $\mathcal{I}^m_{i=0}$ and those of $\mathcal{J}^n_{i=0}$ corresponds to finding "heavy" cliques of $G_A$, if the weight of a vertex $v \in V_A$ (i.e. of a potential match) is again given by $\sigma(v)$. Unfortunately, the problem of finding a clique with maximum total weight (corresponding to a consistent mapping with maximum total consistency) is NP-hard [2]. In the following we can only guarantee to find a clique with maximal weight, i.e. one that cannot be enlarged without loosing the property of being a clique. Note that a maximal clique in $G_A$ corresponds to a consistent mapping that cannot be extended without loosing consistency.

The rest of this section is devoted to a heuristic for finding "heavy" cliques of $G_A$. The plan is to start with a small clique of the association graph and iteratively enlarge it by single vertices in a greedy way. The enlargements are done so as to create favorable conditions for further enlargements. We propose a look ahead-rule for the enlargements that stems from a look-ahead rule formulated within a pivoting-based heuristic to the maximum weight clique problem [10]. Specifically, the pivoting-based heuristic was used to solve a linear complementarity formulation [3] of a standard quadratic program which, in turn, is equivalent to the maximum weight clique problem. For the unweighted case Marco Locatelli [9] gave the following combinatorial interpretation of the look-ahead rule in [10].

*For enlarging the current clique, always take a candidate whose degree is maximal in the subgraph induced by all candidates.*

To arrive at high total $\sigma$-values, we adapt the above rule. If $G_A = (V_A, E_A, \iota_A)$ is the topological association graph, $C \subset V$ denotes the set of candidates to enlarge the current clique, $N_C(c)$ denotes the neighborhood of a vertex $c$ in the subgraph of $G_A$ induced by $C$, i.e.

$$N_C(c) = C \cap \bigcup (\iota(e) : c \in \iota(e)), \tag{3}$$

then the adapted look-ahead rule says the following.

*For enlarging the current clique, always take a candidate $c$ such that*

$$\sum_{c' \in N_C(c)} \sigma(c') \quad \textit{is maximal.} \tag{4}$$

## 5. Results

The aim of the experiments is to see whether the requirement of topological consistency in conjunction with an ad-hoc similarity measure is sufficient to yield plausible matches between "similar" panoramic images.

For the experiments we used a sequence of panoramic images provided by the *Cognitive Vision Group* at the *Computer Vision Laboratory*, University of Ljubljana and the *Center for Machine Perception*, CTU, Prague (http://lrv.fri.uni-lj.si/ matjazj/backyard/testimgs/). The sequence simulates a path of a mobile robot through a lab (Figures 4 and 5).

All images were scaled to approximately 15.000 pixels and the hierarchy was always calculated as specified in Section 2.3. Moreover, to reduce memory requirements, we restricted each hierarchy to its upper 14 levels. The weight of a vertex in the association graph corresponding to the potential match $(R_1, R_2)$ was always set to

$$\sigma(R_1, R_2) = ((1 - dx)(1 - dy)(1 - dg)(1 - ds))^\alpha, \tag{5}$$

where $dx$ and $dy$ stand for the normalized absolute deviation of the barycenters in $x$ and in $y$, $dg$ stands for the normalized absolute difference of the mean gray values,

$$ds = \frac{min(area(R_1), area(R_2))}{max(area(R_1), area(R_2))}, \tag{6}$$

and $\alpha = 0.3$ is an empirical value. Typically, the topological association graph is very dense. To save memory, we neglect an edge $e$ between potential matches $(R_1, R_2)$ and $(S_1, S_2)$, if the relative location of $R_1$ with respect to $S_1$ deviates significantly from the relative location of $R_2$ with respect to $S_2$. Formally, $e$ is neglected, if

$$\|b(R_1) - b(S_1) \; - \; (b(R_2) - b(S_2))\|_2 > DEV, \tag{7}$$

where $b(R) \in \mathbb{R}^2$ stands for the barycenter of region $R$ and $DEV$ is a threshold (set to 22).

To evaluate the advantages of fully hierarchical matching over flat matching between the base levels only, we performed both kinds of experiments. In all experiments the total similarity from fully hierarchical matching was about twice of that from flat matching.

A typical example is the pair *cmppath.23* and *cmppath.25* (Figure 4). Also the results of the matching (Figure 5) are typical.

Performing the fully-hierarchical method as described in Sections 3 and 4 yields the result shown in Figure 5a. Constraining the matches to base level regions, however, the result is poorer (see Figure 5b). Indeed, there are less matches, the matched regions are more isolated, and the similarities of the matched regions are lower. Note also that match 6 is not plausible.

**Figure 4. a) Panoramic images** *cmppath.23* **(left) and** *cmppath.25* **(right). b) Base level of hierarchy on** *cmppath.23* **(left) and on** *cmppath.25* **(right).**

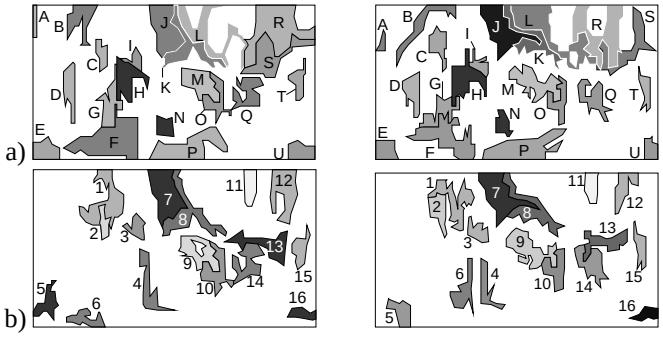

**Figure 5. Matching the hierarchies on the base levels shown in the Figure 4b. The columns refer to** *cmppath.23* **(left) and** *cmppath.25* **(right). a) Fully hierarchical match. (b) Non-hierarchical match of the base levels.**

## 6. Conclusions and outlook

We showed how to build an association graph, the maximal [maximum] weight cliques of which correspond to topologically consistent matches with maximal [maximum] total similarity between the regions of two segmentation hierarchies. The experiments demonstrate that using hierarchies increases the number and the quality of the matches. The very strict requirement that *all* topological relations are preserved by the match has a negative and a positive effect. On the negative side, one has to live with considerable holes between matched regions. On the positive side, the strict topological constraints make the match more reliable.

## References


[1] E. Ahronovitz, J.-P. Aubert, and C. Fiorio. The star-topology: a topology for image analysis. In *Cinqui ème Colloque DGCI*, pages 107–116. LLAIC1, Université d'Auvergne, ISBN 2-87663-040-0, September 1995.

[2] I. M. Bomze, M. Budinich, P. M. Pardalos, and M. Pelillo. The maximum clique problem. In D.-Z. Du and P. M. Pardalos, editors, *Handbook of Combinatorial Optimization (Suppl. Vol. A)*, pages 1–74. Kluwer, Boston, MA, 1999.

[3] R. W. Cottle, J.-S. Pang, and R. E. Stone. *The Linear Complementarity Problem*. Accademic Press, Boston, MA, 1992.

[4] R. Diestel. *Graph Theory*. Springer, New York, 1997.

[5] R. Glantz, M. Pelillo, and W. G. Kropatsch. Using segmentation hierarchies for matching and recognition in computer vision. Technical Report CS-2003-8, 2003.

[6] Y. Haxhimusa, R. Glantz, M. Saib, and W. G. Kropatsch. Logarithmic tapering graph pyramid. In L. V. Gool, editor, *Proceeding of the DAGM Symposium 2002*, volume 1876 of *Lecture Notes in Computer Science*, pages 117–124, Zürich, Switzerland, September 2002. Springer.

[7] V. A. Kovalevsky. Finite topology as applied to image analysis. *Computer Vision, Graphics, and Image Processing*, Vol. 46:pp.141–161, 1989.

[8] W. G. Kropatsch. Building Irregular Pyramids by Dual Graph Contraction. *IEE-Proc. Vision, Image and Signal Proc.*, 142(6):366 – 374, 1995.

[9] M. Locatelli, I. M. Bomze, and M. Pelillo. Swaps, diversification, and the combinatorics of pivoting for the maximum weight clique. Technical Report CS-2002-12, Dipartimento di Informatica, Università Ca' Foscari di Venezia, 2002.

[10] A. Massaro, M. Pelillo, and I. M. Bomze. A complementary pivoting approach to the maximum weight clique problem. *SIAM J. Optim.*, 12(4):928–948, 2002.

[11] A. Meijsler and J. Roerdink. A Disjoint Set Algorithm for the Watershed Transform. In *Proc. of EUSIPCO'98, IX European Signal Processing Conference*, pages 1665 – 1668, Rhodes, Greece, 1998.

[12] F. Meyer. Graph based morphological segmentation. In W. G. Kropatsch and J.-M. Jolion, editors, *2nd IAPR-TC-15 Workshop on Graph-based Representation*, pages 51–60. OCG-Schriftenreihe, Band 126, Österreichische Computer Gesellschaft, 1999.

[13] J. R. Munkres. *Elements of Topology*. MIT Press, 1984.