# A New Graph-Based Method for Automatic Segmentation

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**Abstract.** In this paper, a new graph-based segmentation method is proposed. Various Regions of Interest (ROIs) can be extracted from digital images/volumes without requiring any processing parameters. Only one point belonging to the region of interest must be given.

The method, starting from a single source element, proceeds with a specific propagation mechanism based on the graph theory, to find a Minimum Path Spanning Tree (MPST).

As compared with other existing segmentation methods, a new cost function is here proposed. It allows the process to be adaptive to both a local and global context, to be optimal and independent from the order of analysis, requiring a single iteration step. The final decision step is based on a threshold value that is automatically selected. Performance evaluation is presented by applying the method in the biomedical field, considering the extraction of wrist bones from real Magnetic Resonance Imaging (MRI) volumes.

Keywords: Unsupervised segmentation  $\cdot$  Minimum Path Spanning Tree  $\cdot$  Graph theory  $\cdot$  MRI volumes

# 1 Introduction

Image segmentation, or rather the process of identifying regions of interest starting from a digital image or volume, has been a major problem in image processing.

According to the classical definition, the aim of segmentation is to partition an image into a set of non-overlapping regions whose union is the entire image. In the particular case of ROI segmentation, like in this work, the result is a bi-partition of the image into the so-called foreground and background. In a second time, all the single extracted ROIs could be collected together forming a partition.

More recently, the purpose of segmentation has become more oriented to the detection of image parts that are meaningful within a particular application domain.

One of the most promising segmentation approach refers to the graph-based methods. The graph cuts with respect to regional constraints is a well-studied problem, and many methods have been proposed as a solution. The minimal graph cuts [1] approach calculates how to define an appropriate cut of the graph where objects related to seed-points are separated. Usually the criterion is such that the sum of the edge weights along the cut is minimal. Another family of methods is based on the calculation of a minimum

© Springer International Publishing Switzerland 2015 V. Murino and E. Puppo (Eds.): ICIAP 2015, Part I, LNCS 9279, pp. 601–611, 2015. DOI: 10.1007/978-3-319-23231-7\_54 cost path forest. Examples of this approach include the Image Foresting Transform (IFT) [2], and the Relative Fuzzy Connectedness method [3]. The Random Walker [4] method computes cuts such that each vertex is connected to the seed-point that a "random walker", starting at the vertex, is expected to reach first. The classical watershed approach has recently been reformulated on edge-weighted graphs [5].

One of the major drawbacks in graph-based methods consists in properly taking into account spatial correlation and contextual information during the graph visit. In addition, these approaches aims to find the Minimum Spanning Tree (MST) [8]; here, a new aggregation criterion is defined: the Minimum Path Spanning Tree (MPST). More details will be explained in Section 2.2.

In the present work, a seed-based algorithm which applies a graph-based segmentation driven by the research of minimum cost paths for the analysis of digital images/volumes is described. An optimal grouping algorithm is proposed; it proves to be independent of any model, parameter, threshold, or order of analysis.

The specific tree traversal propagation mechanism, starting from a user-defined seed, adapts to the actual data content and correctly accounts for local and global connectedness relationships in terms both of spatial relation among vertices and feature information. The obtained result is a graph-based segmentation, where a cost value is associated to each analyzed pixel/voxel and represents how it relates to the starting seed-class. During the graph visit, the assignment of the cost function is computed only one time and not reconsidered at each step of the propagation process.

The cost function here proposed is known in the framework of network optimization as the Bottleneck Shortest Path Problem (BSP); its goal is to determine the limiting capacity of any path between two specified vertices of the network [10]. In the context of segmentation, this formula has not explicitly been employed before. In fact, most of the graph-based methods consider as cost function the summation of the edge weights.

The innovative aspect of this work actually regards the MPTS and the cost function previously introduced.

This paper is structured in the following way. In Section 2, the graph-based method is described: initially, some graph notations are recalled, and then the algorithm with a detailed explanation of the different steps is presented. Application cases related to the biomedical domain are shown in Section 3, dealing with MRI volumes of the hand district.<sup>1</sup> In Section 4, the performance of the method is quantitatively evaluated by computing some classical parameters from the confusion matrix and a similarity measure. In addition, a discussion about the choice of the value where computing the graph cut is carried out.

# 2 The Proposed Method

The image is mapped into a graph, where each voxel corresponds to a vertex and pairs of neighboring vertices represent the edges. The objective is to locate and segment different regions of interest from the original volume, i.e., to extract a number of

<sup>&</sup>lt;sup>1</sup> The MRI volumes are available thanks to the Project MEDIARE: "New methodologies of Diagnostic Imaging for rheumatic diseases". PAR FAS 2007-2013 Program 4 – Pos. N. 14.

separated connected components from the graph. In this work, the ROIs are extracted one at a time. The proposed method is an unsupervised and automatic approach, which can be applied to both 2D and 3D digital images. Let us first consider some classical graph notations [9] that will be useful in Section 2.2, followed by a detailed description of the algorithm.

#### 2.1 Graph Notations

Starting from [6], we define a graph as a pair G(V, E), where  $V = \{v_1, ..., v_n\}$  is the vertex set and  $E \subset \{(v_i, v_j) \subseteq V \mid v_i \neq v_j\}$  is the edge set, the set of the pairs of neighboring vertices. The order of *G* is the number of the vertices and it is denoted by |V| or |G| or sometimes n(G).

We define a weighted graph when the vertices and/or the edges are labelled with weights. In the former case, we call the graph a vertex-weighted graph; in the latter case, we call the graph an edge-weighted graph. The weights can be positive or negative and can be assigned by different functions and with different criteria.

We say that two vertices  $v_i$  and  $v_j$  are adjacent if an edge  $e_{ij} = (v_i, v_j)$  connecting  $v_i$  with  $v_j$  exists. A graph G is undirected (or not oriented) if the pairs of the edges are not ordered, i.e.,  $e_{ij} = e_{ii}$ .

Let  $\pi(v_1, v_k) = \langle v_1, ..., v_k \rangle$  be an ordered sequence of vertices.  $\pi$  is a path from  $v_1$  to  $v_k$  if for any  $i \in [2, k]$ ,  $v_i$  is adjacent to  $v_{i-1}$ . If the extremities of the path coincide, we say that  $\pi$  is a cycle. We define G a connected graph if any two vertices of G are linked for G.

Let G(V, E) and G'(V', E') be two graphs; if  $V' \subset V$  and  $E' \subset E$ , we say that G' is a subgraph of G, i.e.,  $G' \subset G$ . If G' is a connected graph without cycle, then G' is a tree.

A spanning tree is a tree containing all vertices of the graph. A Minimum Spanning Tree (MST) is a spanning tree for which the sum of the edges is minimal [8]:

$$c(T) = \min\left(\sum_{e=1}^{n-1} w_T(e)\right)$$
(1)

where T is the tree and  $w_T(e)$  represents the weight assigned to edge  $e \in E_T$  and  $E_T$  defines the set of edges of T.

A Shortest Path Tree (SPT) rooted at a vertex s defines a tree composed by the union of the paths between s and each of the other vertices in G such that [8]:

$$c(s,v) = \min\left(c_G(s,v)\right) \tag{2}$$

where  $c_G(s, v)$  is the cost of the path, i.e., the sum of the weights of the edges belonging to the path.

#### 2.2 Proposed Cost Function and Algorithm

In this work, the authors propose a graph-based segmentation method by defining a new cost function. This function is the formulation of bottleneck single source shortest path, which although commonly known, is not usually considered and employed in the context of graph-based segmentation methods. Unlike the classical graph notations, where the sum of the edge weights is used, the aim of the algorithm is to find the Minimum Path Spanning Tree, that is a spanning tree considering a cost function as this:

$$f_{w_s}(v_i) = \min_{\pi(s,v_i)} [\max_{x \in \pi(s,v_i)} w_s(x)]$$
(3)

where w is the weight associated to the vertices,  $\pi(s, v_i)$  is the path from the seed s to a vertex  $v_i$ . This function minimizes the largest of the vertex weight in the path  $\pi$  and is equivalent to the maximum capacity path problem [11]. By this definition, the algorithm does not consider the length of the path, and consequently the dimension of the object to segment.

A digital image  $I = (D, \vec{I})$  is a pair, where  $D \subset \mathbb{Z}^n$  is the image domain and  $\vec{I}(x) \in \mathbb{Z}^m$  is a vectorial mapping, which assigns a set of values to each  $x \in D$ .

The image (or volume) to be segmented can be interpreted as a graph G(V, E), where  $V \subseteq D$  is the vertex (or node) set, represented by the pixels (or voxels) and  $E \subset D \times D$  is the set of arcs, defined by an adjacent relation, i.e., 4-connected in 2D or 6-connected in 3D space.

The graph is an undirected, vertex weighted, grid graph. In the graph-based approach, a seed-based segmentation, given a seed point *s* belonging to a ROI, is a partition of V into components. Here, the extracted region corresponds to a connected component in a subgraph G'(V, E'), containing the vertex *s*. This vertex encloses all connected nodes that are homogeneous with respect to some properties of the seed point. In other words, the segmentation result is induced by a subset E' of the edges in *E*.

Let  $I: V \to \mathbb{R}$  be the intensity map with  $I(v_i)$  the intensity of the vertex  $v_i$  and L be the maximum grey level value that can be represented in the digital image/volume.

Let  $w: V \to \mathbb{R}^+$  be the weight function with  $v_i \mapsto w(v_i)$ , where  $w(v_i)$  is the weight of the vertex  $v_i$ , with i = 1, ..., |V|.

Chosen a seed point (source) *s* belonging to a ROI, the weights are assigned to the vertices following this criterion:

$$\forall v_i \in V, \qquad w_s(v_i) = |I(v_i) - I(s)| \tag{4}$$

From the previous formula, it follows that the weight function w is a function from V to the scalar domain [0,L].

This vertex weight assignment takes into account the dissimilarity of the pixel as compared to the seed point, like a sort of distance. From the formula, it is possible to observe that vertices with values very close to the seed value have a weight close to zero, while vertices with values different from the seed value have a weight close to L.

To avoid a too strong influence of local noise, the value I(s) has been replaced by the local average value of the 4-connected neighborhood  $N_4$ , instead of the seed intensity value itself:

$$I(s) = \frac{1}{|N_4|} \sum_{v_i \in N_4} I(v_i)$$
(5)

Let define the cost function  $f_{W_s}$  from V to the scalar domain [0,L] as

$$f_{w_s}(v_i) = \min_{\pi(s, v_i)} [\max_{x \in \pi(s, v_i)} w_s(x)]$$
(6)

where  $\pi(s, v_i)$  is the path from *s* to  $v_i$ .

The contextual segmentation problem is comparable to the single-source shortest path problem for a graph with non-negative vertex weights, producing a Minimum Path Spanning Tree. It follows that, starting from the first node, the process oriented to the correct solution moves to each neighbor by computing the cost of the new path from the starting point, taking into account all previous computations.

The purpose of the algorithm is to assign the cost function  $f_{w_s}$  to each vertex,  $v_i$ , according to the best path from the seed s. As a preliminary step, with respect to the seed point, the algorithm computes the  $w_s(v_i)$  value for each seed  $v_i$  representing the dissimilarity with the seed.

The image segmentation method is implemented by performing a particular propagation process, that decides which nodes are the candidate ones to be analyzed (based on the already analyzed nodes) and selects the best paths starting from a fixed seed point. Such a mechanism, being adaptive to the image content, allows a non-iterative approach to account for contextual information.

The seed point represents the generator and the other pixels are initially considered "unvisited". We create two lists of vertices: S is the list of generators with their connected neighbors; T is the complementary set of S. During this process, S is updated with new nodes until T becomes an empty list.

In the following, the main steps of the algorithm are described:

- Input: a non-empty connected, undirected, vertex weighted graph G(V, E).
- *Initialization*: setting the value zero for the seed ("generator") point and its direct neighbors and the value one for the others vertices. This choice is important in case the seed point is a noise pixel.

$$w_s(v_i) = \begin{cases} 0 & if \ v_i = \{s, N_4\} \\ 1 & otherwise \end{cases}$$
(7)

At the beginning, all the nodes are marked as "unvisited" and the generators are the seed point closed neighbourhood:  $S = \{s, N_4\}, T = V \setminus S$ .

- Steps to repeat:
  - 1. For each "generator" or "father", we consider its unvisited 4-connected neighbour pixels (or 6-connected neighbour voxels) and we change their status in "candidates". We choose the minimum weighted vertex considering the weighted function *w*.

The new vertex, "son", is added to the generator, updating the set S, i.e.  $S = S \cup \{v_{new}\}.$ 

2. We consider the neighbour of this new vertex together with the previous and we choose the minimum. If the minimum weight is greater than its "father" then it maintains its weight; if the minimum weight is lower than its "father" then we assign the father value. For two contiguous nodes,  $v_{i-1}$  and the fol-

lowing  $v_i$  belonging to the best path from the seed, the cost function is given by:

$$f_{w_s}(v_i) = \begin{cases} w_s(v_i) & \text{if } w_s(v_i) > f_{w_s}(v_{i-1}) = w_s(f) \\ f_{w_s}(v_{i-1}) & \text{if } w_s(v_i) \le f_{w_s}(v_{i-1}) = w_s(f) \end{cases}$$
(8)

Such a value will not be checked again; its cost as recorded is now final and will never be changed.

In the case that the minimum weight corresponds to two vertices, we choose arbitrarily one of the two nodes. All the new vertices considered are chosen so that no cycles in the path are created.

- 3. We continue to apply this criterion of growing and labelling until all the nodes are considered (all nodes are marked as visited), i.e.,  $S = V, T = \{\emptyset\}$ .
- Output: the obtained paths are a Minimum Path Spanning Tree.

The described algorithm starts from a seed point and successively analyzes all image sites at recursion steps. The steps are organized into a sequential order dependent on the image content. This adaptive procedure performs selective propagation steps based on the computed intermediate cost vertex. The order of visited sites leads to the generation of a tree, whose root is the seed point and where a node is instantiated for each analyzed image site.

The approach proceeds selecting the best path and producing a Minimum Path Spanning Tree. In the literature, different algorithms exist for obtaining the Minimum Spanning Tree (such as Kruskal's Algorithm, Prim's Algorithm), the shortest path (such as Dijkstra's Algorithm), the shortest path tree [8]. All these methods consider the cost of the path as the sum of the edges.

The proposed method utilizes the same criterion of propagation of Prim's Algorithm, but with some differences in the intermediate steps.

The Prim's Algorithm finds a Minimum Spanning Tree from a connected weighted undirected graph, minimizing the cost of the sum of the edges.

Through the proposed approach a spanning tree is found, that is minimum with respect to the cost function defined in Equation (3). This gives to the algorithm an innovation aspect. The main advantages are that the segmentation can be obtained in oneshot and without considering the spatial information. In addition, the Equation (8) ensures that the paths from the seed to each vertex are optimal and that the method is good from a computational point of view, because after the cost value is assigned, it will never be changed during the graph visit.

### 2.3 Graph Cut

The algorithm generates a spanning tree, whose root is the seed point. In order to obtain the region of interest, a graph cut is applied: the image can be represented by two disjoint sets, A, B where  $A \cup B = V$ ,  $A \cap B = \emptyset$ .

The figure below describes the criterion followed to identify the ROI. We start from a single source (red point) and its 4-connected neighbors. Each level corresponds to a value of the cost function  $f_{w_s}$ . For each level, the graph order (i.e., a summation of the vertices) is computed and updated according to the previous level value.

Let  $n(v_{l_i})$  be the number of vertices at level *i*.We compute

$$\sum_{i=1}^{l_i} n(v_{l_i}) \tag{9}$$

The meaning of such a sum relates to the size of the region that can be obtained with a cut at this level.

We propose to cut the tree at a certain level, in order to cut the edges connecting these levels; thus, one connected component including the source point is obtained. The rest of the graph can consist of one or more connected components, depending on the shape of the ROI.

In particular, we define a "gap" when there is a large difference between the orders of two consecutive levels. This happens in presence of contrast or edges. When a graph cut is performed, corresponding to a gap it means that a region made of very similar voxels is extracted. On the contrary, if homogeneity property is relaxed a graph cut can be chosen after a gap. This means that the ROI expands out of a significant border if the gap is larger than the gradient value.

Such a result can be interpreted as a multi-level segmentation: with a cut just before the gap, we obtain the region of interest. After the gap there can be an enlargement of the region until the entire image is covered.



Fig. 1. Scheme of the criterion used to make the graph cut.

# **3** The Application Case

For the experiments five volumes of T1-weighted magnetic resonance of the hand district, affected by Rheumatoid Arthritis (RA) are considered. Rheumatic disease involves in particular the joints, the bones and the muscles. RA is one of the most common autoimmune rheumatic disease; it is a chronic and progressive inflammatory polyarthritis. According to current recommendations, MRI is used to asses three main signs of RA based on manual evaluation of MR images: synovitis, bone edema, and bone erosions [7].

The graph-based approach is applied to these volumes in order to segment the main wrist bones: capitate, trapezium, trapezoid, pisiform, scaphoid, lunate, triquetrum, hamate.

The results are compared with ground references delivered by Softeco Sismat Srl [9]. For the latter, a quantitative evaluation through statistical values of sensitivity, precision and Dice coefficient is performed.

For each volume (of size 256×256×102), starting from a seed point decided by the user, the wrist bones are extracted separately. To prove the independence of the method from the seed choice, the fuzzy graph-based approach is applied several times to the various volumes of interest.

Figure 2 shows the different phases from the original image to the final result: (a) the original image; (b) the map of the final cost function (inverted grey levels); (c) the image after the graph cut, with the identification of the region of interest in red color; (d) the binary map of the capitate bone; (e) the boundary of the bone overlapped to the original image; (f) the 3D visualization of the segmented bone.

After detecting all the bones individually, we perform a composition of the segmented images by overlapping to the original image.

Figure 3 shows the original image (on the left) and the segmented bones overlapped to the original image. It is possible to observe how the edges are very precise and accurate with respect to the original one. From a qualitative point of view, the segmentation gives good results; in the next section, we will confirm this statement by means of a quantitative evaluation.





Fig. 2. Phases of graph-based method, from the original image to the bone extraction.



Fig. 3. The original image (on the left); the segmented bones overlapped to the image with colored boundaries.

# 4 Quantitative Evaluation

To establish the performance quality of the proposed segmentation, different evaluation measurements are computed, referring to the ground truth. In particular, the following parameters have been extracted for each region of interest: Sensitivity, Precision and the similarity measure, Dice Coefficient.

The indices are given by these formulae [12]:

$$Sensitivity = \frac{TP}{TP+FN}, \ Precision = \frac{TP}{TP+FP}$$
(10)

$$DICE = \frac{2 TP}{(TP+FP)+(TP+FN)}$$
(11)

where TP are the True Positives, TN are the True Negatives, FP are the False Positives, FN are the False Negatives, P are the Positives and N are the Negatives.

Sensitivity informs about how many data are correctly evaluated as positive on the total positive observations, while precision is the proportion of the predicted positive cases that are correct. Dice coefficient is a similarity index, which measures the overlap of two sets. A value of 0 indicates no overlap; a value of 1 indicates perfect agreement. Higher numbers point out better agreement in the sets, so when we apply this index to evaluate the agreement of segmentation results, the goal is to get as close to 1 as possible.

The parameters presented in table 1 are the mean values of three patients. The evaluation shows promising results, since the method does not use a-priori knowledge or models. In particular, precision shows high values, close to 1. Sensitivity values are lower, a sign of an under segmentation. Possible post-processing steps can be applied in order to improve the results. In addition, Dice coefficient provides values ranging from 0.69 to 0.83.

As regards the graph cut phase, analyzing these five patients it is possible to note that usually the value of the cut is around 200.

The figure below represents the values of the cut for the different wrist bones, for the five patients. For each bone, there are 5 values corresponding to the patients: it is possible to observe that the values range from 180 to 250. The value of the cut has been chosen by an adaptive method, since a fixed value should have led to bad results.

	Sens	Prec	DICE
Capitate	0,7056	0,9986	0,8258
Triquetrum	0,5392	0,9978	0,6952
Pisiform	0,5746	0,9962	0,7217
Scaphoid	0,6570	0,9997	0,7886
Lunate	0,6204	0,9978	0,7647
Trapezium	0,7147	0,9983	0,8320
Trapezoid	0,6905	0,9979	0,8130
Hamate	0,6605	0,9966	0,7852

 Table 1. The quantitative evaluation of the method: a comparison between sensitivity, precision, and Dice Coefficient.



Fig. 4. Histogram of the values of the cut for the different wrist bones, for each patient.

### 5 Conclusions

In this work a new graph-based method has been proposed for analyzing digital volumes. An unsupervised approach that, starting from a single source, extracts the regions of interest one by one. Unlike other methods, it considers only one seed in the foreground and not in the background, with no further user interaction or a-priori model.

The aim of the algorithm is to find a Minimum Path Spanning Tree, whose root is the seed point, through the definition of a cost function. This function maximizes the minimum of the weight vertex over the path, without considering the sum of the edges like many algorithms present in literature. The innovative aspects of this work are exactly the aggregation criterion of MPST and the cost function.

The main advantage of the presented method is the independence on the image content and resolution, so it works well for any kind of image. Furthermore, this approach is simple to use and very fast. It is a robust method, since it does not depend on the choice of the seed point and it is also adaptive; in fact, the value of the graph cut is not fixed at first, but it is chosen considering the content of the image.

This approach has been applied to real RMI volumes in order to extract the wrist bones and to identify the presence of pathology in the hand, more precisely the manifestation of the rheumatoid arthritis.

The robustness of this method is investigated through the analysis of statistical parameters, and the first results are very good. The evaluation of the approach, in terms of Sensitivity, Precision and Dice coefficient produced very promising results.

At the same time, good qualitative results are obtained in the segmentation of the total volume of the hand. Other cases will be analyzed in order to make more robust the method and increase the significance of the quantitative evaluations.

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