Portal Vein Registration for the Follow-Up of Hepatic Tumours

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Abstract. In this paper, we propose an original method which permits a follow-up of intra-patient evolution of tumours in the liver by using a registration of the portal vascular system.

First, several methods to segment the liver data structures (liver, vascular systems and tumours) on computed tomography scans are presented. Secondly, the skeleton of the vessels is computed and transformed into a graph representation. Then, the intra-patient graph registration is computed to determine an approximation of liver deformation. Finally, the deformation permits to match tumours to diagnose their evolution.

For each step, we present the methods we used and their results on CT-scan images.

1 Motivations

Liver surgery is a field in which computer-based surgery planning has great impact on selection of therapeutic strategy. In this paper, we focus on the follow-up of tumours from the same patient between two acquisitions. We propose an automatic method which permits to show how tumours evolve. The main purpose is to match tumours between two different moments.

Tumour matching provides an automatic framework to diagnose their evolutions. The comparison amongst matched tumours permits to see their evolutions by comparing their volumes. A tumour cannot be matched if it appeared or disappeared between the two acquisitions.

Tumour matching can not be accurately performed by using only their localization information. Indeed, between two acquisitions, their localization and shape can vary a lot. The shape deformation is due to disease development and the localization changes are due the deformation of liver.

The liver deformation gives an estimate of tumour displacement that helps to track them. The liver is lacking of reference points allow the estimation of its deformation, so its inner vascular system is preferred, particularly the portal system. On the CT-scan images, hepatic vessels are enhanced with a contrast medium. The vascular system gives a better reference point set in two respects: a) topologically, by providing junction points as reference points, b) geometrically, with diameter and orientation information of incident branches.

Fig. 1. Component extraction: **[left]** Slice obtained by CT-scan of a liver. The vascular systems are highly contrasted and tumours are poorly contrasted. **[center]** Liver surface obtained by robust segmentation of the CT-scans. **[right]** Visualization of different components of the liver (portal vein, hepatic vein and tumours).

To compute the deformation, the portal vein is modeled as a directed tree from the skeleton of segmented CT-scan images, then graph vertices are matched together. These matchings define a transformation which helps in tracking tumours. This method differs from traditional methods which generally work on grey level image registration [2,3]. Our approach is inspired by some methods employed to register airway tree [6,10] but whose purpose is to search for local liver deformations.

The remainder of this paper is organized as follows. Section 2 deals with the computation of the vascular graph from CT-scan images. Section 3 describes our graph registration algorithm. It also introduces energy functions used to measure resemblance between edges. Section 4 is dedicated to tumour registration. We finish with a discussion on future possible improvements.

2 Preprocessing: Segmentations and Thinning

Segmentation: Some methods are proposed in the literature to segment liver structures [4,8]. To extract them, we have used an automated algorithm [9] based on three segmentation steps. First, an approximation of the other structures allows to obtain a good localization of the liver in the image. A deformable model is used to segment the liver [5] (see fig. 1). Then, the method estimates the intensity distributions of three tissue classes: tumours, parenchyma and vessels, and classifies them. Finally, to separate hepatic and portal vascular systems, the skeleton of systems is computed and inconsistent links between graphs are removed to obtain two dissociated graphs.

Graph representation: The graph representing the portal system is constructed from a skeleton. The thinning skeleton (see fig. 2) is obtained by iterative removing points (except end points) where removal preserves the topology

Fig. 2. Skeleton creation: **[left]** Voxel visualization representing the portal vascular system segmentation of a liver. **[center]** Thinning result of the portal vascular system. **[right]** 3D representation of the graph structure data obtained starting from previous skeleton.

Fig. 3. Graph registration: **[left]** This figure shows the superimposition of two portal vascular systems created from two images of a same patient acquired at two different times. On this figure, only the node root has been registered. **[right]** This figure shows the good result of the registration graph (all nodes registered). Some differences appear between graphs, as some branches were detected in only one of the graphs.

(called simple points [1]). Then, the edges (resp. vertices) of graph are generated by branch voxels (resp. junction nodes). Furthermore, a few operations improve visualization and keep significant edges [4,8,9].

3 Graph Registration

Once the graph of the portal vascular system is created for both acquisitions of the same patient, we register their graphs. There are many approaches for graph matching in the graph theory, especially on the matching of hierarchical structures using weighted association graphs [7]. The algorithm proposed in this paper is simplified, faster and more specific although it strongly related to these concepts. Figure 3 shows the result of this registration.

3.1 Algorithm

The method is very fast (see alg. 1): a) roots are matched and registered, b) the first edge set is matched with the second set, c) local deformations are computed and d) we repeat this operation with child nodes. Figure 4 shows some steps of the iterative registration evolution.

Fig. 4. Graph registration evolution: Images represent the evolution of graph registration (left $\rightarrow$ right, up $\rightarrow$ down) of a real patient case showed on fig. 3. Step by step, the graph matching evolves with a depth-first search.

3.2 Vessel Registration

The first step of the algorithm requires a matching of nodes in both graphs and tries to match the out-edges. This step is difficult because blood vessels are not always well segmented due to contrast medium propagation time. Two matched edges can have different lengths or can be slightly displaced in space. Sometimes edges have no match in the other graph.

To determine the best out-edges matching for a given node pair, the method minimizes an energy function. For this, an energy function f_g between two edges (see eq. 1 and fig. 5) is used and all possible one-to-one functions for the matching between $E_1 = \{e_1^1, e_1^2, \dots, e_1^n\}$ first graph edge set and $E_2 = \{e_2^1, e_2^2, \dots, e_2^m\}$ second graph edge set are tested. Finally, the function which minimizes the global matching energy is chosen (see eq. 2).

$$\begin{aligned}
f_g(e_1, e_2) &= f_1(e_1, e_2) \times f_2(e_1, e_2) \\
f_1(e_1, e_2) &= \frac{1}{l_{min}} \times \sum_{i=1}^{l_{min}} \|p_1^i - p_2^i\|^2 \\
f_2(e_1, e_2) &= \sin\left(\frac{\hat{\theta}(e_1, e_2)}{2}\right)^2 \times e^{\frac{l_{max} - l_{min}}{l_{max}} - 1}
\end{aligned} \tag{1}$$

where e_1, e_2 are edges (vessels) which are registered in their first node, l_{min} (resp. l_{max}) is the shortest (resp. longest) edge length between e_1 and e_2 and where p_k^i is the i^{th} point of e_k .

$$F_g(E_1, E_2) = \min_{\sigma} \sum_{k=1}^n f_g(e_1^k, e_2^{\sigma(k)}) \tag{2}$$

where $\sigma : [1...n] \rightarrow [1...m]$ is an injective function of correspondence and thus it is supposed that $n \leq m$. If this is not the case, E_1 and E_2 are permuted in equation.

The robustness of this method depends on the ability of the energy function to describe the matching between two edges. To improve this, the function f_2 is introduced in eq. 1 to influence small angles between edges with $\hat{\theta}(e_1, e_2)$ (the angle created by vectors $(p_1^1 p_1^{l_{min}}, p_2^1 p_2^{l_{min}})$) and the matching edge of same length with $e^{\frac{l_{max} - l_{min}}{l_{max}} - 1}$.

However, to improve matching quality, work on other energy functions is being study. These functions will focus on the matching impact on the subgraph or on the quality of the transformation to deform the edge.

Algorithm 1 Graph registration

{Initialization}

- 1/ Register graph roots which correspond to the entry of the portal vein.
- 2/ Compute their associated transformation.
- 3/ Push the common node in the process stack.

{Principal loop}

while all nodes are not registered (process stack is not empty) **do**

Step 1/ Vessel registration (see sec. 3.2)

 From two already matched nodes, compute the best set of out-edge pairs (without parent edge) within both graphs. Some out-edges can have no match.

Step 2/ Junction node registration (see sec. 3.3)

 If end points from edge pair do not match, a new artificial node has to be inserted in the graph at the longer edge. Go to step 1 and recompute with new edges.

Step 3/ Local transformation (see sec. 3.4)

 A local transformation for each edge pair is computed to superimpose them and deform the edge subgraph.

Step 4/ Push registered nodes of out-edges.

end while

Fig. 5. Process registration visualization: **[left]** This figure shows how to compute the energy function f_g to know if two edges match (see eq 1). **[center]** This figure explains the problem of matching group for out-edges of a registered node and shows the problem of missed edges. For instance here, the best matching is: $((e_1^a, e_2^a)(e_1^b, e_2^b)(e_1^c, e_2^c))$, e_1^d has no correspondence. **[right]** Problem of junction node matching when edges and nodes miss.

3.3 Junction Node Registration

In this step, the best one-to-one function which matches the first edge set with the second edge set is found. However, some matched edges do not have the same length, due to squeeze pressure on the liver, methods used to compute the graph representation and injection time. If the end node of each edge match, they are registered together. It is also possible, that during the segmentation process, some edges are not segmented on one of the graphs. In this case, junction node does not appear in one of the graphs. This node will be inserted into it to preserve the efficiency of matching in the process continuation and to obtain in the end, a better registration (see fig. 5).

The difficulty is to distinguish between these two cases. Currently, the method is just a simple test on the relative length difference. But, in the future, criteria will take the impact of such a decision on the subgraph into account in terms of register costs.

3.4 Local Transformation Computation

At the beginning of this step, pairs of edges match between themselves due to step 1 (see sec. 3.2) and edge endings (node ends) are equivalent due to step 2 (see sec. 3.3). It is now necessary to compute the local transformation T (translation, rotation, ...) to be applied to these edges to obtain the deformation that the subgraph of each edge will undergo.

$$T_{sol} = \min_T \sum_i \|p_1^i - T(p_2^i)\|^2 \quad (3)$$

Equation 3 shows the best local transformation which is chosen to minimize the euclidean distance error between edge points and the projection of associated points of the other graph. Currently, a translation is applied to register

Fig. 6. Tumour registration: [left] This figure shows the tumours superimposition before tumour registration. The graph and tumours with the surface point represent the first acquisition. [right] This figure shows the tumour superimposition (associated with an id number) after tumour registration. All tumours have an improved matching (good correlation or reduction of the distance separation (see table 1)) but some of them did not overlap perfectly (2,4).

Table 1. Tumour registration results: This table shows some results on each tumour matching. Tumour numbers indicated in the table are shown in fig. 6. All measurements are in millimetres (excluding similarity) and are computed before and after registration.

Group id	Min $\min_{a \in A, b \in B} d(a, b)$	Max $d_{Hausdorff}(A, B)$	Center $d(c_a, c_b)$	Similarity $\frac{2 \times vol(A \cap B)}{vol(A) + vol(B)}$	Tumour to graph distance
1	0 $\rightarrow$ 0	35.5 $\rightarrow$ 16.5	27.7 $\rightarrow$ 9.5	12.1 $\rightarrow$ 58.0 %	11.6
2	14.8 $\rightarrow$ 2.5	22.1 $\rightarrow$ 10.7	21.6 $\rightarrow$ 10.4	0 $\rightarrow$ 0 %	22.6
3	14.8 $\rightarrow$ 0	22.5 $\rightarrow$ 4.0	22.1 $\rightarrow$ 2.4	0 $\rightarrow$ 48.2 %	7.7
4	25.4 $\rightarrow$ 7.6	37.8 $\rightarrow$ 19.6	35.8 $\rightarrow$ 16.7	0 $\rightarrow$ 0 %	6.1
5	9.5 $\rightarrow$ 0	25.1 $\rightarrow$ 2.4	25.4 $\rightarrow$ 0.9	0 $\rightarrow$ 81.8 %	1.8

node ends. In future works, this transformation will be approximated by a rigid transformation (rotation, translation). Finding the right 3D rotation is necessary to increase the robustness of the method with other patients.

4 Tumour Registration

In this part, lesion matching is evoked. From the local transformation computed in each node, a global transformation in the liver can be approximated. This transformation is applied to tumours in order to superimpose them.

Nowadays, the deformation applied to each tumour is only the local transformation of its graph closest node.

Figure 6 and table 1 show the result of tumour registration. The projection of tumours in the first patient acquisition is represented before and after regis-

tration. All tumour distance separations decrease with the matching. Groups 1, 3 and 5 have an efficient matching (good similarity).

However, groups 2 and 4 do not overlap, although the distance between them decreases. The worst matching can be explained for group 2 by a large separation between vessels (graph) and tumours, and for group 4 by a too simple deformation model. In a future work, it will be interesting to compute and merge sub-hepatic vascular system and liver surface deformations which will provide more information on liver deformation.

5 Discussion and Perspectives

We have presented a new method for tumour registration. It permits an automatic follow-up of tumour evolution. Our method works by registering the vascular system to approximate the liver deformation. The registration process is robust to topological changes within the vascular graph. Preliminary results promise an efficient approach.

However, this study must be tested on a larger database to be correctly evaluated. Future work will be directed towards defining a more complex local deformation model and improving the robustness of the energy function. We will also be able to introduce Kalman filtering to estimate a global deformation of the liver.

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