A Hierarchical Layered Graph Approach for Multi-Label Segmentation in 2D Medical Images

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Abstract

A method for the multi-label segmentation in medical images must attend all the individual priors of each object such as shape constraints or boundary polarity, as well the structural relations between them. However, many existing classical approaches do not include these high-level priors into a single energy optimization, or are only restricted to some particular cases. We proposed a novel method that uses a weighted digraph, named as *layer*, associated to each object attending its individual high-level priors. All the layer graphs are then integrated into a hierarchical graph, considering the hierarchical structural relations of inclusion and exclusion. A *single* energy optimization is performed in the hierarchical layered weighted digraph leading to globally optimal results satisfying all the priors and hard constraints such as seeds. Our experimental evaluations indicate promising results. Compared to min-cut/max-flow algorithm, our approach is less restrictive, leading to globally optimal results in more general scenarios, and has a better running time.

1 Proposed method

In graph-based methods, an image is modeled as a connected graph, because it can naturally represent the objects and their relationships **[1]**. Then, the image segmentation task can be interpreted as a graph partition problem subject to hard constraints. We propose a new graph-based method named as *Hierarchical Layered Oriented Image Foresting Transform* (HLOIFT). This method was firstly introduce in **[2]** and an extended version was submitted to a journal **[3]** which is still under revision. Figure 1 shows an overview of our framework. For a given input image, seeds sets for some objects, and the tree of relations between objects, the HLOIFT method has three principal steps which are briefly described below.

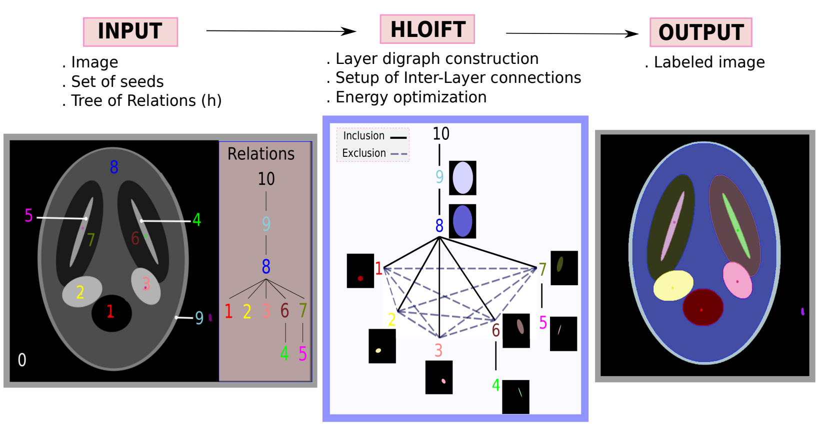

Figure 1: Framework: given the input parameters, HLOIFT constructs a hierarchical layered weighted digraph using individual and structural constraints. As output, we have a multi-labeled image.

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Layer digraph construction : We first create a set of m layers, where each layer represents a single corresponding object O_i, $i \in \mathcal{L} = \{1, \ldots, m\}$, of an (*n-dimensional*) image $\mathcal{I} \subset \mathbb{Z}^n$. A layer $\mathcal{H}_i = (\mathcal{N}_i, \mathcal{A}_i, \omega_i)$ is a weighted digraph, where $\mathcal{N}_i = \{i\} \times \mathcal{I}$ and each node $t = (i, v) \in \mathcal{N}_i = \{i\} \times \mathcal{I}$ correspond to the image pixel $p(t) = v$. We define the intra-layer adjacency $\mathcal{A}_i$ on $\mathcal{N}_i = \mathcal{I}$ as this $\mathcal{A}_\mathcal{I}$, that is, $(s,t) \in \mathcal{A}_i$ if, and only if, $(p(s), p(t)) \in \mathcal{A}_\mathcal{I}$. Usually, $\mathcal{A}_\mathcal{I}$ is the 4- or 8-neighborhood adjacency. Similarly, we have defined an intra-layer weight function ω_i for every $(s,t) \in \mathcal{A}_i$. Of course, ω_i should highlight the priors for O_i whenever it is appropriate. We based on the regular OIFT method **[4]**, for **boundary polarity** priors, and the **geodesic star convexity prior**, prioritizing the O_i with more regular shape as in **[5]**.

Setup of inter-layer connections : In this step, HLOIFT generates a *hierarchical layered* weighted digraph $\mathcal{H}$ as the union of all layered graphs $\mathcal{H}_i$, $i = 1, \ldots, m$, with the additional *inter-layer* arcs connecting only some of the distinct layers, based on the priors h (a *tree*) and ρ (distance parameter). The hierarchy prior (h) between any pair $\langle O_i, O_j \rangle$ of objects is understood: either $O_i \cap O_j = \emptyset$ (**exclusion**), or one of them is properly contained in the other (**inclusion**), and defined as follows. If $O_{m+1} = \mathcal{I}$ (the image domain and the root of the tree). Then $h(i) = j$ if, and only if, O_j is the smallest of the objects properly containing O_i, and we will refer to O_j as the *parent* of O_i. We say that the objects O_i and O_j are *siblings*, provided $i, j \in \mathcal{L}$ are distinct and $h(i) = h(j)$. We will use the distance parameter $\rho \geq 0$, where

(C) for siblings O_i and O_j we will assume that $\|s - t\| > \rho$ for every $s \in O_i$ and $t \in O_j$, while for parent-offspring pair $\langle O_j, O_i \rangle$ that $t \in O_j$ whenever there exists an $s \in O_i$ with $\|s - t\| \leq \rho$.

The weights of the inter-layer arcs for **inclusion**, is $\omega(t,s) = \infty$ and $\omega(s,t) = -\infty$, and for the special arcs ($\mathcal{A}_s$) of **exclusion**, $\omega(s,t) = \omega(t,s) = -\infty$.

Energy optimization : Finally, we execute the HLOIFT algorithm **[3]**, which is a modified and very efficient Jarník-Prim-Dijkstra algorithm: quasi-linear w.r.t. the size of the graph. It is applied to the hierarchical layered graph $\mathcal{H}$ constructed above and its output maximizes a single energy ε^h_{min} defined to ensure that the output satisfies also the hierarchical constraints imposed by h and ρ. Specifically, for a binary map $X \colon \mathcal{N} \to \{0, 1\}$ (segmentation) the energy ε^h_{min} of X is defined as

$$\varepsilon^h_{min}(X) \quad = \quad \min\{\varepsilon^{incl}_{min}(X), \varepsilon^{excl}_{min}(X)\}, \tag{1}$$

where $\varepsilon^{incl}_{min}(X) = \min\{\omega(s,t) \colon (s,t) \in \mathcal{A} \setminus \mathcal{A}_s \ \&\ X(s) > X(t)\}$, and
$\varepsilon^{excl}_{min}(X) = \min\{\omega(s,t) \colon (s,t) \in \mathcal{A}_s \ \&\ X(s) = X(t) = 1\}$. As result we have the Theorem 1, which proof of correctness is in **[3]**.

Theorem 1 (Cut optimality by HLOIFT) *For every image $(\mathcal{I}, I)$, a hierarchy tree h, a distance parameter $\rho \geq 0$, and a sequence $\langle \mathcal{S}_0, \ldots, \mathcal{S}_n \rangle$ of seed sets consistent with (C), the binary map $X \colon \mathcal{N} \to \{0,1\}$, computed by the HLOIFT Algorithm in* **[3]**, *maximizes the energy $\varepsilon^h_{min}(X)$ given by (1) among all solutions satisfying the seed constraints and the requirement (C).*

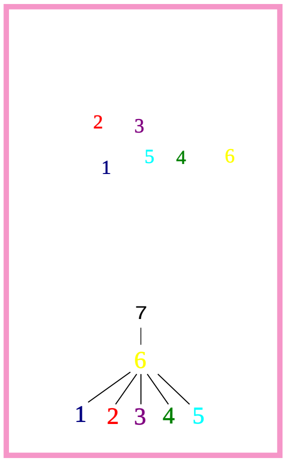
2 Experimental evaluation

We used a medical image to compare the result obtained by HLOIFT against the IFT method **[7]** for multi-object segmentation by seed competition. OIFT is not included here since it is restricted only to binary segmentation **[4,8]**. Another experiments are described in**[2,3]**. In Figure 2, we used a thoracic-abdominal CT image, extracted from 3D-IRCADb-02 **[9]**, to segment six objects: right lung (O_1), liver (O_2), heart (O_3), left lung (O_4), aorta (O_5) and the thoracic-abdominal region (O_6). As input we have the image, the tree of relations (h) and only **some** user seeds. We used ω^i defined by a dissimilarity measure. We also used $\rho = 3.5$, boundary polarity from dark to bright pixels for O_1, and from bright to dark pixels for O_5 and O_6, and O_4 shape constraint by geodesic star convexity for O_2 and O_3. Clearly, the HLOIFT results are closer to the ground-truth compared to the IFT results.

3 Conclusion

In the context of multi-label segmentation is advantageous to explore the own distinctive features of each object as the structural relations between the different objects in the image. Therefore, our main contributions are: **Theoretical:** a new method, named *HLOIFT*, allowing the integration of high-level priors for the objects and their hierarchical constraints, into a single energy optimization in a hierarchical graph of layers; **Generality:** leads to globally optimal results in more general scenarios; and **Complexity:** lower computational complexity as compared to methods based on the min-cut/max-flow algorithm **[10]**, as was shown in **[3]**. Our experiments show good segmentation results, even considering a simple measure of dissimilarity. As a future work, we are interested in use a machine learning method to generated ideal weighted graphs. Also now we are extending our method to work with 3D medical images.

INPUT



OUTPUT

Figure 2: A thoracic-abdominal CT image segmentation with six objects. HLOIFT obtain a result similar to the ground-truth (manual segmentation), in contrast to the IFT method.

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