

A Fast Algorithm for Liver Surgery Planning

Fajie Li, Xinbo Fu, Gisela Klette, and Reinhard Klette

Xiamen (China) and Auckland (New Zealand)

DGCI, Sevilla - March 22, 2013

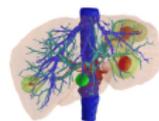
Slide 1: Introduction

- ▶ Liver cancer is the 5th most common malignancy in men and the 8th in women worldwide. In 2000 there were 564,000 new cases.
- ▶ **Liver resection** often the cure for primary liver cancer.
- ▶ Existing **liver surgery planning** usually requires surgeons' personal expertise to interact during surgery.
- ▶ For example, there is branch labelling at some planning stage; this is the most time-consuming step in the planning procedure.

Slide 2: Related work

Mint Liver, 3D image analysis software for liver resection from Germany for hepatic surgeons

*mint Liver*TM – Liver Resection Planning



Your solution for advanced liver diagnostics and therapy planning
*mint Liver*TM offers valuable and efficient methods and workflows to support diagnosis and therapy planning of liver diseases. By using advanced PACS interfaces and fully automated analysis of your image data, *mint Liver*TM finishes tedious image processing tasks before you even start to diagnose your patient. During therapy planning, a palette of intuitive tools provides you with the opportunity to model and compare various, alternative therapy strategies in a short time to assess the best possible treatment for your patient.

- ▶ (1) a deformable 2D manifold for resection; 3D interaction to specify and modify this manifold by medical doctors
- ▶ (2) a probabilistic atlas
- ▶ (3) squared Euclidean distance transform for approximately computing the liver part that should be removed
- ▶ (4) calculates the vascular perfusion area, based on direction and diameter of the portal vein branch

Existing algorithms compute only 'heuristically' the liver part that should be removed.

Slide 3: The problem

We model the problem in terms of digital geometry and propose an algorithm for computing the diseased part of a liver.

The problem to be solved is as follows:

- ▶ Let S_l be the set of cells (i.e., voxels) in the given 3D input image classified to be **liver cells**.
- ▶ Set S_h contains all cells classified to be **healthy vein cells**.
- ▶ Set S_d contains all the detected **diseased vein cells**.
- ▶ We have to specify and then to calculate that part of the liver which is **affected by** diseased vein cells.

Slide 4: Considered subsets

Our **accurate** solution for this problem is defined by the maximum subset $A \subseteq S_I$ such that A is **affected by** the set S_d of diseased cells.

- ▶ We compute three subsets $S_{a_{h+d}}$, S_{a_h} , and S_{a_d} such that

$$S_I = S_{a_{h+d}} \cup S_{a_h} \cup S_{a_d}$$

where $S_{a_{h+d}}$ is affected by both S_h and S_d , S_{a_h} by S_h only, and S_{a_d} by S_d

- ▶ $S_{a_{h+d}}$ are boundary cells between healthy liver cells and diseased liver cells.
- ▶ Set $S_{a_{h+d}} \cup S_{a_d}$ of liver cells should be removed (our solution).

Slide 5: Definition of “affected by”

Discussion for plane and 2D images only for simplicity.

$d_e(p, q)$ – Euclidean distance between p and q in the plane

Planar sets A and B : $d_{min}(A, B) = \min\{d_e(p, q) : p \in A \wedge q \in B\}$

$d_{min}(p, B) = d_{min}(A, B)$ if $A = \{p\}$.

- ▶ Set $S \subseteq S_l$ is *only affected* by S_h if for each cell $p_l \in S$,
 $d_{min}(p_l, S_h) < d_{min}(p_l, S_d)$.
- ▶ Analogously: set $S \subseteq S_l$ is *only affected* by S_d .
- ▶ $S \subseteq S_l$ is *affected* by both S_h and S_d if for each cell $p_l \in S$,
 $d_{min}(p_l, S_h) = d_{min}(p_l, S_d)$.

Slide 6: We use cells and supercells

h for cell of type- h , d for type- d , and l for type- l .

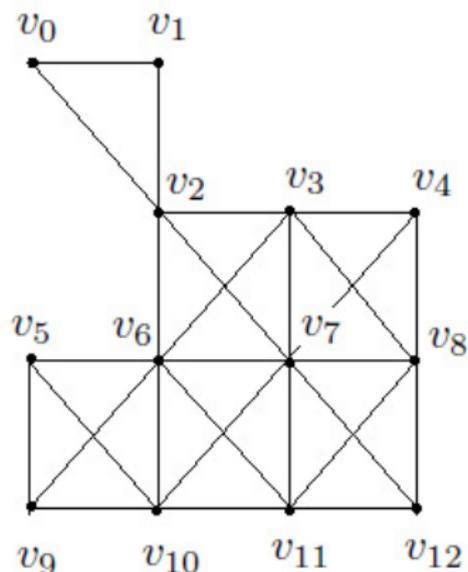
h	h	h	h	l	l						
	h	h	h	h							
	h			h	h						
				h	h			l	l	l	
				h	h	h	h	h	d	l	
				h				d	d	l	
				h			d	d	d		
l	l	h	h	h				d	d		
	l	l						d	d		
l	l	l	l					l	d	d	
l	l	l						l	d	d	
	l							l	l	l	

h	h	h	h	l	l						
	h	h	h	h							
	h			h	h						
				h	h				l	l	l
				h	h	h	h	h	h	d	l
				h					d	d	l
				h				d	d	d	
l	l	h	h	h					d	d	
	l	l							d	d	
l	l	l	l						l	d	d
l	l	l							l	d	d
	l								l	l	l

Left: Set S of labelled cells for original grid constant θ_0 .

Right: Supercells for grid constant $\theta = \theta_0 \times 3$.

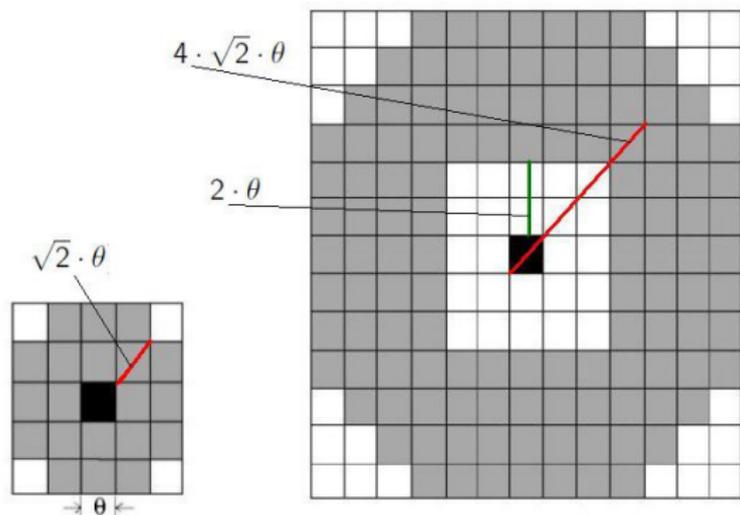
Slide 7: We use θ -graphs for 8-adjacent supercells



8-adjacent occupied θ -supercells (for figure before)
weights are either θ or $\theta\sqrt{2}$

Slide 8: Two types of used adjacency sets for supercells

Just for illustrating that we also use two types of adjacencies.



Left: type-1 adjacency set $N(C, 3, \sqrt{2} \cdot \theta)$ for a type-*sldoh* supercell C .

Right: type-2 adjacency set $N(C, 4, 4, 2)$ for a type-*sl* supercell C .

Slide 9: A brute-force subroutine for subset assignments

The idea of this brute-force routine is simple:

- ▶ For each cell $p_l \in S_l$,
- ▶ go through S_h for computing $d_{min}(p_l, S_h)$;
- ▶ go through S_d for computing $d_{min}(p_l, S_d)$;
- ▶ If $d_{min}(p_l, S_h) < d_{min}(p_l, S_d)$, then let $S_{a_h} = S_{a_h} \cup \{p_l\}$;
- ▶ else, if $d_{min}(p_l, S_h) > d_{min}(p_l, S_d)$, then let $S_{a_d} = S_{a_d} \cup \{p_l\}$;
- ▶ otherwise $S_{a_{d+h}} = S_{a_{d+h}} \cup \{p_l\}$.

Slide 10: An improved version

The idea of its improved version is also simple. Assume that $|S_h| \leq |S_d|$.

- ▶ We may not have to go through S_d for computing $d_{min}(p_l, S_d)$:
- ▶ If there exists a cell p_d such that $d_e(p_l, p_d) < d_{min}(p_l, S_h)$ then let $S_{a_d} = S_{a_d} \cup \{p_l\}$,
- ▶ and we break then both this for-loop and the outer for-loop,
- ▶ and test the next cell after p_l in S_l .

Slide 11: The decomposition algorithm

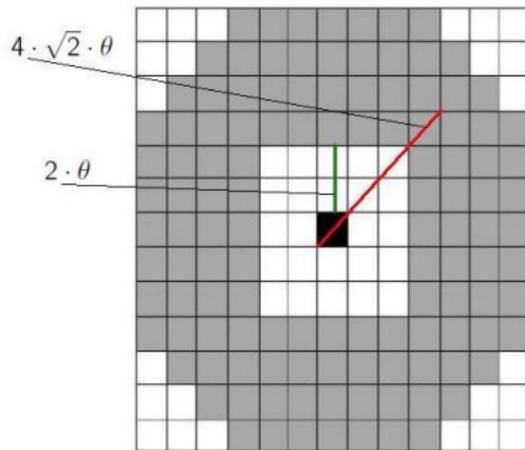
Main ideas:

- ▶ decompose the liver into some supercells
- ▶ remove unnecessary supercells (that are “too far” from the current supercell)
- ▶ reuse the improved version of the above brute-force routine

Main steps:

- 1 For each supercell C , if C is of type-*sldoh* then compute type-1 adjacency set $N(C, 3, \sqrt{2} \cdot \theta)$
- 2 The candidate sets are reduced from S_d and S_h to $S_d \cap N(C, 3, \sqrt{2} \cdot \theta)$ and $S_h \cap N(C, 3, \sqrt{2} \cdot \theta)$.

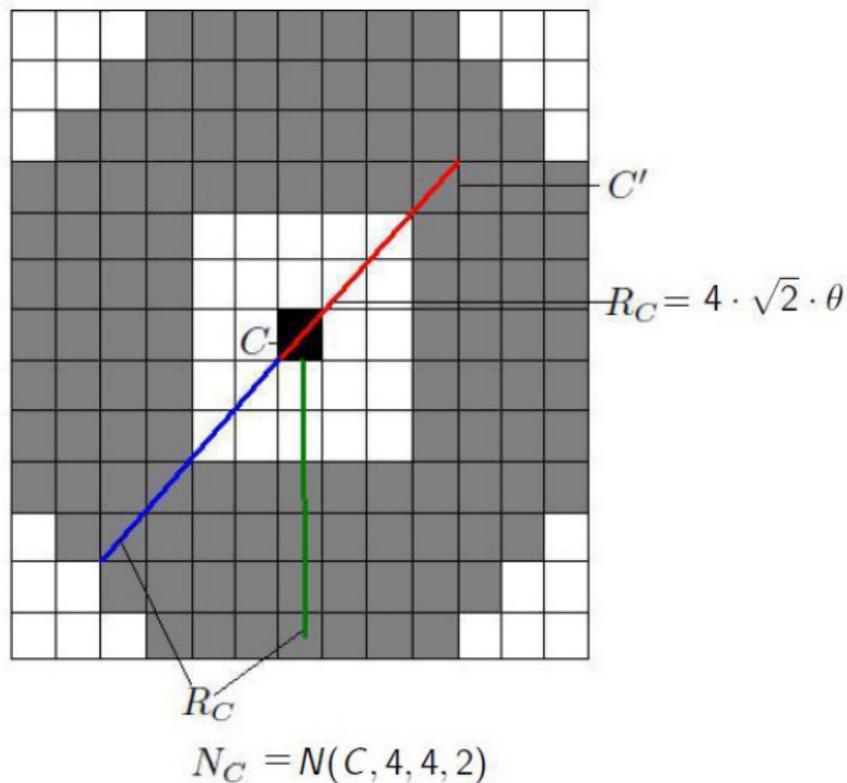
Slide 12: Algorithm continued



$N(C, 4, x, y)$, where $x = 4, y = 2$

- 3 For each supercell C , if C is of type- $s/$ then compute type 2 adjacency set $N(C, 4, x, y)$, where parameters x and y depend on the supercell C .
- 4 The candidate sets are reduced from S_h and S_d to $S_h \cap N(C, 4, x, y)$ and $S_d \cap N(C, 4, x, y)$, respectively.

Slide 13: Correctness of the algorithm.

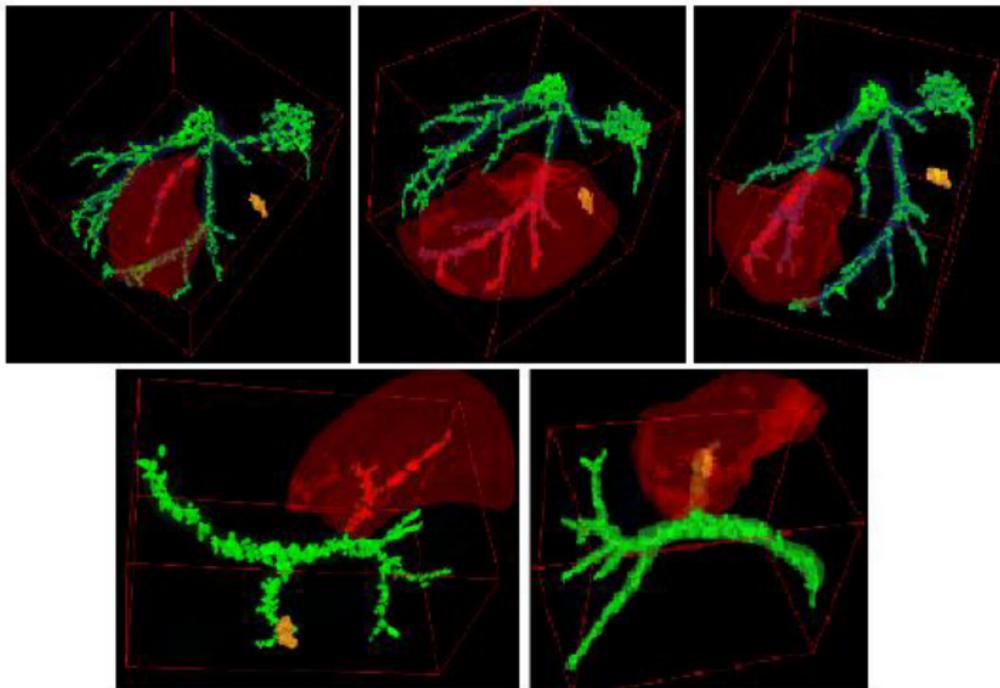


Slide 14: Time Complexity

The runtime of algorithm is in $\mathcal{O}(m^i \times n \times n_{ave})$, where m satisfies $\theta = m \times \theta_0$, n is the number of supercells, n_{ave} is the average value of all supercells in type 2 adjacency sets $N(C, 4, x, y)$'s, and $i = 2$ for the 2D case, and $i = 3$ for the 3D case.

- ▶ Exact Euclidean Distance Transform takes $\mathcal{O}(m^i \times n)$ operations.
- ▶ The decomposition algorithm may be slower than the exact Euclidean Distance Transform depending on the value of n_{ave} that depends on the distribution of input type- j cells, for $j = d, h, l$.
- ▶ Some literature reports about an average labelling time of about 17 minutes, depending on the data set.
- ▶ Our algorithm takes about 30 seconds on the data set $324 \times 243 \times 129$ (PC: 2.4GHz CPU, 2.0Gb RAM)

Slide 15: Examples



Slide 16: Concluding remarks and future work

Concluding remarks:

- ▶ propose a time-efficient algorithm for separating liver cells
- ▶ In contrast to existing methods, our algorithm is not only independent of a surgeons' personal interactive manipulations,
- ▶ but also outputs an exact solution.
- ▶ Exact Euclidean Distance Transform may not work correctly if the input liver is non-convex.

Future work:

Generalize the algorithm for non-convex liver inputs.