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Segmentation of 3D tubular objects with adaptive front propagation and minimal tree extraction for 3D medical imaging

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We present a new fast approach for segmentation of thin branching structures, like vascular trees, based on *Fast-Marching* (FM) and *Level Set* (LS) methods. FM allows segmentation of tubular structures by inflating a "long balloon" from a user given single point. However, when the tubular shape is rather long, the front propagation may blow up through the boundary of the desired shape close to the starting point. Our contribution is focused on a method to propagate only the useful part of the front while freezing the rest of it. We demonstrate its ability to segment quickly and accurately tubular and tree-like structures. We also develop a useful stopping criterion for the causal front propagation. We finally derive an efficient algorithm for extracting an underlying 1D skeleton of the branching objects, with minimal path techniques. Each branch being represented by its centerline, we automatically detect the bifurcations, leading to the "Minimal Tree" representation. This so-called "Minimal Tree" is very useful for visualization and quantification of the pathologies in our anatomical data sets. We illustrate our algorithms by applying it to several arteries datasets.

Keywords: Segmentation; Fast-marching; Level set; Minimal paths; Skeletonization; 3D medical imaging

1. Introduction

We are interested in this paper in segmentation of branching tubular objects from 3D images, motivated by medical applications related to vascular trees. Much work has been done on surface extraction since the introduction of deformable models (see references in McInerney and Terzopoulos 1996) and their first use for medical images in Cohen and Cohen (1993). The recent trend in this domain makes use of Level Set (LS) methods (for example Malladi *et al.* 1993, 1995, Caselles *et al.* 1996, Yezzi *et al.* 1997).

A major drawback of the LS methods is their huge computation time, even when using a narrow band. *Fast-Marching* (FM), introduced in Sethian (1999) allows fast surface segmentation when the evolution is always going outward like a balloon (Cohen 1991, Malladi and Sethian 1998). Using FM as a region-growing method, we can for example extract the surface of the colon out of a CT scanner, starting from an initial seed point inside the object of interest (Deschamps and Cohen 2001). An important question is when to stop the propagation in order to get the desired segmentation.

In Deschamps (2001)and Deschamps and Cohen 90 (2001), we have demonstrated that the front propagation could be stopped on the basis of a distance traveled by the front corresponding to the known length of the object, by computing the length of the minimal path to the starting point while the front is propagated. When the propagation 95 speed is almost constant inside the tubular structure, this length is almost the geodesic distance to the starting point inside the tubular object. Figure 1 illustrates this idea by showing iterations of this front propagation in a 3D image with a speed chosen in order to segment the colon. 100

However, classical segmentation problems do not provide an excellent contrast like the air-filled colon on a CT scanner, and the front usually flows over the boundaries of longer and thinner objects when propagating. Our aim in this article is to show how the FM surface segmentation can be specifically optimized for this target. If the propagation of a front could be restricted to the part of the image occupied by those structures, the computing time could be divided by almost

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Figure 1. Segmenting the colon volume (orthogonal CT slices above) with FM: the user locates a starting point at one particular recognizable part of the colon, then a front is propagated from this seed point until a maximum path length is reached (below).

five, since arteries in a typical MR-Angiography image donot exceed 10% of the whole volume.

The FM algorithm is also a very powerful tool to extract minimal paths in images, as shown in Cohen and Kimmel (1997). Starting from the 3D implementation of the minimal path tracking, previously used for virtual endoscopy (Deschamps and Cohen 2001), we show that it can be extended to automatically extract the trajectories in each branch of a tree-like object. Finally, we explain how to build a *Minimal Tree* from this trajectories. This *Minimal Tree* is the underlying skeleton of our branching tubular shapes. We show on several medical images the gain that results in terms of visualization and quantification of the pathologies concerned.

This paper is organized as follows: In Section 2, we summarize the method detailed in Cohen and Kimmel (1997) for minimal path tracking, and the application to segmentation of the minimal path algorithm (Malladi and Sethan 1998). In Section 3 we detail the *Freezing* approach: a front propagation technique for thin and elongated shape extraction. Finally, in Section 4 we explain how to extract efficiently the *Minimal Tree* of the resulting segmented objects, showing the improvement brought to the examination of anatomical objects and their pathologies.

2. Minimal paths, FM and surface segmentation

2.1 Minimal paths extraction

2.1.1 Global minimum for active contours energy. We present in this section the basic ideas of the minimal path method introduced by Cohen and Kimmel (1997) to find a curve in a 2D or 3D image that reaches the global

minimum of the active contour energy. The energy to minimize is similar to classical deformable models (Kass *et al.* 1988) where the curve is evolving under the influence of both smoothing and image features attraction terms:

$$E(C) = \int_{\Omega} \{w_1 \| C'(s) \|^2 + w_2 \| C''(s) \|^2 + P(C(s)) \} ds.$$
(1)

where C(s) represents a curve drawn on a 2D or 3D image, Ω its domain of definition, and *P* the potential function or penalty image term, being small where the curve should be attracted. Authors Cohen and Kimmel (1997) avoided the energy minimization problem of getting stuck at local minima by considering a simplified energy model leading to a global minimum solution. Dismissing the second derivative term and using the arc-length *s* parametrization in the energy leads to the expression

$$E(C) = \int_{\Omega} \{w + P(C(s))\} \mathrm{d}s.$$
 (2)

where $\Omega = [0, L]$, and *L* is the length of the curve. We now have an expression in which the internal forces are included in the external image term and where the regularization is now achieved by the constant w > 0. In Cohen and Kimmel (1997), this problem is related to the paradigm of the LS formulation, by showing that its Euler equation is equivalent to the geodesic active contours (Caselles *et al.* 1997).

Given a potential P > 0 that takes lower values near desired features, and two end points \mathbf{x}_0 and \mathbf{x}_1 , we are looking for paths along which the integral of $\tilde{P} = P + w$ is minimal among all paths that join \mathbf{x}_0 and \mathbf{x}_1 . In order to

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[¶] This means that $C(0) = \mathbf{x}_0$ and $C(L) = \mathbf{x}_1$.

(3)

find a curve minimizing this energy, the minimal action map $T(\mathbf{x})$ is defined as the minimal energy integrated along a path starting at point \mathbf{x}_0 and ending at point \mathbf{x} :

$$T(\mathbf{x}) = \inf_{\mathcal{A}_{\mathbf{x}_0,\mathbf{x}}} E(C) = \inf_{\mathcal{A}_{\mathbf{x}_0,\mathbf{x}}} \left\{ \int_{\Omega} \tilde{P}(C(s)) \mathrm{d}s \right\}.$$

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where $A_{\mathbf{x}_0,\mathbf{x}}$ is the set of all paths joining \mathbf{x}_0 and \mathbf{x} . Assuming $T(\mathbf{x})$ has been computed over the image domain, a minimal path between \mathbf{x}_0 and any point \mathbf{x}_1 in the image can be easily built out of this minimal action map: the potential *P* being always positive, the minimal action map will have only one local minimum which is the starting point \mathbf{x}_0 . The minimal path indicating the smallest weighted length trajectory to go from \mathbf{x}_0 to \mathbf{x}_1 , it will be built by a simple back-propagation on the image domain, following the gradient descent of the energy $T(\mathbf{x})$ from \mathbf{x}_1 to \mathbf{x}_0 (see Ardon *et al.* 2007 for proof). More than simplifying the minimization process, this method even reduces the initialization to the selection of the two extremities of the path, rather than a whole curve for active contours.

2.1.2 Fast-marching resolution. In order to compute minimal action map *T* in equation (3), we solve the related front-propagation equation $((\partial C)/(\partial t)) = (1/\tilde{P})\vec{n}$, where \vec{n} is the normal vector to *C*, and the speed is inverse proportional to the potential. It evolves a front starting from an infinitesimal circle shape around \mathbf{x}_0 until each point inside the image domain has been visited by the front. *T*(\mathbf{x}) being the time *t* at which the front passes over the point \mathbf{x} , it represents the minimal cost to go from \mathbf{x}_0 to \mathbf{x} , i.e. the energy of the minimal path between \mathbf{x} and the start point \mathbf{x}_0 .

The **FM** algorithm, introduced by Sethian (1999), was used by Cohen and Kimmel (1997) noticing that the map T in equation (3) satisfies the Eikonal equation:

$$\|\nabla T\| = \tilde{P}, \quad T(\mathbf{x}_0) = 0. \tag{4}$$

One way to solve equation (4) is to use upwind finite difference schemes and iterate the solution in time. In other words, the scheme relies on one-sided differences that looks in the upwind direction of the moving front, thereby picking the correct viscosity solution. In order to solve equation (4) in a 3D image (Deschamps and Cohen 2001), we write that at each voxel (i, j, k), the unknown *T* satisfies the quadratic equation:

$$\left(\frac{\max\{T - T_{i-1,j,k}, T - T_{i+1,j,k}, 0\}}{\Delta x}\right)^{2} + \left(\frac{\max\{T - T_{i,j-1,k}, T - T_{i,j+1,k}, 0\}}{\Delta y}\right)^{2}$$
(5)

+
$$\left(\frac{\max\{T - T_{i,j,k-1}, T - T_{i,j,k+1}, 0\}}{\Delta z}\right)^2 = \tilde{P}_{i,j,k}^2$$
.

giving the correct viscosity-solution t for $T_{i,j,k}$, with Δx , Δy and Δz being the pixel anisotropy.

The improvement made by the FM proposed by Sethian (1999) is to solve this equation rapidly by introducing order in the selection of the grid points. This order is based on the fact that information is propagating *outward*, because the minimal action T can only grow due to the quadratic equation (5).

The algorithm is detailed in table 1.

The FM selects at each iteration the *T*rial point with minimum energy. This technique of considering at each step only the necessary set of grid points was originally introduced for the construction of minimum length paths in a graph between two given nodes in the A^* algorithm (Dijkstra 1959).

Thus it needs only one pass over the entire image. To perform efficiently these operations in minimum time, the *Trial* points are stored in a min-heap data structure (see details in Sethian 1999). Since the complexity of the operation of changing the value of one element of the heap is bounded by a worst-case bottom-to-top proceeding of the tree in $O(\log_2 N)$, the total work is about $O(N \log_2 N)$ for the FM algorithm on a N points grid.

Once the front has been propagated, we can *back-track* a minimal path inside the image. The minimal path between any point **x** and the start point \mathbf{x}_0 is found by sliding back the map *T* until it reaches to \mathbf{x}_0 . It can be achieved by a simple steepest gradient descent with a pre-defined descent step on the minimal action map *T*, choosing

$$\mathbf{x}_{n+1} = \mathbf{x}_n - \operatorname{step} \times \nabla T(\mathbf{x}_n). \tag{6}$$

More accurate gradient descent methods like Runge–Kutta midpoint algorithm or Heun's method can be used for this back-tracking.

2.1.3 Calculation of the length of the minimal path. The length of the minimal path between \mathbf{x}_0 and \mathbf{x} is a very valuable indication. It is the *Euclidean* distance traveled by the front from our starting point \mathbf{x}_0 to reach \mathbf{x} , and it is

Table 1.	Algorithm	for 3D	Fast-Marching
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• Definitions:	
 Alive set: grid points at which the values of T have been reached and will not be changed; 	320
 Trial set: next grid points (6-connectedness neighbors) to be examined. An estimate T has been computed using discretized equation (5) from Alive points only; 	
- Far set: all other grid points, there is not yet an estimate for T;	
Initialization:	
- Alive set: start point \mathbf{x}_0 , $T(\mathbf{x}_0) = 0$;	325
- Trial set: reduced to the six neighbors \mathbf{x} of \mathbf{x}_0 with initial value	525
$T(\mathbf{x}) = \tilde{P}(\mathbf{x});$	
- Far set: all other grid points, with $T = \infty$;	
• Loop:	
- Let \mathbf{x}_{\min} be the Trial point with smallest T;	
- Move it from the Trial to the Alive set;	
- For each neighbor \mathbf{x} of \mathbf{x}_{\min} :	330
*If x is Far, add it to the Trial set and compute a first estimate of	
$T(\mathbf{x})$, solving equation (5);	
*If x is Trial, update $T(\mathbf{x})$, solving equation (5).	

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something we would like to use while we are propagating a front in an image.

Once the path is extracted by gradient descent (6), we can easily compute its length. But this is a very time consuming process to systematically do this at each point visited.

Therefore, we propose to compute on-the-fly an approximation of the distance traveled by the front, while it is propagating according to the Eikonal equation (4), with a method originally introduced in Deschamps and Cohen (2001).

Notice first that when $\forall \mathbf{x}, P(\mathbf{x}) = 1$, energy *E* is proportional to the length of the path, a minimal path is a shortest path, and if we call *d* the minimal action defined by (3), it is proportional to the distance to the starting point, and it can be obtained by solving

$$|\nabla d|| = 1 \, d(x_0) = 0. \tag{7}$$

This means that when propagating a front with a constant speed equal to 1, the minimal energy obtained at each point represent the *Euclidean* distance d to the starting point.

350 Now, in the general case for P, in order to compute the Euclidean length D of the minimal path at each point, at the same time we make the FM to compute T, we can compute an estimate by solving locally equation (7), using the same neighbors involved for solving T in equation (5). As detailed 355 for example in Cohen (2005), equation (5) is solved at each grid point as a quadratic equation involving at most three of the six neighbors that appear in equation (5). This comes from the fact that for each of the three frame directions i, j, k, only the neighbor reaching the max is involved, or none if 360 that max is 0. Let us denote i_0, j_0, k_0 such that $i - 1 \le i_0 \le$ $i + 1; j - 1 \le j_0 \le j + 1; k - 1 \le k_0 \le k + 1$ the indexes which reach the max in each direction, with the convention that if $i = i_0$ that term is void, and the same for $j = j_0$ or $k = k_0$. We then solve in the FM for T and D the quadratic 365 equations:

$$\begin{cases} \left(\frac{T-T_{i_0,j,k}}{\Delta x}\right)^2 + \left(\frac{T-T_{i,j_0,k}}{\Delta y}\right)^2 + \left(\frac{T-T_{i,j,k_0}}{\Delta z}\right)^2 = \tilde{P}_{i,j,k}^2. \\ \left(\frac{D-D_{i_0,j,k}}{\Delta x}\right)^2 + \left(\frac{D-D_{i,j_0,k}}{\Delta y}\right)^2 + \left(\frac{D-D_{i,j,k_0}}{\Delta z}\right)^2 = 1. \end{cases}$$
(8)

The corresponding algorithm is described in table 2.

This algorithm was already used for reducing userintervention in the Virtual Endoscopy process (Deschamps and Cohen 2000). If we evolve a front inside a tubular object (like the colon) and compute at the same time the Euclidean distance travelled with the algorithm detailed in table 2, the first improvement is that the propagation can be automatically stopped when a chosen length has been traveled. The second improvement is that we can automatically pick the furthest visited point as extremity to extract a minimal path between this point and the starting point inside a tubular structure. Therefore, the user interaction is limited to locating the start point in the

Table 2.	Algorithm for computing the euclidean distance traveled by
	the front.

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- A starting point **x**₀ manually set;
- The minimal action map T, a min-heap \mathcal{H}_T and a potential image P_{390} as defined in equation (4);

• A distance map *D* to compute the Euclidean minimal path length; Initialization

• Initialize the front propagation method, by setting $T(\mathbf{x}_0) = D(\mathbf{x}_0) = 0$ and storing \mathbf{x}_0 in min-heap \mathcal{H}_T ;

Loop: at each iteration, consider \mathbf{x}_{\min} be the *T*rial point with smallest *T* • Move it to Alive set, and remove it from \mathcal{H}_T

- For each neighbor **x** of **x**_{min}:
 - Proceed according to the classical FM algorithm: update T(x) and re-balance H_T;
 Update D(x) according to equation (8) using the same
 - neighbors of **x** that were involved in updating $T(\mathbf{x})$

dataset, and it is very important when studying such a complicated object as the colon or a brain vessel (Deschamps and Cohen 2001).

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2.2 Segmentation with the Eikonal equation

Many approaches are possible to segment the external surface of an object starting from inside, like a balloon model (Cohen 1991) or its LS implementation (Malladi 410 et al. 1995, Tek and Kimia 1995). FM can be used as well to perform this kind of monotone surface evolution (Malladi and Sethian 1998). When computing the minimal energy from a starting point, the Trial points correspond to the boundary of the visited points (a contour in 2D or a 415 surface in 3D). If the potential \tilde{P} is much larger on the external surface of the object than inside it, then, since its speed is inverse proportional to P, the front moves slowly when it reaches the boundary, and that surface acts as a barrier for the front propagation. In this case, the Trial 420 points define a surface segmenting the object, and satisfying the front propagation equation $(\partial C/\partial t) =$ $(1/\tilde{P})\vec{n}$ as mentioned in previous section.

Let us see the relation with LS methods and consider the usually solved evolution equation of an interface (2D 425 curve or 3D surface):

$$\begin{cases} \frac{\partial C}{\partial t}(x) = F\vec{n}, \\ C(x,0) = C_0(x), \end{cases}$$
(9)
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If we assume that the speed of the interface $F = 1/\tilde{P}$ is strictly positive, the front moves always outside, in the normal direction \vec{n} like an inflating balloon (Cohen 1991), but with a non constant speed. The idea of the LS method is to solve the evolution equation

$$\phi_t + F \|\nabla\phi\| = 0. \tag{10}$$

where C(t) identifies § with the zero LS of ϕ .

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[§]The relation between equations (9) and (10), detailed in Sethian (1999), can be understood from the fact that the normal \vec{n} to the LS of ϕ is in the direction of $\nabla \phi$, used in a way similar to equation (11) below.

 $T(C(\mathbf{x}, t)) = t \Rightarrow \nabla T \cdot C_t = 1$

A different way to find the location of the interface is to compute the arrival time $T(\mathbf{x})$ of the curve C when it reaches each point of the image. This map T is characterized by the fact that for all points of C(., t), the curve position at time t, we have T = t(C(., t) corresponds)to the t LS of T). Using simple derivation with respect to t and the classical property that the gradient of a function is normal to its LS, and thus $\vec{n} = (\nabla T / ||\nabla T||)$, the following equations are obtained from the evolution of C in equation (9):

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$$\Rightarrow \nabla T \cdot (F\vec{n}) = \nabla T \left(F \frac{\nabla T}{\|\nabla T\|} \right) = 1 \qquad (11)$$
$$\Rightarrow F \cdot \|\nabla T\| = 1$$

where we find again the same Eikonal equation as above in 460 equation (4). This equation was used in (Malladi and Sethian 1998) for surface segmentation since it has the same advantages as the LS method, but can be implemented much faster. Discretized with an upwind scheme, it is then solved using the FM algorithm (table 1), 465 given an initial starting point \mathbf{x}_0 . In practice the front is propagated until a given time is reached. This corresponds to the set of *Trial* points when reaching a given energy since each new alive point has larger value of T than all previous ones, that set correspond to a LS.

470 Figure 1 shows iterations of this front propagation in a 3D image with an image term defined in order to segment the colon. Evolution is stopped when a given geodesic length has been traveled by the front, as described in Subsection 2.1.3.

475 As refinement process, the front is evolved to sub-pixel accuracy, using a more complicated scheme, as in Caselles et al. (1997) or Caselles et al. (1996):

$$\phi_t + (1 - \varepsilon \kappa) F_\sigma \|\nabla \phi\| - \beta \nabla g \cdot \nabla \phi = 0$$
(12)

where the equation contains the following terms:

- an inflating force, analogous to the balloon force (Cohen 1991), here defined by $F_{\sigma}(\mathbf{x}) = 1/(1 + \|\nabla I_{\sigma}(x)\|)$ where I_{σ} is the image convolved with a Gaussian kernel of size σ ; this inflating force vanishes to zero in region of high gradients (i.e. near object boundaries);
- a curvature term $-F_{\sigma}\varepsilon\kappa$ which controls the smoothness of the iso-contours of $\phi(\cdot, t)$, as originally introduced in Caselles et al. (1993) and Malladi et al. (1993);
- an external force, similar to the snake image force (Cohen • 1991, Kass et al. 1988), which role is to attract the surface toward the boundary of the object of interest. This term is a vector flow which denotes a projection of an attractive force vector on the surface normal. The image term can be defined as $g(\mathbf{x}) = - \|\nabla I_{\sigma}(\mathbf{x})\|$ or $g(\mathbf{x}) = F_{\sigma}(\mathbf{x})$.

3. Design of a segmentation method for tubular objects

Setting up a framework for the segmentation, visualization and quantification of thin tubular structures, based on the use of the FM as an initialization step, we show in this section how this method, which is not tuned for this kind of thin and long objects, can be specifically optimized for this target.

3.1 The overflowing problem

Segmentation problems do not always provide as an excellent contrast as the air-filled colon on a CT scanner of figure 1. In more complex cases, the propagation leaks through the object walls, as it is illustrated in figure 2. The front flows over the boundaries of the object and floods the background image. The resulting surface cannot be used as an initialization for a refined segmentation, as it is done in the previous section when combining FM and LS methods (Malladi and Sethian 1998).

When the front propagates in a thin structure, there is only a small part of the front, which we could call the "head", that really moves. Most of the front that is located close to the boundary of the structure or to the starting 520 point (the "tail" of the front) moves very slowly. However, since the structure may be very long, in order for the "head" front to reach the end of the structure, the "tail" voxels may flow out of the boundary since their speed is always positive, and integrated over a long time. This is 525 illustrated in figure 2, where we applied FM in the dataset shown in figure 2-top with a potential based on the gray level with contrast enhancement. The resulting front propagation (figure 2-bottom) leaks through the object walls and does not give a valuable surface description.

3.2 Propagation freezing for thin structures

From the description of the overflowing process above, it appears inefficient to use all of the voxels in the computation of the arrival time in Eikonal equation. The idea we introduced is that some of them located in the tail could be considered as walls, thus blocking the leakage that occurs. This *Freezing* process can be done by setting their speed to zero, and has been first proposed in Deschamps and Cohen (2002)) and used in Lin (2003).

Freezing points during propagation means that we consider the front has reached the object boundaries when it visits them. The question is now to design the appropriate criterion to choose these points. We illustrate this method on a synthetic branching structure in 2D and then propose two criteria.

3.2.1 Synthetic test problem. We would like to extract in a very fast process the multiple branches of the synthetic example of a tree structure shown in figure 3. The left binary image represents both the data image and the potential (i.e. P is small on the object and large in the

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Figure 2. 3D contrast enhanced MR image of the aorta (above) and front propagation (below): these three images represent different steps of the propagation inside the aorta MR dataset using Eikonal equation with a potential given as a simple function of the gray levels either linear or non-linear. Compare to figure 6 to see what should be correct.

background). Setting an initial seed point at the left corner point, the front propagates quickly in the three branches and much slower in the background. Figure 3-right shows the action map computed with the classical FM algorithm applied until the whole object has been flooded. The LS of the action map are visible on the white background of the image domain which has not yet been visited by the front. The shape of the set of points visited is a whole "bloblike" structure that does not delineate the correct boundaries of the tree and cannot be of any use. It emphasizes the limited use of this method, without a clear constraint on the domain of points visited.

590 **3.2.2 Time based Freezing**. The first idea is to freeze the points of the front that are spending a long time in the propagating front, i.e. points that remain *T*rial (table 1) for



Figure 3. Synthetic test problem: the left image is the medium where a front has been propagated, starting at the root of the three branches, and stopping when a maximum distance criterion of 300 has been reached; right image is the corresponding action map for time $T \in [0, T_{\text{max}}]$ with T_{max} user defined.

a given number of iterations. Unfortunately, the results of this criterion are non-predictable, as illustrated in figure 4. The reason might be that the time spent in the front for a point is related to the local potential value at this point and not its location in the object that we are trying to segment. What we want is to differentiate the *tail* of the front from its *head*, in order to prevent propagation leakage in nondesired areas of the data.

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3.2.3 Distance based freezing. We now propose a criterion based on the Euclidean Distance $D(\mathbf{x})$ traveled by the front from the starting point \mathbf{x}_0 to any point, point \mathbf{x} , using the principle detailed in Section 2.1.3, based on 645 equation (8).

It seems far more "natural" to use the distance relatively to the starting point or to the *head* of the front. Actually this information is now related to the geometry of a tubeshaped object where the diameter should be small compared to the length. And we can use the algorithm detailed in Section 2.1.3 for computing this Euclidean path



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Figure 4. Instability of the time criterion for Freezing: Left image is the action map T obtained with a maximum time criterion of 100 iterations; Other images are freezing maps (white pixels) with respectively from left to right 100, 80 and 60 iterations as maximum time spent in the front.

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Figure 5. Using distance for freezing: left and middle images are action maps T with distance criterion (13) of respectively 100 and 50; right image is a zoom on the freezing map for a distance criterion $\tilde{d} = 50$: the frozen points are set in black.

⁶⁷⁵ length $D(\mathbf{x})$, that was already very helpful in a virtual endoscopy application (Deschamps and Cohen 2001).

We can easily define several *Freezing* criteria based on the current maximum distance value d_{max} computed. For example, we can decide that a point **x** of the propagating front (i.e. *Trial* points) should be frozen (i.e. set as Alive point) if its path length distance is small relatively to the largest value d_{max} :

$$D(\mathbf{x}) < \max(d_{\max} - \tilde{d}, 0), \text{ with } \tilde{d} > 0 \text{ chosen}$$
 (13)

The results are now predictable (see the 2D example on the synthetic test shown in figure 5). The Euclidean distance to the starting point is a measure which contains information about the geometry of the surface extracted, and in particular its length. This is less related to the local potential at each point, and more to the location of this point in the object. The strict inequality in (13) ensures that no point is frozen till one point on the front has traveled at least the Euclidean distance \tilde{d} .

At each time step, we can now discriminates the front *tail* points, by comparing their distance to the maximum distance which has been traveled by the front *head*. If the distances satisfy our distance criterion (13), we "freeze" those points by setting their speed artificially to zero. It enables to stay inside the object when it is long and thin like a tubular structure, as shown in figure 5. The domain visited by our algorithm is slightly smaller than the previous one (figure 4-right) and this domain shortens with the distance criterion (13), when we compare left and middle images in figure 5. Figure 5-right clearly demonstrates that the FM with *Freezing*, that we denote FFM algorithm in the following, discriminates the points located far (depicted in black) from the propagating front.

3.2.4 Algorithmic implementation for distance based freezing. Just like we were ordering the energy values in the FM algorithm (table 1), we are going to use an additional heap where the ordering key is the computed

Notations

- A starting point \mathbf{x}_0 , located at the root of the tree structure;
- The usual action map T, a min-heap \mathcal{H}_T and a potential image P used in table 1
- The distance map D, and another min-heap H_D, where the ordering key for any point x is the value of D(x) (the first element of this heap will be the Trial point with smallest D);
 Several counters d_{max}, *d*, d_{stop}

Initialization

Initialize the front propagation method, by setting $T(\mathbf{x}_0) = D(\mathbf{x}_0) = 0$ and storing \mathbf{x}_0 in both min-heaps \mathcal{H}_T and \mathcal{H}_D ; $d_{\text{max}} = 0$

 \tilde{d} and d_{stop} are parameters for tuning the algorithm (user defined).

- Loop: at each iteration, consider x_{min} the *T*rial point with smallest *T*Proceed according to the FM algorithm as in table 2, by examining
 - its neighbors, updating T and the min-heap \mathcal{H}_T , as well as D using equation (8) and \mathcal{H}_D ; Take $d = \max(d = D(x - y))$.
 - Take $d_{\max} = \max(d_{\max}, D(\mathbf{x}_{\min}));$
 - Consider \mathbf{q}_{\min} , the first element of \mathcal{H}_D , (Trial point with the smallest D). While $D(\mathbf{q}_{\min}) < \max(d_{\max} \tilde{d}, 0)$ do - Set $D(\mathbf{q}_{\min}) = T(\mathbf{q}_{\min}) = \infty$;
 - Set \mathbf{q}_{\min} in the Alive set, then \mathbf{q}_{\min} will not be used for computing the energy/distance at its neighbors location.
 - Delete \mathbf{q}_{\min} in both \mathcal{H}_D and \mathcal{H}_T ; If $d_{\max} > d_{\text{stop}}$, exit the loop.

distance. It means that the element at the top of this second heap will be the *T*rial point that is the closest to the starting point. Thus knowing d_{max} at each iteration, we are able to remove all the points who satisfy our criterion (13). In table 3 is detailed an implementation of the FFM. The same algorithm can be used with any other distance-based or time-based *Freezing* method.

3.2.5 Illustration on the vascular tree extraction problem. Using the method explained previously, we segment a vascular tree very quickly, starting from a seed point at the top of the tree hierarchy. Figure 6 displays the successful result of this algorithm on the data of figure 2 where FM previously failed. The distance threshold \tilde{d} is a parameter which is not very sensitive, and we usually choose a value related to the *a priori* dimensions of the object. Since it represents the portion of the branches that are not surrounded by frozen points, it is important to have some kind of understanding about when the front does leak through the object. The only important condition is that \tilde{d} should be larger than the expected maximum section of the object, otherwise the algorithm will wrongly freeze points inside objects.

3.3 Suitable stopping criterion

Having designed an adequate algorithm to prevent the front *tail* from "overflowing", we now explain our strategy to automatically stop the propagation whatever the number of branches, based on the same FFM method.

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Table 3. FFM algorithm.

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^{||}Previous strategy was to use a maximum Euclidean path length to stop propagation, like for the virtual endoscopy application. In virtual endoscopy, the user can set both extremities of the trajectory, if he has an *a priori* knowledge of the anatomical objects. Extraction of tree-like structures cannot use such an assumption: the number of branches in our structure is undefined, the only assumption being that the user can fix a point inside the structure, at the beginning of the segmentation process.

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Figure 6. Using distance for freezing in the aorta: from left-to-right, images show iterations of the segmentation process on the former examples of figure 2; the propagating front is in red, and the frozen points are in white.

If we plot the maximum distance d_{max} visited by the front, as a function of the number of iterations of the algorithm detailed in table 3, we obtain the profile shown in figure 7. We observe that the evolution of d_{max} can be broken into two quasi-linear parts separated by a huge change of the slope.

By definition of the FM method, the number of iterations is equal to the number of points that are alive, and is thus an estimate of the volume inside the front. If we are propagating in a tube-shaped object with constant section area *A*, then the number of points visited should be proportional to the length of the tube. Thus the slope is the ratio between the length and the number of points visited, and it is inverse proportional to *A*. This should remain true for anatomical branching objects in their large parts as long as the sum of all sections areas remains constant. But this should no longer hold in the very thin parts of the vessels and arteries due to the fact that the front starts to leak, and this is as though the area of the section becomes very large. The slope becomes then much smaller.

Therefore, the slope abrupt change indicates exactly when the the front *head* flows out of the object, i.e. when front propagation should be stopped. This slope collapse can be detected using a simple threshold, depending on the object we want to extract, and indicate when we should stop propagation. Notice that even in pathological cases (aneurysms), we can assume that we do not want to extract an object which is more than a maximum section radius r_{max} . The slope being inversely proportional to the square of the tube radius we can add to our criterion another condition on the maximum radius.

815 **3.4 Discussion and results**

The level of accuracy of LS implementations dedicated to tubular shape extraction (Lorigo *et al.* 2001, Vasilevskiy and Siddiqi 2001), cannot be of course outperformed by the FFM method. However, solving the Eikonal equation in $o(n \log(n))$ is much faster than any time-dependent scheme, since this is the stationary case of Hamilton–Jacobi equation (Sethian 1999). This is why in this article, the aim is not to implement dedicated algorithms based on the LS methods, but to use them afterwards for sub-pixel accuracy results, once preliminary results have been obtained with our fast algorithms. Moreover, the FFM algorithm reduces the number of points visited to a small portion of the image, leading to accurate segmentation in a total of 10 s, for the MR datasets shown in figure 2, on a commercial computer.

The FFM and the LS algorithms are used in four steps:

- (1) the user manually initializes a seed point inside the object of interest;
- (2) the FFM algorithm (table 3) propagates a front from this point;
- (3) this evolution is stopped using our automatic criterion (Section 3.3). First row of figure 8 shows the surfaces of several tubular structures extracted with the FFM algorithm; and
- (4) a LS deformable model is evolved according to equation (12) for a small number of iterations, until the final surfaces which are shown in the second row in figure 8.

Since our freezing method gives a very good estimate of the surface, this step is quite fast.

4. Extracting the Minimal Tree of the branching structures

Once the contour a tubular anatomical object is obtained (figure 8), we can extract trajectories inside it with minimal path techniques (see Section 2). Along a centered trajectory, we can either quantify numerically the extent of pathologies, or assess them visually (virtual endoscopy).

In this section we show how to obtain the *Minimal Tree* of a branching structure, as a set of bifurcation points and extremities connected by minimal trajectories, using its shape and the user-defined seed point of the segmentation. Our method will be illustrated on a 3D rotational angiography (D-RA) dataset (Kemkers *et al.* 1998) of a stenosed artery shown in figure 9.

4.1 Multiple trajectories extraction

We have shown in Deschamps and Cohen (2001) how to extract a centered trajectory inside a tubular structure. In this section, we extend this single trajectory extraction method to the case of multiple trajectories.

The dataset displayed in figure 9-left with three orthogonal views is a branching structure in which pathology—a stenosis—is clearly visible on the Maximum-Intensity-Projection (MIP) view in figure 9-right.

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the maximum distance reached by the front propagation across iterations; it emphasizes that the decrease in the slope is related to the "overflowing" out of the aorta.



Figure 8. Segmentation of vascular objects: first row shows different vascular objects that have been extracted with the FFM algorithm — except the example shown in last column on the right, where the method used was the competitive fronts algorithm; second rows is the final result of the segmentation after 40 iterations of the LS method.





Figure 9. 3D-RA dataset of a stenosed artery: left image shows three orthogonal views of the dataset; right image is a MIP view of the same dataset.

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The complete study of this pathology involves to be able to inspect its surface and to measure the extent of the stenosis. This can be done with minimum interactivity using the Minimal Tree.

In some cases the stenosis will be so important that the artery will appear as two or more disconnected parts in the image. In this case, we have devised a method to reconnect those parts with minimal path techniques adapted in a perceptual grouping perspective (Deschamps and Cohen 2002).

4.1.1 Previous work and principle of the method. The combination of path and shape representation is a framework already studied in Computer Graphics as well 1005 as in Computer Vision. In Computer Graphics, cylindrical shapes description is done by implicit surfaces (in the sense of Bloomenthal 1997, p. 223]) defined by the convolution of a filter kernel with a skeleton. In other words, this distance surface is a surface that is defined using the 1010 distance to some set of skeletal elements. But in graphics, the target is to improve visualization and interactivity over the representation of the object. However, it connects to vision because it is often convenient to model a shape as a generalized cylinder (O'Donnell et al. 1994), for 1015 reconstruction of anatomical shapes (Terzopoulos et al. 1987) by combining the fitting of a generalized cylinder and its symmetry axis. In those methods, the central axis constrains the extraction, and models the tubular shape of the final object extracted. 1020

> In our case, even if it is initialized by a minimal path tracking method (FFM algorithm in table 3), the principle is the opposite: the shape constrains the path, because the final set of trajectories (i.e. the skeletal information of our object) is built from the surface extracted by the LS method.

> Our method is based on the construction of a connectivity map of the propagating front (i.e. the Alive points), at several chosen iterations, as shown in figure 10. Defining a distance step d_{step} , each time the front travels this distance we change the label of the visited points, and we thus detect when a front separate at a branch into several unconnected sets. When the whole object has been visited, we take for each separate set the furthest point from the starting point, according to minimal path length, and we set it as a candidate extremity for back-tracking a trajectory.

 d_{step} defines at the same time the accuracy and the computation cost of the method: if it is big, it decreases the computation cost of keeping track of the connectivity of the front. At the same time, it misses branches smaller than

 d_{step} : on figure 10-right, only one of the two extremities of region 3 will be eligible for back-tracking.

4.1.2 Multiple path tracking algorithm. The algorithm 1050 we devised for multiple path tracking is mostly inspired from works on skeleton extraction from binary or scattered data. However it has one advantage over morphological techniques: the accuracy, or scale, is an explicit parameter that we can derive from anatomical 1055 knowledge of the data studied. This scale is the length of the minimal path extracted at each step.

Our framework detailed in table 4 relies on a binary mask \mathcal{M} that defines our object and which can be obtained by the FM as well as the LS methods. Figure 11 illustrates 1060 this algorithm by showing several label maps $\mathcal L$ with different values of the scale d_{step} .

4.1.3 Illustration on the vascular tree extraction and 1065 discussion. Using FFM segmentation followed by several iterations of LS methods to build the mask \mathcal{M} we illustrate the extraction of multiple trajectories inside two different datasets in figure 12. Moreover, the computation for the paths is constrained to a small number of points located 1070 inside the objects of interest (usually less than 20% of the whole volume) defined by \mathcal{M} . Figure 13 shows the result of the same algorithm on the dataset of figure 2. This set of paths can lead to apply quantification techniques on the Abdominal Aortic Aneurysm (AAA) it contains. 1075

The advantages of our framework are numerous:

- Initialization: user input is limited to the setting of the seed point for the segmentation.
- Adaptability: the front propagation techniques enable 1080 any change in topology, have no constraints on the initialization, and can segment any branching object;
- Accuracy: the surface definition is at the sub-voxel level, thus our method increases the accuracy of both trajectories extracted and measures of the pathologies;
- Interactivity: while the set of endpoints is manually drawn in the original image for most of the front propagation techniques applied for multiple path extraction (Lavialle et al. 1999), all our trajectories are extracted automatically;

4.2 From multiple trajectories to minimal tree

The multiple trajectories obtained previously can guide virtual endoscopes or be used to quantify pathologies by



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Figure 10. Multiple path tracking algorithm: from left to right, these are connectivity tests made on the propagation of a wave inside a segmented object, starting from the point designated by label 0, until the whole domain is visited.

Table 4. Multiple path tracking algorithm.

Notations
rotations

- A binary mask \mathcal{M} defines the region of interest in the image;
- A potential image P will drive the front propagation (usually computed using the centering method Deschamps and Cohen $200\bar{1}$):
- A distance map D (the Euclidean length of the minimal path computed with the method of Section 2.1.3), and a user-defined distance step d_{step} controls the accuracy of the end-point extraction:
- A counter c_d records the iteration number of the loop in our algorithm;
 - A label map \mathcal{L} labels each branch detected with a counter $n_{\mathcal{L}}$, and an array ε records the hierarchy of the branches detected; $\varepsilon[l]$ is the label of the neighbor region that was found in the tree structure previously to region of label l.
- A starting point \mathbf{x}_0 , located at the root of the tree hierarchy. Initialization

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- $\mathcal{M}(i,j,k) = 1$ for all point in the region of interest, elsewhere $\mathcal{M}(i,j,k) = 0;$
 - $\mathcal{L}(i,j,k) = -1$ for all point in the image domain, $n_{\mathcal{L}} = 0$, and all elements of $\varepsilon[I]$ are set to -1;
- We initialize the usual set of data-structures for front propagation, including an action map T, the distance map D, and a min-heap;
- We initialize a classical front propagation method, setting $T(\mathbf{x}_0) =$ 0 and storing \mathbf{x}_0 in the min-heap;
- The counter $c_d = d_{\text{step}}$.

Loop

- We propagate the front with Eikonal equation, computed with potential P on the domain defined by the mask \mathcal{M} ;
- For each Trial point x visited in the FM algorithm, $\mathcal{L}(\mathbf{x})$ is set to the label of its current Alive neighbor with minimal energy:
 - If we visit a point **x** with $D(\mathbf{x}) \ge c_d$:
 - We consider the set of Trial points \mathcal{T} , that are all stored in the 1) min-heap, we consider t_1, \ldots, t_n its *n* subsets of connected components (with 26-connectedness in 3D), obtained through a simple connectivity algorithm;
 - 2) For each subset $t_r, r \in [1, ..., n]$
 - Passing from the old label $l_{r_{old}}$ to the new label $l_{r_{new}}$: we set $n_{\mathcal{L}} = n_{\mathcal{L}} + 1, \ l_{r_{\text{new}}} = n_{\mathcal{L}}, \ \text{and} \ \varepsilon[l_{r_{\text{new}}}] = l_{r_{\text{old}}};$ For all the points $\mathbf{x} \in t_r$, we set $\mathcal{L}(\mathbf{x}) = \overline{l_{r_{new}}}$;
 - 3) $c_d = 2 \times c_d$:
- 4) We stop if the whole domain defined by \mathcal{M} is visited. Termination
- - We consider all LS $\mathcal{L}_p, p \in [1, \ldots, n_{\mathcal{L}}]$ defined by the label map \mathcal{L} with different labels;
 - We select the sets \mathcal{L}_p such that $\varepsilon[l_p] \neq -1$ and $\forall n > l_p, \varepsilon[n] \neq l_p$; This means that such labels have no neighbor regions that follow them in the tree structure.
 - $\forall \mathcal{L}_p$ selected, we find the voxel (i, j, k) with maximum distance D(i, j, k) and set it as end point for back propagation;
 - We back-propagate from all final point selected and extract a set of multiple trajectories.

measuring the variation of the section of the object along one of the path extracted. But a trajectory is just the centered minimal path between two extremities of the branching structure without any spatial relationship between the paths and the surface. These trajectories cannot be used for further developments like automatic labeling of the branches and accurate localization of pathologies.

In order to extract the information which is relevant to analyze the surface of the tree-shaped object extracted, we need to transform these multiple minimal paths into a Minimal Tree as done in figure 14. The process of building the Minimal Tree is rather simple: during back-tracking of the trajectories, we create branching points where couples of them are close enough, therefore, the only parameter is the definition of proximity between trajectories.

The initialization use the same input as the multiple path tracking, including the final end points extracted. The algorithm is presented in table 5. Figure 15 displays the result obtained on the D-RA image of figure 9. From the set of multiple trajectories, branching points are extracted, as shown in figure 15-right.

4.3 Other methods for skeletal representation

4.3.1 Skeletonization by expansible trees. In Verroust and Lazarus (1997), authors build a skeletal representation of an unorganized collection of scattered data points lying on a surface. They capture branching shapes, using a 1185 distance step similar to ours, by computing the k LS from the user-defined root of the tree; and for each of those LS, they extract the centroids of connected components. In our case it is not necessary to extract the centroids, because it introduces uncertainty in the location of the branching 1190 points. With a centering potential P, we aggregate the paths that are under a user-chosen distance d_{paths} . This method based on the centroid extraction can be compared to the very interesting work of Angella et al. (1996), which presents a deformable and expansible tree as a skeleton 1195 extractor, where each node of the tree is a free particle that propagates into the data, pushed by repulsive forces coming from other particles and contours. The set of free particles describes the tree hierarchy. In our case, the sub-



Figure 11. Labeling algorithm for multiple path tracking: from left to right, the images show the label map obtained with the algorithm of table 4 applied with path steps 10, 30 and 50 respectively.

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Figure 12. Complete method applied to several objects: first row is the framework applied to the stenosed artery of D-RA image of figure 9 and second row concerns an aneurysm in a 3D-RA image — left column is the initialization given by the FFM method; middle column is the surface obtained after a small number of iterations of the LS method; right column shows the multiple trajectories extracted with the labeling algorithm, by transparency (color images are available through the online version).



Figure 13. Multiple trajectory extraction from only one seed point: projection on three orthogonal views of the complete set of trajectories tracked in the aorta MR dataset which was segmented in figure 8 in the second row; the FFM algorithm has been used to extract centered trajectories.

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voxel precision is very important for visualization and measurements, and the needed number of particles for achieving this task would lead to huge computing times.

4.3.2 Morphological skeletonization. Very similar work can be found in Serra (2002), where the author use wavefronts to extract morphological descriptions of binary



Figure 14. From multiple trajectories to minimal tree representation: left image is a set of trajectories extracted in a segmented object. Right image represents the minimal tree needed.

images, in particular binary tree structures. However, bifurcations are detected on a projected image in 2D, then this information is upgraded to 3D, but still the method is applied iteratively, looking for bifurcations at each iteration. Our method uses a scale parameter d_{step} , as a distance step in our wavefront, only looking for bifurcations every time the front has crossed a multiple number of this distance. It reduces greatly computations, and can be parameterized by the user, who can only look for branches lower than a typical value d_{\min} which is the upper-bound of our scale parameter.

Mathematical morphological techniques (Serra 2002) are the main tool used for tree extraction, and lots of techniques, like thinning algorithms are already used in medical imaging. They start from volume images so that the traditional medial axis transform (Blum 1967) can be applied (Pisupati et al. 1995, Naf et al. 1996). However, the purpose of our application is to have a smooth set of

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Table 5. Tree extraction algorithm.	it acts as a <i>scale</i> paramete
Notations	undesirable small parts of
 A binary mask <i>M</i> defines the region of interest in the image; A potential image <i>P</i> drives the front propagation (usually computed using the centering method Deschamps and Cohen 2001); The minimal action map <i>T</i> computed with this potential during the 	scale is also an input in the the use of morphologic description we are looking
 initial multiple path tracking; The starting point x₀, located at the root of the tree hierarchy; The set of end points e_l l ∈ [1;N_e] where N_e is the number of end points extracted. 	pathologies. We thus no information: a tree which
 A distance d_{paths} which defines the maximum distance between two trajectories (chosen bigger than the gradient descent step). A map L labels the points that are neighbors of a path (at a distance smaller than d_{paths}); An array ε to record the branches detected 	topology of the object of section of a tubular shap axis transforms, and to techniques to <i>clean</i> the ske
Initialization	does not need
 <i>L</i>(<i>i,j,k</i>) = −1 for all point in the image domain; <i>n_e</i> = <i>N_e</i> and ∀<i>p</i> ∈ [1; <i>n_e</i>], <i>ɛ</i>[<i>p</i>] = 0. 	does not need.
Loop: for $l \in [1; N_e]$ • We back-propagate from e_l on the minimal action map T using a	1.1 Application to magaul
simple gradient descent method, as described in equation (6);	4.4 Application to vascula
• At every path step, the position of the new path point is defined by	4.4.1 Previous work. I
$x = (x, y, z) \in \mathbb{R}^3$ We consider the yoyals $\mathbf{n} = (i, i, k) \in \mathbb{IN}^3$ that surround x which	quantification among othe
satisfy $D(\mathbf{x}, \mathbf{n}) < d_{\text{norths}}$, where D is the Euclidean distance:	thesis of Frangi (2001). H
• If, for all those vertices $(i, j, k) \in IN^3$, $\mathcal{L}(i, j, k) = -1$, we set	method based on path and
$\mathcal{L}(i,j,k) = l$, and continue back-tracking for e_l ;	
• Else, if one of the vertices (i, j, k) satisfies $\mathcal{L}(i, j, k) \neq -1$, a	1777].
branching point is detected, then: Depend the label $L = C(i, j, k)$	
- Record the label $L = \mathcal{L}(l, j, \kappa);$ - $n = n + 1, e = (i, j, k);$	• he first set the two ext
$- e[l] = e_n \text{ and } e[n_e] = 0;$	surface extracted;
- Stop back-tracking for e_i ;	• the minimal path is ext
- Continue back-tracking, this time for e_{n_e} , substituting all	the surface, using a tec
$\mathcal{L}(i,j,k) = L$ by $\mathcal{L}(i,j,k) = n_e$, until another branching point or \mathbf{x}_0 are	Sethian (1998):
detected;	Settian (1998),
• If we reach \mathbf{x}_0 , then stop back-tracking for e_l .	• a centering force, base
Termination	filtering (Frangi et al. 19
• For all end point e_j , $j \in [1; n_e]$, we can consider the couples of endpoints (e_i, e_j) as extremities of linear parts of the skeleton	the center of the tube-sh
(with $e_0 = \mathbf{x}_0$)	• a circular cross section

The multiple paths between couples of points $(e_p, e_{\varepsilon[p]}), p \in$ $[1; n_e]$ build the skeleton of our object, at scale d_{step} , and distance d_{paths}

multiple trajectories. This smoothness is needed for accurate measurements and visualization along the 1360 trajectories. Morphological techniques require postprocessing in order to remove undesirable small parts of the skeleton. Since the distance step d_{step} chosen in our algorithm is the minimum size of the trajectories detected,

er which smooths and removes of the skeleton, similarly to and Kimia 2001), where the e algorithm. To conclude with al techniques, the skeletal g for corresponds to the need servation and measurements of eed a smooth and accurate ch describes the cylindrical bserved. The variation of the 1385 pes leads to error in medial the need of post-processing leton obtained, that our method

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ar quantification

mportant work on vascular ers can be found in the PhD e developed a very interesting shape extraction (Frangi et al.

- tremities of a path on an iso-
- racted on the representation of hnique similar to Kimmel and
- d on multi-scale enhancement 1405 998) drives the minimal path in haped object;
- a circular cross section approximating the artery is swept along the central axis extracted previously (swept surface), and creates a deformable cylinder; and
- this cylinder initiates a tensor product B-spline surface (Piegl and Tiller 1996), that fits the boundaries of the artery.

Using both path and shape representations in the same 1415 framework, Frangi et al. (2001) proposes an elegant method for quantification of vessel morphology. In the following we will demonstrate the benefits of our methods toward Frangi's.



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Figure 15. Obtaining a tree hierarchy from a set of trajectory: left image is the segmented artery extracted from the dataset shown in the D-RA image of figure 9; middle image is a zoom on two bifurcations of the object, wherethe trajectories extracted are displayed; right image is the same point of view on the translucent surface extracted with the tree extracted from the set of paths.

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4.4.2 Comparison. In order to highlight important benefits of our method, we are going to compare our results to Frangi method. Even if our method is not specifically dedicated to quantification of vascular diseases in MRA images, we propose an alternative that may overcome several limitations of his. This method is illustrated by the figure 16.

4.4.2.1 Initialization requirements

For the initialization, we provide the measures in the 1440 whole set of branches of our objects, setting a unique tree root seed for segmentation and path tracking. Frangi (2001) gives the measure between the user defined end points (he gives also an interesting study of the variability of the results across the user initialization). In our case, only one point is needed.

4.4.2.2 Complexity of the object extracted

Concerning the topology of the objects observed, in Frangi (2001) the bifurcations in carotid arteries introduce errors in the measurements of the stenoses. With our



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Figure 16. Comparison of measurements on the tree and on a trajectory: Two different datasets are presented, each one in a column (left column dataset present a stenosed vessel). First row (a,b) displays segmented surfaces and extracted trees. Second row (c,d) displays the sub-volume of interest in both cases where sections are performed. Third row (e,f) shows plots of the section measured along a trajectory. Fourth row (g,h) displays the same result using branches extracted between two bifurcations.

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method, bifurcations are localized and wrong measures near branching points can be omitted. It enables to reconstruct the whole set of trajectories inside the object, but it converts this information into a tree hierarchy, where important information can be separated from the whole.

In particular, figure 16(g) is the information contained in the interval [40; 60] in figure 16(e). It is the same process for figure 16(h) which corresponds to the sub-plot contained in the interval [190; 250] in figure 16(e). Therefore, the tree extraction enables to localize accurately the information needed, as the stenosis extent for the case presented in the left column of figure 16.

4.4.2.3 Accuracy of the model

- The B-spline that extracts the vessel boundaries in Frangi *et al.* (1999) is an approximation of the surface, whereas the zero-LS embedded in $\tilde{\phi}$ has sub-pixel precision.
- The computational cost of the tree extraction finds its justification in the improvement of the measurements along the new set of trajectories available. The tree extraction enables to measure the section along the necessary subset of the object, delimited by the two branching points (this subset has been colorized in green in figure 16(c-d)). If this information is plotted across a trajectory in the entire object, it is not useful for two reasons
 - section information is not valuable at the branching points; and
 - the location of the region of interest along the trajectory cannot be obtained straightforwardly.

We finally have a method which provides a sub-pixel information of the position of the shape. Based on the paths extracted with our fast and robust algorithm, the quantification relies on an accurate centered position of the path points. **4.4.3 Minimal vascular tree and virtual endoscopy.** Having obtained the *Minimal Tree* in the vascular structure, it is now possible to interactively navigate inside the object, by choosing at each bifurcation point which branch to follow (figure 17). Measures and visualization are thus enhanced (figure 17). Moreover, once paths and shapes are extracted this fly-through is real-time due to the fast rendering of the triangulation of our implicit model.

4.4.4 Minimal vascular tree and computational fluid dynamics. Antiga *et al.* (2003) presented a method to create patient-specific models of the arteries, based on a LS segmentation. In order to produce a relevant body-fitted finite-element representation of a vascular object, they smooth and correct the surface. They also extract centerlines with a method based on Voronoi diagrams in order to edit the branches and produce a mesh usable by computational fluid dynamics methods.

Our method is much faster since the segmentation is rather fast due to the FFM algorithm. However it is necessary to convert the surface extracted (zero LS) into a computational domain appropriate for the CFD solver, involving the construction of a mesh on the surface and 1620 in the 3D domain surrounding it (Cebral et al. 2004). Fast adaptive remeshing could also be used for his task (Peyre and Cohen 2003). But recent techniques in CFD make easy use of the LS representation in the generation of computational grids: the Embedded-Boundary rep-1625 resentations (Deschamps et al. 2004) on the Cartesian grid enables to simulate the blood-flow in these realistic models. The advantage of this technique is that neither a finite-element representation is needed nor the smoothing of the surface, since the fluid equations can be discretized 1630 on the Cartesian grid where the signed-distance to the surface is defined (see Deschamps et al. 2004 for details). The process becomes then quicker and automatic.



Figure 17. Endoscopic view along one trajectory of the minimal tree: the whole set of trajectories is displayed (in yellow) simultaneously with the surface rendering: the user does not miss any bifurcation since he can see all branches. Videos are availableonline at http://www.ceremade.dauphine.fr/ \sim cohen/MPEG.

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5. Conclusion

We have presented a complete framework for automatic segmentation, labelization, quantification and visualization of tubular tree structure in 3D medical images. A rough estimate is found, based on the Freezing FM algorithm and the stopping criteria of Section 3.3. The shape is then refined by a LS method. Multiple paths are extracted from the branching object giving a complete description and allowing various applications.

A first improvement brought by our freezing method is to accelerate the computation, by visiting a very small number of points during propagation, and to segment thin tubular structures, therefore, enabling the centering of trajectories inside those tubular structures. The second part of our contribution emphasizes how we extract the *Minimal Tree*, starting from the segmented surface and using the same fast technique.

This *Minimal Tree* is very valuable for visualization and quantification of pathologies. The structure enables the clinician to make accurate measurements of the extent of pathologies, and to visually inspect them at the same time. Those trajectories can also be the input to an endoscopic tool (Deschamps and Cohen 2001).

1675 The method presented here could be extended to extract bronchial tree and other branching objects. The most difficult aspect of this extension is in handling properly the segmentation task.

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