# 3D Coronary Vessel Tree Tracking in X-Ray Projections

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**Abstract.** CTA angiography brings potentially useful information for guidance in an interventional procedure. It comes with the challenge of registering this 3D modality to the projection of the coronary arteries which are deforming with the cardiac motion. A tree-spline i.e. a tree with a spline attached to each edge and shared control points between these points describes a 3D coronary tree and is able to represent its deformation along the time. We combine this description with a registration algorithm operating between the tree-spline and the angiographic projection of the coronary tree. It starts by the estimation of a rigid transformation for the iso cardiac phase time followed by a non-rigid deformation of the tree driven by the pairings formed between the projection of the edges of the tree-spline and the observed x-ray projection of the coronary arteries. The pairings are built taking into account the tree topology consistency. Anatomical constraints of length preservation is enforced when deforming the arteries. The proposed approach has been evaluated with clinical data issued from ten different clinical cases which enabling to form twenty three different experimental conditions. Encouraging results have been obtained.

**Keywords:** Deformable registration, tracking, coronary arteries, x-ray, computed tomography angiography, CTA

## 1 Introduction

Coronary artery narrowings are commonly treated in Percutaneous Coronary Intervention (PCI) procedures. These procedures are performed under the guidance of an x-ray imaging system and implies the use of iodinated contrast agent to opacify the lumen of the coronary arteries. Once the vessel, which is going to be the object of the procedure, has been imaged, the operator modifies the orientation of the image chain to place it such that vessel superimposition and projective foreshortening of this vessel is minimal. The angiography depicts the lumen of the artery with an excellent spatial and temporal resolution. It is limited in its capacity to depict the characteristics of the vessel wall as for example the existence of calcifications. Computed Tomography Angiography (CTA) is

more able to provide this additional information. Most of the times and for the benefit of limiting the dose delivered to the patient, it comes as a static image which depicts the vessel anatomy in diastolic phase. Physicians are eager to see both modalities in the same referential which is the one defined by the angiographic image in the configuration selected for the patient treatment. In this article, we propose and evaluate an algorithmic approach to bring these two imaging modalities in the same referential while keeping the dynamic of cardiac motion. [3,1,8] have proposed different strategies applicable solely to data in the same cardiac phase. The registration requires then the estimation of a rigid transformation followed by the conic projection with the x-ray source being the focal point. To extend to the cardiac cycle, [2] has proposed to adapt a generic model of the cardiac motion to end-diastolic CTA. This strategy raises the question of the validity of the generic model. [7] proposed to focus the attention of the algorithm to the vessel of interest and to track it along the cardiac sequences. It takes profit of a spline representation of the vessel of interest. The spline can be smoothly warped to follow the observed coronary artery deformation in the artery. The optimization of the control points is made with the double constraint of minimizing the distance to the projection of the vessel of interest and keeping the vessel length constant, which is anatomically meaningful. Encouraging results with an accuracy of 2 mm for the tracking of a landmark were observed. This approach is only applicable when the operator has avoided vessel superimposition over the vessel of interest. To further extend the concept, we explore here the benefit of doing the deformable registration over the whole coronary tree. This benefit is illustrated through tracking videos presented in https://3dvttracking.github.io/. In the following, we will describe the proposed method and explain the assessment strategy which includes metrics evaluating the registration and a specific metric related to the consistency of the position along the vessel.

## 2 Method

Before introducing the method, we first describe the data we have at hand. The 3D information is extracted from a CTA scan by a fully automated commercial product, *Auto-Coronary-Analyis* from GE Healthcare, providing a segmentation of the coronary vessel structure. The coronary vessels are separated between the right and the left coronary and the different branches are represented by their centerlines. So the anatomic structure is described by a tree $\mathcal{T}$. The aim of this work is to track $\mathcal{T}$ along the consecutive images of the x-ray record sequence. Even if the 3D model of the coronary vessels can be depicted by a tree, this may not be the case for the x-ray projection. Indeed, self superimpositions create crossings. The vessel segmentation may also cause over segmentation or miss some vessels. X-ray projections are segmented with an Hessian based vessel enhancement technique, and vessel like structures are extracted forming a set of curves which corresponds to the centerlines of the vessel. The segmented object is organized in a graph by applying standard processing methods to connect

neighboring centerlines. Considering the consecutive images obtained in the sequence of $N$ images by performing the acquisition after injection of the contrast agent, we obtain a set of graphs $\boldsymbol{\mathcal{G}} = \{\mathcal{G}_1, \ldots, \mathcal{G}_N\}$.

We initiate the registration by identifying the initial rigid transformation, $T^\circ$ which maps $\mathcal{T}$ to the element $\mathcal{G}_1 \in \boldsymbol{\mathcal{G}}$ corresponding to the same diastolic cardiac phase as the pre-operative CTA image [3].

The aim of the proposed tracking method is to track the tree $\mathcal{T}$ in all the consecutive phases of the cardiac cycle, which necessitates to deform it. A spline description [7] is a tool suited for a one vessel deformation which can be represented by the optimization of its control points. Nevertheless, the tree structure implies a vessel connectivity preservation. A tree-spline structure (as in [10]) makes this preservation possible. The registration itself is based on a two steps mechanism with first the determination of pairings between the projected edges of $\mathcal{T}$ and the centerlines represented through a graph structure. Second, the control points are adjusted by minimizing an energy depending on the distance between the paired points and constraints on edges.

### 2.1 Problem modeling

The 3D temporal tracking requires a priori 3D model of the tree as introduced in [10,5]. The tree is represented as a set of centerlines which is a set of 3D curves. The different 3D curves are not completely independent: the extremity of a 3D curve is either a leaf of the tree and as such can move independently or is either the common extremity of other 3D curves. It is the case when the considered extremity is an anatomical bifurcation and in this case, it is the extremity of three different 3D curves. The representation of this tree shall support deformation of each 3D curves while keeping coherency between them when they share extremities. As seen in [7], the spline functions support a compact and smooth description of curves which can be continuously deformed by changing the position of the control points. We thus fit an approximating cubic ($C^2$ continuity) spline curve $C^k$ for each edge $A^k$ as in [6], using a centripetal method such that, $A^k \approx \{C^k(u) \mid u \in [0,1]\}$. More precisely the spline is defined as $C^k(u) = \sum_{i=1}^{n^k} N_{i,p}(u) P_i^k$, where $N_{i,p}$ is the $i$th B-spline of degree $p$, $P_i^k$ the $i$th control point of $C^k$, $u$ the spline abscissa (between 0 and 1), $n^k$ the number of control points. To reach the goal of representing a tree, we assign a multiplicity of $p+1$ to the first and last element of the associated knot vector $U_k$ as below:

$$U_k = \{\underbrace{0, \ldots, 0}_{p+1}, u_{p+1}, \cdots, u_{m-p-2}, \underbrace{1, \ldots, 1}_{p+1}\}$$

with $m$ the size of the vector. Given the description of the spline, the curve has to pass by the first (respectively last) control points (see [4] for details). Then we parametrize the set of splines such that the control points of 3D curves with a common extremity are also shared. Deformations are obtained by the optimization of the spline parameters. The set of control points to register the

3D vessel tree with the graph $\mathcal{G}_t$ is determined by solving this optimization problem:

$$\begin{cases} \hat{\mathcal{P}}_t = \text{argmin}_{\mathcal{P}=\{P^1,\ldots,P^{n^a}\}\in\Omega} \sum_{k=1}^{n^a} E_d(C_{P^k}, \mathcal{G}_t) + \beta E_r(C_{P^k}) \\ \Omega = \{P \in \mathbb{R}^3 \mid P^k_{n^k} = P^j_0 \text{ if } A^j \text{ is a daughter artery of } A^k\} \end{cases} \quad (1)$$

$t$ denotes the temporal index of the frame, $E_d()$ and $E_r()$ are respectively the data attachment and the regularization energy terms, $C_{P^k}$ the spline built with the control points $P^k$. In the following $\mathcal{P}_t$ denotes the set of control points for frame $t$ while $\mathcal{P}_1^{init}$ denotes the set of control points for the 3D vessel tree after the pose estimation $T^\circ$ for frame 1. An initial position is used for the 3D vessel tree to build the data attachment term: it is the 3D vessels/splines $\mathcal{T}_{\mathcal{P}_1^{init}}$ issued from the pose estimation for the first frame $t = 1$ or $\mathcal{T}_{\mathcal{P}_{t-1}}$ for frame $t > 1$. For the sake of simplicity, $t$ will be omitted in the following. Every 3D edges $C^k$ are projected onto the angiographic frame and are denoted $c^k$. A 2D curve $v^k$ corresponding to the projected 3D curve is extracted from the graph $\mathcal{G}$ as described in [3]. In the sequel, the registration between one couple of curves will be explained, therefore $k$ will also be omitted.

**Data attachment term** The data attachment term $E_d()$ is a sum of 3D residual distances issued from 3D to 2D pairings. The simplest method to build pairings is to use the closest neighbor scheme (as in the ICP). In [9], a variant of this approach is proposed: the idea is to represent the cardiac motion by covariance matrices on the different parameters describing the coronary tree. For this one, a generative 3D model is employed, i.e. a model including a probabilistic distribution of position for the arterial segment. The concept of distance is then extended from standard Euclidean distance to Mahalanobis distance. This geometrically oriented analysis does not include the constraint of ordered pairing as proposed in [3] where it is shown that a point pairing that respects the order along paired curves yields better results than the closest neighbor scheme. Such an ordered pairing was obtained by the means of the Fréchet distance, that allows *jumps* between paired points. In presence of vessel deformation, we observed that the coherency of the obtained pairings is sometimes lost. So we propose to constrain the pairing construction with a 2D elongation preservation. We first recall the Fréchet distance and its induced pairing [3]. Let $c = \{c_1, \ldots, c_{n^c}\}$ and $v = \{v_1, \ldots, v_{n^v}\}$ be the 2D curves to be paired. The points $c_i$ are obtained as projection of points $C_{\mathcal{P}}(\bar{u}_i)$ from the 3D spline which represents the vessel. The points $v_i$ are the discrete points forming the centerline of the vessel extracted from the angiographic images. The point pairings are entirely defined by a single injective function $F : \mathbb{N} \to \mathbb{N}$. The Fréchet distance is defined as:

$$\begin{cases} F(1) = \text{argmin}_{i_v \in I_v} \|v_{i_v} - c_1\| \text{ with } I_v = \{1, \ldots, jump\} \\ F(i_c) = \text{argmin}_{i_v \in I_v} \|v_{i_v} - c_{i_C}\| \text{ with } I_v = \{F(i_c - 1), \ldots, F(i_c - 1) + jump\} \end{cases}$$

with $jump$ a parameter controlling the length of allowed jumps in pairings. Looking at the pairing produced by this metric (as in Fig. 1, left), we observed that the simple application of the criteria of minimizing consecutively the pairing length may lead to irregular pairings. Inspired by the Fréchet distance, we present

a pairing function which aims to build a pairing function that advances at the same speed along the 2D curves to be paired. We define $d(p_1, p_2) = \sum_{i=p_1+1}^{p_2} \|c_i - c_{i-1}\|$ and $F$ as:

$$\begin{cases} F(1) = \text{argmin}_{i_v \in I_v} \|v_{i_v} - c_1\|^2 + \lambda d(v_1, v_{i_v})^2 \text{ with } I_v = \{1, \ldots, jump\} \\ F(i_c) = \text{argmin}_{i_v \in I_v} \|v_{i_v} - c_{i_c}\|^2 + \lambda (d(v_{F(i_c-1)}, v_{i_v}) - d(c_{i_c-1}, c_{i_c}))^2 \\ \qquad \text{with } I_v = \{F(i_c - 1), \ldots, F(i_c - 1) + jump\} \end{cases} \quad (2)$$

with $\lambda$ proportional to the local distance between the neighborhood of $i_c$ and $i_v$. This function favors point pairings between points which are approximately at the same distance from their respective neighborhoods.

Fig. 1 shows the pairings obtained with this weighted Fréchet distance. It is especially useful when the two curves to be paired have experienced a non-rigid transformation with respect to each other. This is exactly the case as our objective is to follow the cardiac deformation. $F()$ provides 2D point pairings $(v_{F(i)}, c_i)$ between the 2D curves $v$ and $c$. To compute 3D deformations, we have to define 3D point pairings. $c_i \in c$ is associated to its corresponding 3D point $C_{\mathcal{P}}(\bar{u}_i)$. The 3D point $V'_{F(i)}$ corresponding to $v_{F(i)}$ is the point from the backprojected line issued from $v_{F(i)}$ that is the closest to $C_{\mathcal{P}}(\bar{u}_i)$. The data attachment term is finally, $E_d(C_{\mathcal{P}}, \mathcal{G}_t) = \sum_{i=1}^{n_C} \|V'_{F(i)} - C_{\mathcal{P}}(\bar{u}_i)\|^2$

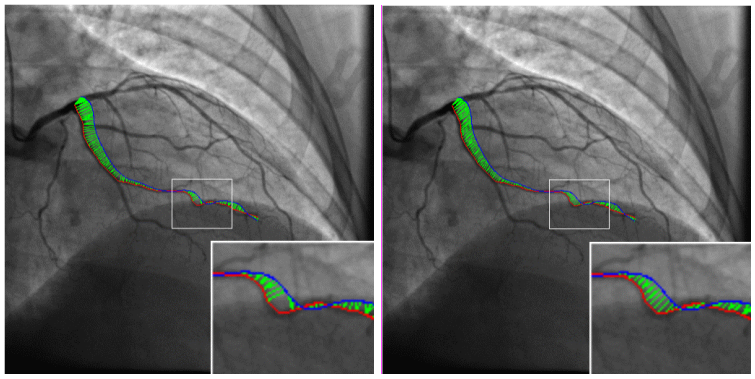


Fig. 1: Pairings (green) between a projected 3D vessel $c$ (blue) and a 2D vessel $v$ (red). Left, with the Fréchet distance; right, with the weighted Fréchet distance.

**Regularization term** The regularization term aims at minimizing the 3D elongation of $C$: $E_r(C_{\mathcal{P}}) = \sum_{j=1}^{J} (\|C_{\mathcal{P}}(e_j) - C_{\mathcal{P}}(e_{j-1})\| - l_j)^2$ with, $e_j = \frac{j}{J}$ , $l_j = \|C_{\mathcal{P}_1^{init}}(e_j) - C_{\mathcal{P}_1^{init}}(e_{j-1})\|$, $J$ is the number of interval used to enforce the length constraint all along the vessel.

**Energy minimization** d This global energy $E_d(C_{\mathcal{P}}, \mathcal{G}_t) + \beta E_r(C_{\mathcal{P}})$ is minimized via a gradient descent. Thanks to the spline description of the 3D curve, the analytic expression of the gradient is used for the gradient descent. The pairings are recomputed along the descent every 1000 iterations. The minimization

is stopped when the gradient norm is below a threshold, whose value has been chosen in preliminary experiments.

## 3 Performance evaluations

Qualitative evaluation of the performance can first be done by a visual control of the deformation of the projected deformed vessel of interest over the angiographic image along the cardiac cycle. We also propose two quantitative measures. The first derives from methodological expectations on the performance but does not cover directly the intended clinical application. The second one replicates more closely the expectations from a clinical standpoint.

**Shape preservation** For this analysis, we start from the idea that the vessel tree shall return to its initial state if the tracking is performed on a series of consecutive images which start and end by the same image. Let $N$ the number of angiographic images in a sequence which covers a cardiac cycle, the tracking is done from the frame 1 to the frame $N$, resulting in $N$ 3D trees corresponding to the same vessels temporally tracked, $\mathcal{T} = \{\mathcal{T}_1, \ldots, \mathcal{T}_N\}$. One can then generate the reverse sequence starting from image $N-1$ down to image 1 and continue to apply the tracking algorithm. The result is an other set of 3D trees $\mathcal{T}' = \{\mathcal{T}'_{N-1}, \ldots, \mathcal{T}'_1\}$. To measure the similarity, we chose to compare the projections of $\mathcal{T}_1$ and $\mathcal{T}'_1$ on the vessel of interest $W$ i.e. the vessel which is pathological and going to be fix in the intervention. Let $I_w$ be the set of edge index which correspond to edges owing to the vessel of interest, we define the vessel as $W = \{C^j\}_{j \in I_w}$. We retain as a measure of shape preservation, the percentage of points which get close enough to their initial position $sp$ and the percentage of points which get close enough to a point owing to $W$, $sp^{cl}$, these measures are defined as $sp = \frac{|E| * 100}{n^w}$ and $sp^{cl} = \frac{|E^{cl}| * 100}{n^w}$ with $E = \{i \in [1, n^w] \mid \|w_1(i) - w'_1(i)\| < l\}$, $E^{cl} = \{i \in [1, n^w] \mid \|w_1(i) - w'_1(k)\| < l\}$, with $w_1$ and $w'_1$ the projections of $W_1$ and $W'_1$, $k$ the index of the closest point of $w_1(i)$ owing to $w'_1$, $n^w$ the number of points in $W$ and $l$ a parameter which controls what close means here.

The point of computing this measure and not the distance between points is to detect when the tracking has followed a wrong vessel (as illustrated in the videos https://3dvttracking.github.io/), which in this case would give a low score of $sp$ and $sp^{cl}$.

**Landmark tracking** The idea is to evaluate if a location defined along $W$ is correctly tracked. A location in the vessel $W$ is defined by its curvilinear abscissa. In the angiographic image, identifying a fixed point is more challenging.

For the purpose of the evaluation, we first manually point an easily identifiable landmark along the 2D vessel. Vessel bifurcations are natural candidates for such landmarks. To decide whether the same 3D point of the tracked vessel is paired to this landmark, we use the curvilinear abscissas $u$ (along the vessel) of the paired 3D points to it. A perfect tracking (along with a perfect manual identification of the landmark) should yield the same curvilinear abscissa for all paired 3D points, thus the standard deviation of all curvilinear abscissas is an adequate measure to assess the tracking.

Formally, let $U = \{u_1, \ldots, u_N\}$ be the $N$ abscissas of the paired 3D points, eg. $W(u_t)$ is paired with the bifurcation/landmark in frame $t$, and $\bar{u}$ be the average value over $U$, the proposed measure is $lt = \sqrt{\frac{1}{N}\sum_{i=1}^{N}(u_i - \bar{u})^2}$.

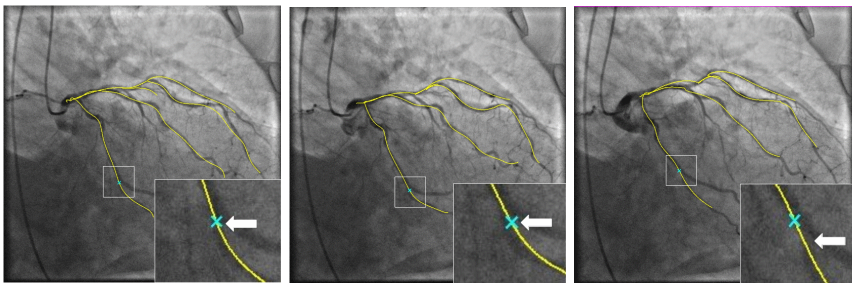
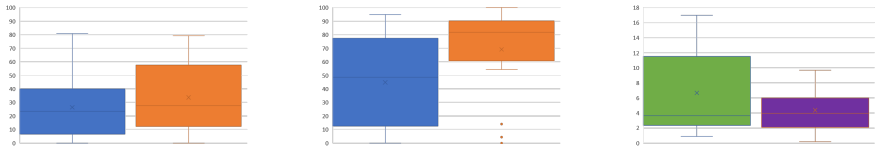


Fig. 2: Tracking results for one patient over one cardiac cycle. The yellow curve represents the projected 3D vessel, the blue cross represents the point tracked as the bifurcation, and the white arrow points to the bifurcation. Those images come from a 15 frames sequence. This figure shows the frames 1, 6, 15, from left to right. More tracking results are available on https://3dvttracking.github.io/

## 4 Results

To assess the performance of the proposed approach, we use anonymous data collected after informed patient consent for use in this type of investigation. These data come from ten different patients. Both the CTA and the angiographic images are available. We selected in the angiographic sequences a sub-sequence which covers a full cardiac cycle or a bit more depending on the patient case. The CT scans have been pre-processed to extract the coronary vessel trees as described above. Several x-ray projections with different angulation may have been selected for a given patient, yielding a total of 23 different tracking experiments. Each of them is analyzed separately from the other. Selection is based on the available angiographic views and the vessels are selected as the ones that could be the object of an interventional procedure. In the following, we propose to compare the trackings on the vessels of interest made thanks to the registration of the single vessel of interest as in [7], and the registration of the vessel of interest made thanks to the registration of the vessel tree as described in this work. Fig. 2 is an example of the obtained results in one case. The method has been implemented through a $C++$ program on a standard modern processor, given an execution time of 18 seconds per image.

**Shape preservation** Fig. 3, (a) and (b), shows the results obtained thanks to the registration of only the vessel of interest (in blue), and the results obtained



(a) $sp$ with $l = 5$ mm (b) $sp^{cl}$ with $l = 5$ mm (c) $lt$

Fig. 3: Each subfigure compares the one-vessel tracking (left, [7]) to the vessel-tree tracking (right). (a) and (b) present the shape preservation measures with respectively the point-to-point and the point-to-closest distances. (c) presents the landmark tracking measure.

| Evalutation | Previous method | Actual method |
|---|---|---|
| $sp$ | 26% | 31% |
| $sp^{cl}$ | 45% | 70% |
| $lt$ | 6.7mm | 4.3mm |

Table 1: Average results for each evaluation, for the previous method presented in [7] and the actual method presented in this work.

thanks to the registration of the entire tree (in orange), with $l = 5$ mm. In (a) the evaluation is computed point to point, in (b) point to closest point. For both, the method presented in this work clearly outperforms the method of [7]. [7] and our method obtained respectively in average for the first evaluation 26% and 33%, and 45% and 70% for the second evaluation (see Tab.1).

**Landmark tracking** The results of this measure are shown in Fig. 3c. The values are the standard deviation of the curvilinear abscissa of points associated to the bifurcations for each projection of the vessel of interest. On the left, the measures (average 6.7 mm) are obtained with the approach presented in [7]. On the right, the measures (average 4.3 mm) are obtained thanks to the registration of the entire tree i.e. the measure described in this work (see Tab.1).

## 5 Discussion and conclusion

Fusing the anatomical content of a CTA scan with angiographic images of the same patient for guidance in interventional procedure is a common request from operators. One of the challenge is the management of the cardiac motion. In this paper, we have explored an approach involving the deformation of the 3D arterial tree represented by a tree-spline. The proposed approach involves several algorithmic steps: a rigid registration of the tree to an iso-cardiac phase projection followed by a deformation of the tree represented as a tree-spline. Encouraging

results have been obtained and the use of the full tree in the different steps of the algorithms improves the accuracy of the approach. Indeed, the algorithm is more able to manage superimpositions of different branches over the vessel of interest which happens along the cardiac cycle. We observed 4.3 mm in average for the task of landmark tracking compared to 6.7 mm following the approach described in [7] which performs the deformation on the vessel of interest only. The considered dataset covers a larger set of clinical situation. Interestingly, the algorithm is able to perform a self-assessment of its performance using the shape preservation. Indeed this measure does not require any pre-defined ground truth. The obtained result shows that there is, in some cases, a "slipping" of the vessel of interest. This "slipping" is possible while keeping the 3D length of the vessel constant. The artery deforms itself in the direction of projection. Future works will be done to solve this. It may require improvement in the creation of the pairings.

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