# Efficient 3D Reconstruction of Vessels from Multi-views of X-Ray Angiography

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## I. MOTIVATION

Intra-operative X-Ray is essential during some surgeries, such as percutaneous coronary intervention. The 2D X-Ray images have many shortcomings such as viewing angle dependence, magnification factor, overlapping, and the blurring between vessels, background, and other tissues/organs. Great efforts have been carried out on 3D reconstruction of coronary arteries to overcome the shortcomings of 2D images. Current 3D reconstruction methods mostly rely on the registration between image pairs, which are generally hard to enforce constraints such as consistency and continuity. To overcome these shortcomings, we develop an efficient vessel reconstruction system based on multiple X-Ray views. We demonstrate our system in coronary artery reconstruction for percutaneous coronary intervention surgery to help doctors understand the spatial configuration of coronary arteries of specific patient during operation.

## II. METHOD

- A. Data acquisition and preprocessing. For all procedures, we use two types of data. One is the synthetic data from our simulation system. Another one is the real data from clinical angiogram. We select one image from each view within mostly the same cardiac cycle and use them to reconstruct the vessels. To overcome the shortcomings such as the low image contrast, the low lumen with the wide dynamic range of original angiograms, we apply multi-scale retinex (MSR) enhancement proposed by Rahman [1] on each image.
- **B. Vessel extraction.** After obtaining the high-contrast images pre-processed by MSR, we use the approach proposed by [2]. It relies on a multi-scale Hessian matrix that enhances the vascular structure. After processing the image, we compute the connectivity of the entire image using a cross template so that line segments whose length are smaller than a typical value are regarded as noise, and the similar thresholding process is applied to noisy points produced by enhancement during MSR.
- C. Centerline tracking. After getting the binary images of vascular structure, we apply the centerline extraction method using multi-stencils fast marching (MSFM). Our method is based on Hassouna's work [3] and by solving the Eikonal equation at each point under several stencils which cover eight neighbors in 2D space and selecting the

one which satisfies the upwind condition the most, this way we can achieve better accuracy.

**D. 3D reconstruction of coronary arteries.** In our method, we treat the space between the image intensifier and the optical center of the X-Ray machine as an Markov Random Field. The 3D space is divided into 2D slices which we call layer  $L=(l_1,l_2,...l_n)$  using a given depth increment. Each depth can be assigned with a label  $l_i$ . Meanwhile, each skeleton point on reference view  $I_1$  corresponds to a projected line from the source to the intensifier through all the layers.

Therefore, for a given pixel p on  $I_1$ , the pair  $(p,l_i)$  uniquely identifies a point in 3D space. So, the goal of 3D reconstruction is to optimally assign a label  $l_i$  to each p on the centerline of the reference view  $I_1$ . This problem can be formulated as an energy minimization problem subject to the constraint of connectivity and topological structures. Our goal is to find the minimum energy and we use the belief propagation (BP) [4] method to derive the solution. In our method, we define  $V_{p,q}(f_p,f_q)$  as the Euclidean distance between point p and q. We define  $D_p(f_p)$  as the color consistency which can be formulated as  $D_p(f_p) = \frac{1}{(n-1)} \sum_{i=2}^n P_i(x,y)$ , where  $P_i(x,y)$  is the projection value of point p on the i-th view, and we define it as

$$P_{i}(x,y) = \begin{cases} W_{h}, & p(x,y) \in I_{i} \\ W_{l}, & \mathcal{N}(p(x,y)) \notin I_{i} \\ W_{a}, & \text{otherwise} \end{cases} , \tag{1}$$

$$W_a = \frac{1}{N} \sum_{i=1}^{N} V_i(x, y),$$
 (2)

where  $p(x,y) \in I_i$  means that p(x,y) is a valid centerline point of  $I_i$ ,  $W_h$  and  $W_l$  are two constants that control the highest and lowest value, respectively. For a grey scale image,  $\mathcal{N}(p(x,y))$  includes 8 neighbors of point p(x,y). If p(x,y) can not be found in  $I_i$ , we will compute its 8 neighbors and obtain the average value as the value of point p(x,y). If none of its neighbors is valid, it could be assigned with  $W_l$ . Our algorithm includes two main steps, message propagation and energy minimization computation. In the message propagation, the color value of point  $p(x,y) \in I_1$  is updated as  $V_p = V_{p-1} + \alpha \min D_{p,q}(f_p, f_q) + (1 - \alpha)V(p_{min})$  where  $\alpha$  is a constant controlling the weight its neighbors' color consistency and distance consistency. And  $D_{p,q}(f_p, f_q)$  denotes the distance from p(x,y) to its

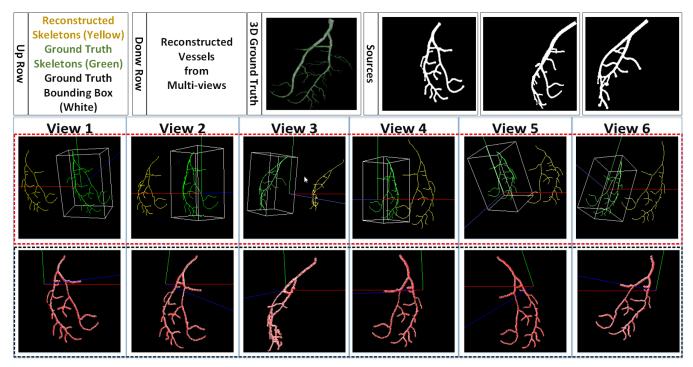


Figure 1: Reconstructed vessels from synthetic data.

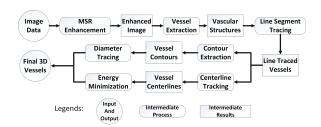


Figure 2: Our system pipeline.

neighbors,  $V(p_{min})$  denotes the value of the minimum distance point.

In our energy minimization, different from typical BP, the current energy of the i-th layer is defined as  $e_i(p_i) = \min[\gamma D(p_i,q) + (1-\gamma)V(q) + e_{i-1}(q)]$  in which q denotes the projected sample depth of  $\mathcal{N}^o(p(x,y))$  which includes all neighbors of  $p_i$  except  $p_i$  itself.

Finally, we compute the minimum sum of all the grouped vessel skeletons' cost, and obtain the optimal solution for the entire vessel skeleton tree. The entire system pipeline is illustrated in Fig. 2.

# III. EXPERIMENTS

We test our reconstruction method on synthetic data and real clinical data, respectively. Compared with real data, the reconstruction of synthetic data is easy to assess because of the vessel ground truth. The final reconstruction results of synthetic data are shown in Fig. 1.

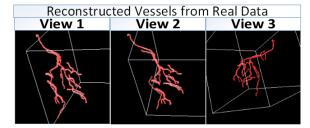


Figure 3: Reconstructed vessels from real data.

In the top row of Fig. 1, the yellow lines indicate the reconstructed skeleton using our method. The green lines indicate the ground truth obtained in our simulation platform. The white box is the bounding box of the ground truth. For the real data reconstruction results, the views and reconstructed results can be found in Fig. 3.

#### IV. CONCLUSION

We have presented a novel method of reconstructing 3D vessels from angiograms. The fundamental idea is to treat the 3D space from the X-Ray machine optical center (receiver) and the X-Ray machine intensifier (emitter) as slices. In this way, we are able to transform the reconstruction problem into an energy minimization problem. The experimental results from both synthetic and real clinical data show our method is useful and works well.

**Acknowledgment:** This work is supported by National Natural Science Foundation of China (No. 61190120,

61190121, 61190125, 61300067, and 61300068) and National Science Foundation of USA (No. IIS-0949467, IIS-1047715, and IIS-1049448).

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