

3D Vessel Reconstruction from Single Plane Angiograms

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I. INTRODUCTION

We describe a system for constructing time-variant 3D vessel models from single-plane angiograms. Previous work in vessel detection and reconstruction is limited to in vitro bi-plane angiograms. Our extension to the existing methods allows us to build animated 3D vessel models from two single-plane angiogram sequences.

II. SIGNIFICANCE

Angiograms have been used clinically for diagnosing acute heart diseases such as atherosclerosis. Due to the ambiguity arising from a single projected view of a 3D elongated structure a single-plane angiogram alone is unreliable.

3D reconstruction provides many important anatomical measurement that are either not available, or can not be accurately measured in 2D. For example, the projected length of a vessel is shorter in the projected views. Torque and the curvature of a vessel are virtually impossible to estimate from 2D views.

3D reconstruction provides better and cleaner visualization allowing people without extensive training to understand vessel geometry. It saves reviewing time for doctors since 3D reconstruction may be performed by a trained technician, and may also help visualize dynamics of the blood vessel that were not be demonstrated by previous methods.

III. METHOD

We first capture a sequence of angiogram images for 2 heart cycles. The camera is then rotated 90 degrees to repeat the capturing process for two more cycles. With the aid of a technician, we manually identify a pair of angiogram images at the same phase of the heart beat to align the two image sequence.

The first step in reconstructing the 3D geometry is to find point correspondences from the two views. Contrast agent dissipation and image intensity variations invalidate common algorithms for establishing such correspondence so we provide an interface to manually match these points. Note that the global rigid motion (patient motion) is removed through the

point correspondence matching process.

We next detect 2D vessel centerlines from each view of a blood vessel. The detected 2D centerline combined with feature point correspondence allow the reconstruction of 3D vessel centerline. We use linear interpolation to interpolate correspondence relationship of line segments bounded by a pairs of matched feature points.

The reconstructed centerline provides a 3D skeleton, of the vessel. We augment this skeleton by computing the cross sectional shape from each view to build a tubular geometry resembling that of a real blood vessel.

Since detected vessel geometry depends on the amount of the contrast agent injected and its dissipation speed it is very difficult to construct the exact geometry; however, good approximation can be found by normalizing the vessel size with respect to the proximal end of the vessel where there is very little chance of arterial disease and the cross sectional shape is circular.

Lastly we create a triangular mesh by joining the cross sectional curves. To do this, we build the correct curve-linear coordinates by using the Frenet formula. The reconstructed cross-sectional geometry and the curve-linear coordinates define the 3D vessel shape unambiguously.

IV. CONCLUSION

The reconstructions are put together into a 3D time-varied animation. The resulting animation has clear advantages over conventional visualization methods. The ability to rotate the model makes for quicker and more accurate understanding of the vessel geometry.