Kidney and vessel segmentation

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1 Method

We present a method for kidney and vessel segmentation from clinical CTa (i.e., CT artery) data. Our ultimate goal is to obtain high quality segmentations for kidneys, arteries, veins and tumors (4 labels). Currently, only kidney and vessel (without differentiating arteries and veins) segmentations are presented (2 labels).

More specifically, the clinical CTa data comprises of 9 scans, among which two scans are the most useful: the **arterial phase scan** and the **essence phase scan**. We use the two scans as the inputs to our processing pipeline. The main steps of our pipeline are illustrated in Fig. 1.

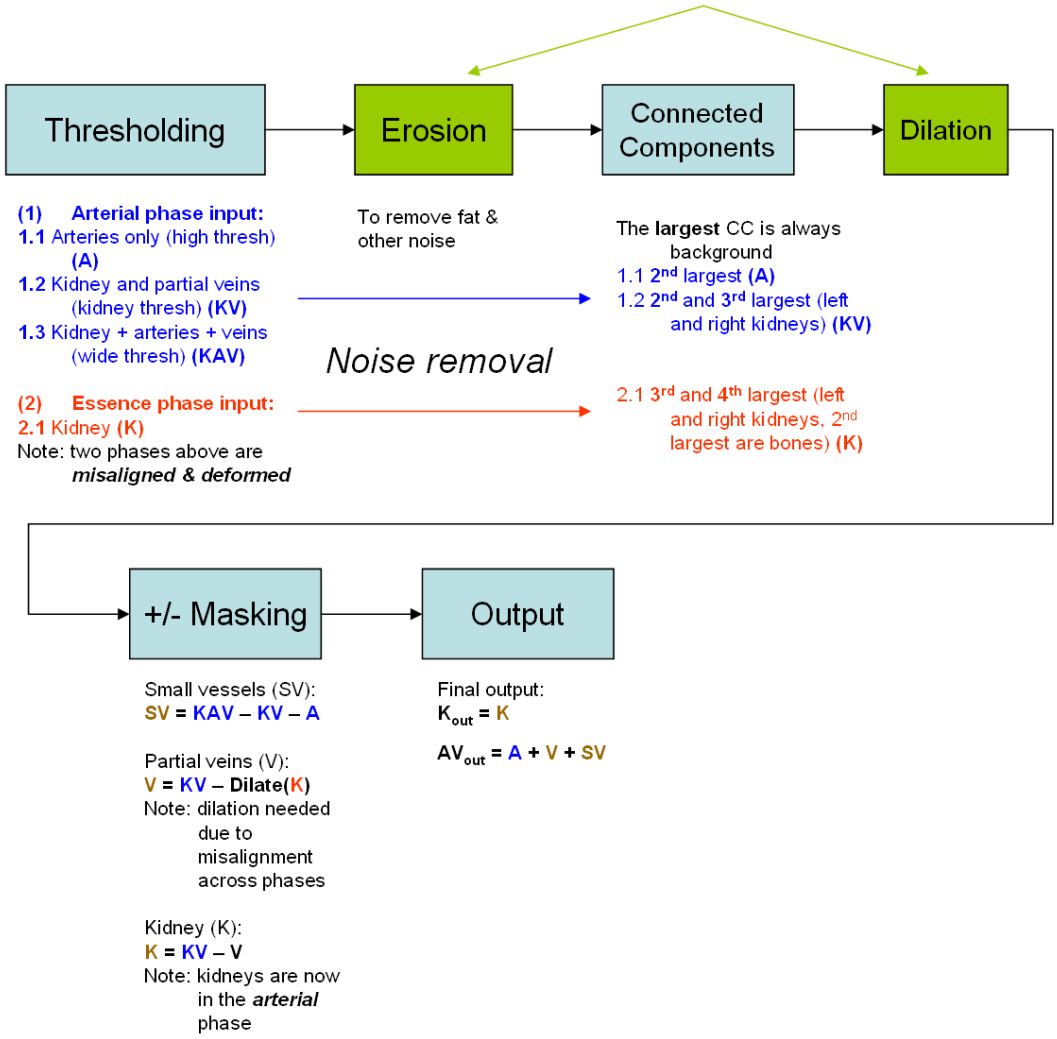

Figure 1: Our processing pipeline.

2 Results

We present some intermediate results from applying our pipeline to the clinical CTa data, as presented in Fig. 2.

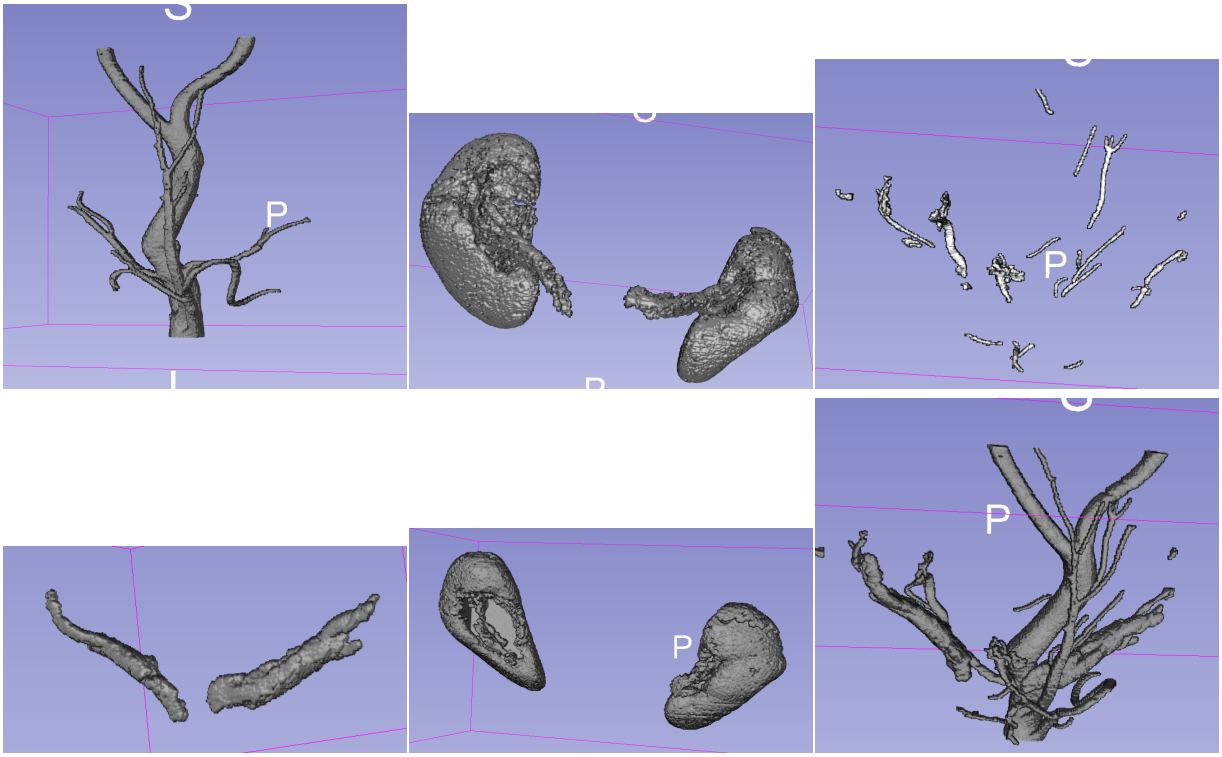

Figure 2: From left to right, top to bottom: arteries only (A), kidney and partial veins (KV), small vessels (SV), partial veins (V), output kidney (K_{out}), and output arteries and veins (AV_{out}).

Final results are shown in Fig. 3.

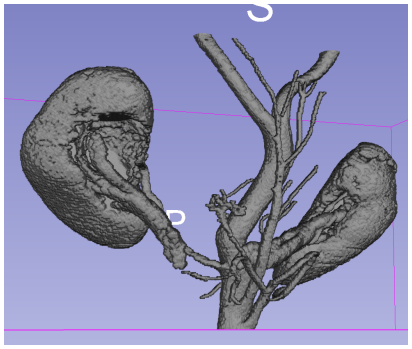

Figure 3: Final results.

3 Discussions

- How to model the vessels (arteries and veins) inside the kidney?
- We applied the Iterative Closest Point (ICP) algorithm to align the arterial and essence phases, however the initial results are poor. Currently, we simply assume that the two phases are roughly aligned, and use a dilated mask of kidneys K from the essence phase, and then apply it to the arterial phase's KV to isolate veins V from KV (see Fig. 1, under the $+/-$ Masking step).
- What is a good visualization tool for our final results?