Homework 5

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https://github.com/Tonight1121/Biology-Image-Analysis

1 Raw Volume Loading and Visualization

I load the mra 3D volume by using the mhd_utils tool.

$fn_mhd =' mra/mra.mhd'$

$rawImg, header = mu.load_raw_data_with_mhd(fn_mhd)$

In such a way, rawImage becomes a 83*512*512 3D array. I used a software called slicer to visualize the 3D volume directly. The software loading result looks like this in Fig. 1.

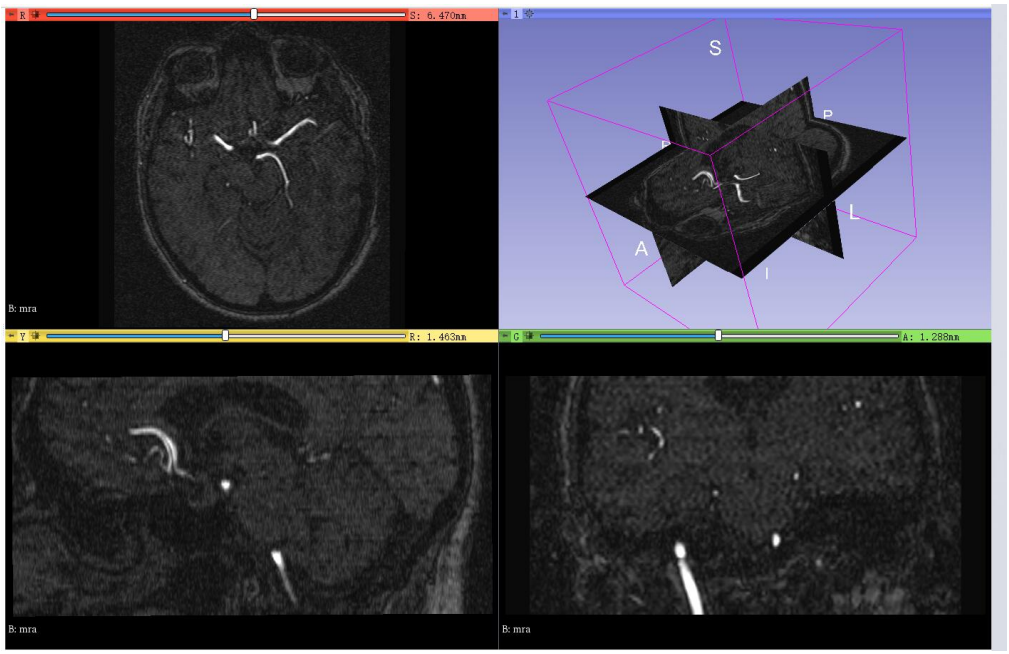

Figure 1: Three views of raw volume. Selected slices with obvious vessel structure.

2 Vasculature Segmentation

Frangi Vesselness Measure is basically based on Hessian matrix decompositiom. I chose to use the built-in library provided by frangi() function in skimage.filter. The arguments of this function and my setting parameters can be seen below:

$frangi(image, scale\_range = (1, 15), scale\_step = 0.05, beta1 = 100, beta2 = 100, black\_ridges = False)$, where

image : (N, M) ndarray. Represents the array with input image data.

scale_range : 2-tuple of floats, optional. This value determines the range of sigmas used.

scale_step : float, optional. Represents the step size between sigmas.

beta1 : float, optional. Frangi correction constant that adjusts the filters sensitivity to deviation from a blob-like structure.

beta2 : float, optional. Frangi correction constant that adjusts the filters sensitivity to areas of high variance/texture/structure.

black_ridges : boolean, optional. When True (the default), the filter detects black ridges; when False, it detects white ridges. In our case, the vessel in brain image appear white according to the observation, so we set this value to False.

3 Segmentation Results

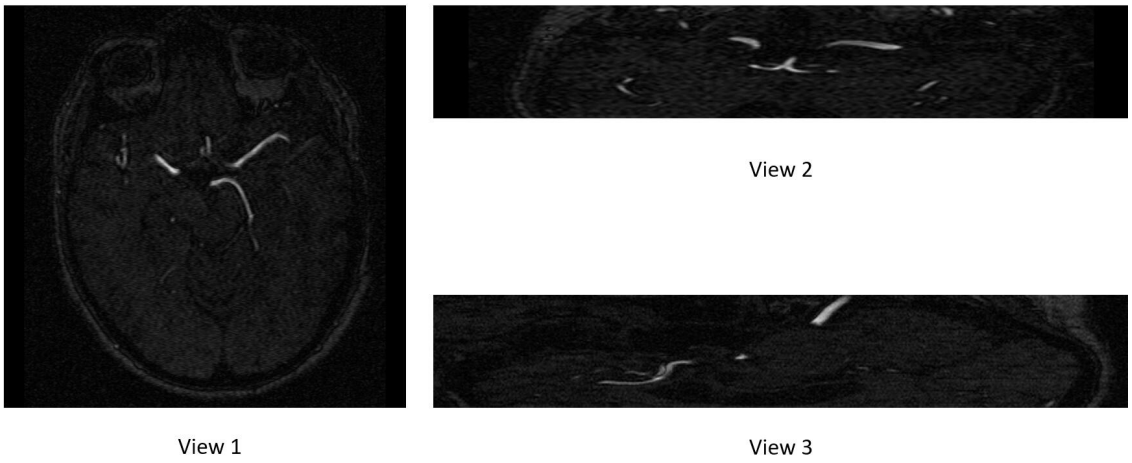

Figure 2: Three view raw images.

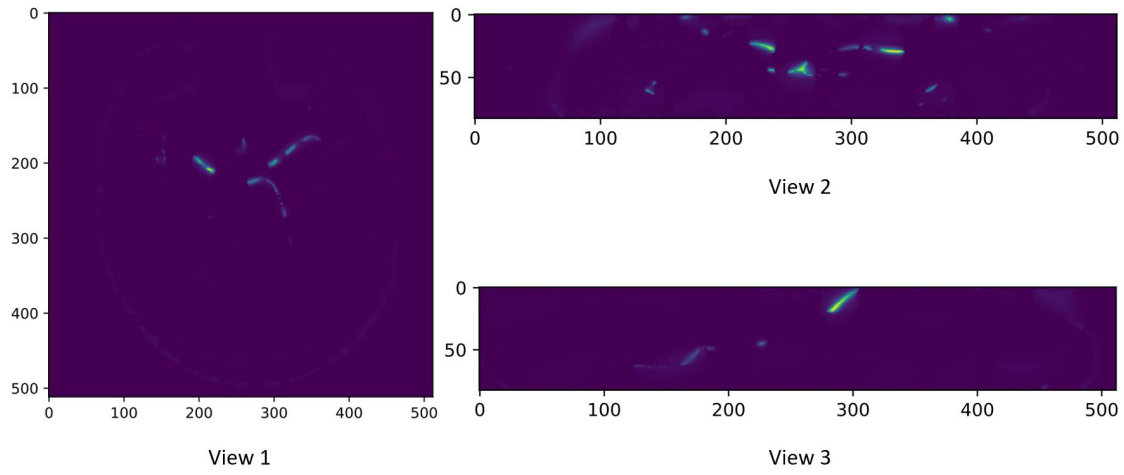

Figure 3: Three view results.