This directory expands upon David Parker's code and uses it to create many training and labeled images for vessel segmentation of medical images. No alteration to the directory make up needs to done.

Environment: img_env.txt

Command Line Call: python3 main.py. This command line call will run everything needed to create images.

Inputs

- 1. All of the models that we'd like to create images for should be in the 'models' folder. These models can be downloaded from the Vascular Model Repository.
- 2. For each model we also need the corresponding 'centerline' data which should go in the 'centerlines' folder.

Outputs

1. In the 'files' folder, the generated training and labeled images are found with the suffix 'X.png' and 'Yc.png'. It is however important to note that Dr. Gabriel Maher's code needs the images in numpy files, so there are also 'X.npy' and 'Yc.npy' files. Dr. Gabriel Maher's code also requires a 'yaml' file for each image pair, and this is also produced by the code. The 'Y.png' and 'Y.npy' is for an intermediate step which is also used by Gabe.

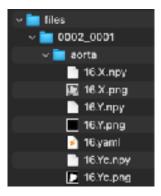


Fig 1. This is an example of how the resulting directory might look: Patient 0002_0001's aorta at point 16 has all of this information.

2. The other important output is 'files.txt'. This file lists all of the yaml files for all of the images that were created. The reason this file is created is because Dr. Gabriel Maher's code requires a file like this.

```
./files/0063_1001/LCCA/83.yaml
./files/0063_1001/LCCA/76.yaml
./files/0063_1001/LCCA/60.yaml
```

This is an example of what *files.txt* looks like.

3. Other outputs include the '3D_points' sub-directory, 'results' directory, and *temp.png*. The *3D_points* subdirectory is an intermediate step for my code. The *results* directory is a byproduct of David Parkers code, and the *temp.png* file is a byproduct of my code.

Important Functions:

util.create_slices(model,path)

Information: This file is called in util.create_images(). You don't need to explicitly call this function at any time.

Inputs:

- 1. Model: This refers to a patient number such as 0002_0001, 0003_0001, etc.
- 2. Path: This refers to a path such as 'aorta', 'LAD', 'SVC', etc. Any vessel is a path.

HardCoded Inputs:

- 1. Slice_Increment: This refers to how often in a pathway you'd like to extract slices. For instance, setting this value to 10 will yield ten times as many images as setting this value to 1 will. The default is 10.
- 2. Slice_Width: The default for this value is 5 in Dave Parker's code.

Supplemental Code/Features:

More files can be found in 'extra_tools' although these were used for my personal use. However, one may find them useful.

Perimeter.py:

Command Line Call: python3 perimeter.py

Explanation: This can be run only once 'python3 main.py' has been called. This will produce images showing the perimeter vessel.

Xo.py:

Command Line Call: python3 Xo.py

Explanation: This can be run only once 'python3 perimeter.py' has been called. This will produce images showing the perimeter of the vessel on top of the original ground truth images.

GUIXo.py:

Command Line Call: python3 GUIXo.py

Explanation: This can be run only once 'python3 Xo.py' has been called. This will produce a GUI showing all of the Xo.png images in an easy to scroll through format.

GUI2.py:

Command Line Call: python3 GUI2.py

Explanation: This can be run only once 'python3 main.py' has been called. This will produce a GUI showing all of the *X.png, Y.png, and Yc.png* images in an easy to scroll through format.

sobel.py:

Command Line Call: python3 sobel.py

Explanation: This can be run only once 'python3 main.py' has been called. This will produce an alternate filtered list of images like 'files.txt' however this file only include files such that the average gradient of the images is equivalent to some hard-coded value (target_mean). The default for this value is 87 because this is the value for the images Dr. Gabriel Maher used.