**INSTRUCTIONS ON RUNNING THE CLASSIFICATION MODEL**

1. Duplicate the CancerData folder and rename one (you could use CancerData\_FE for instance).
2. Download and Install [Anaconda](https://repo.anaconda.com/archive/Anaconda3-2019.10-Windows-x86_64.exe) package for Python 3.7 to your local machine.
3. After Installing Anaconda, open Jupyter Notebook either by opening the Anaconda package and opening the Jupyter Notebook module or opening your local search window and searching for Jupyter Notebook then opening it.
4. Upon opening, it will load a prompt and thereafter open a local environment in your default browser where it will list your system directory.
5. Navigate this list to the location of the ipynb file which contains the model and open it.
6. Go to the local search window again and search for Anaconda prompt and open it.
7. This will open up a command prompt styled window. Enter the following code into the prompt to install libraries which were not pre-installed but are necessary for the model

***pip install scipy-stack, seaborn, skimage, Pillow, scikit-learn, opencv-python***

1. Go back to the notebook and go to the cell toolbar and click run all.
2. At the data processing part, you will need to enter the path to the original and duplicate images during runtime. If this isn’t done, it would just keep loading without doing anything. Enter the path like ***C:/Users/PRUNEDGE/Documents/FE\_CancerData/benign/*** starting from your root directory (C:) to the file location (e.g. benign or malignant) using forward slashes (/). Errors would cause an error in the next cells and the path entering cell would have to be re-run before running all again.
3. Notebook should run without any errors with this and the entire running process should take about 8 minutes.