1. Download the INbreast 1.0 dataset (can be downloaded from <https://drive.google.com/file/d/19n-p9p9C0eCQA1ybm6wkMo-bbeccT_62/view?usp=sharing>)
2. Run the code present on the dataset at INBreast Release 1.0\ALLDICOMs\
3. Run tablePreprocessing.m code that creates a table tbl\_inbreast which contains information on label and corresponding .dcm file
4. Import INbreast.xls as INbreast1 variable
5. Run massData.m to create mass data table tbl\_inbreast\_mass
6. Run defineClass.m which defines original label to label for malignant and benign
7. Make a folder named Datastore with two subfolders Malignant and Benign
8. Run createDS.m. This creates an image datastore.
9. Finally, run classificationCancer.m file to start training and look at progress and metrics

Test.dcm can use used to check the image processing part.