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The code used was borrowed from Abhinav Sagar on Towards Data Science in an article called "Convolutional Neural Network for Breast Cancer Classification." In this code, I altered the deep neural network used as well as the batch size, learning rate, dropout rate, and number of epochs hyperparameters in order to compare model performances. There is a folder called data that has images of both benign and malignant tumors. In the benign and malignant folders, there is a train and a test folder. The train folder has 1000 images and the test has about 250 images. The code takes in these training images which train a classifier to learn what the benign and malignant classes look like. Then this classifier is tested by predicting labels for new sets of test images and compares the actual labels to the labels made by the classifier which gives us the accuracy. These images were put into arrays. Arrays of 0s were used to represent benign tumors and arrays of 1s were used to represent malignant tumors. The 8th cell is where you can see what the images look like that are being examined. The 9th, 10th, 11th, and 12th cells are the main cells that you should be running in order to see the accuracies produced by the different models. In the 11th cell, this is where you can see all the different models that can be implemented in addition to the learning rate and dropout parameters. The 10th cell has the batch size and then 12th cell has the number of epochs. The 12th cell is the one to run in order to see the accuracies. After these cells, the rest are there to produce different graphs and a confusion matrix in order to properly visualize what is going on. When you open the code, there are already results that are present for you to see.

Link to the code:

<https://colab.research.google.com/drive/1qxcAXDSVJavzQ67-4NS2pzbZZ3Jw53bu?usp=sharing>

Link to GitHub where code was borrowed:

<https://github.com/abhinavsagar/Breast-cancer-classification>