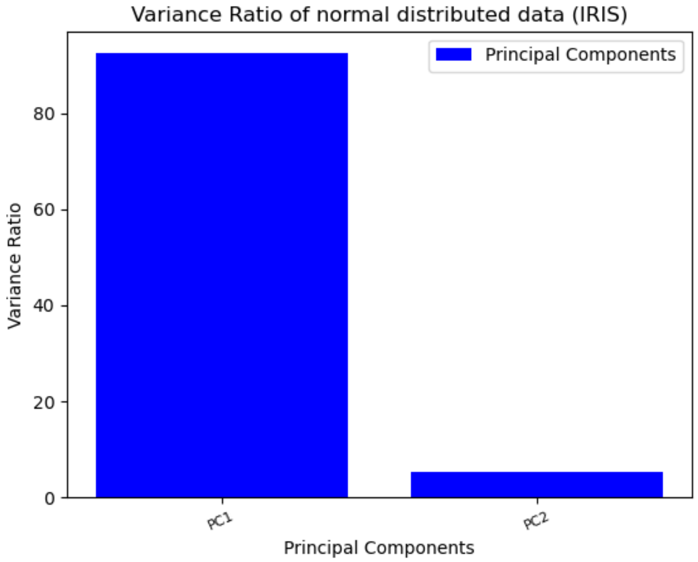
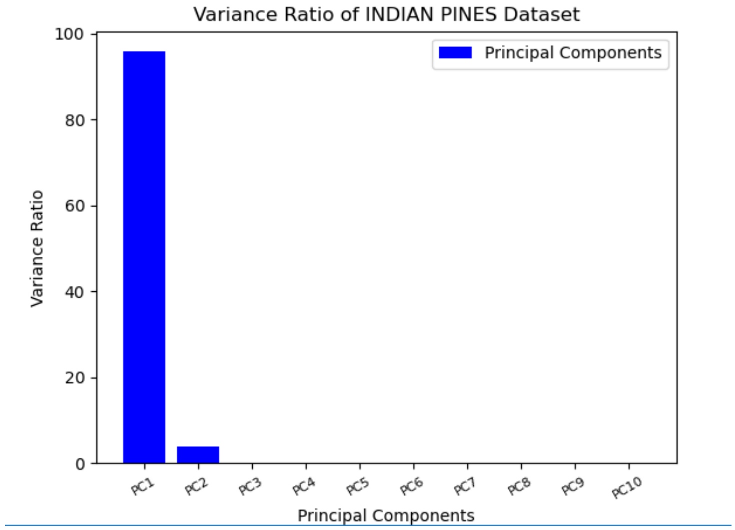
Ian McNichols, CS 488-01, 11/2/2021

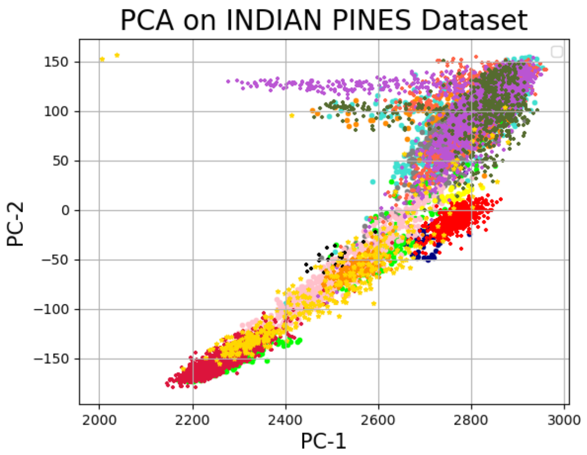
1a) Dimensionality reduction using PCA and LDA on the Iris and Indian Pines dataset

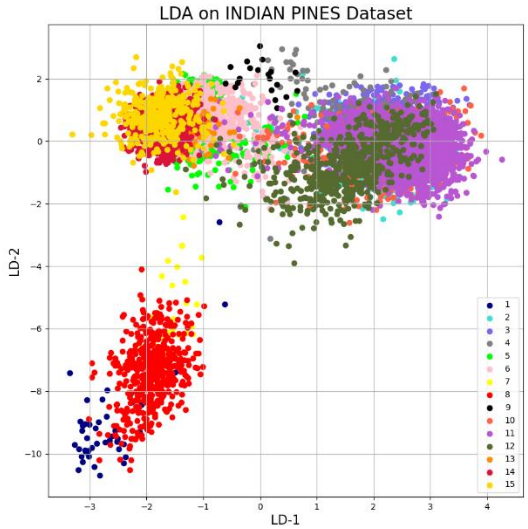
i) Figures 1 and 2 respectively: Plots of variance ratios of the Iris and Indian Pines dataset

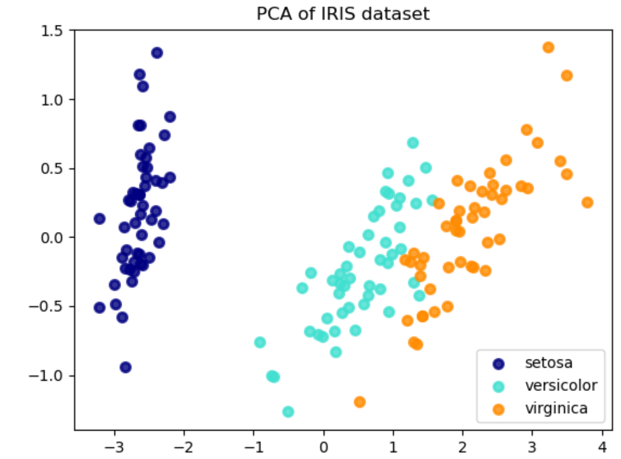


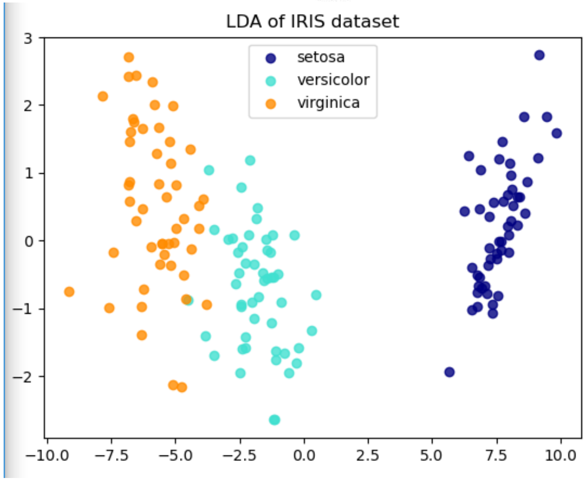


ii) Figures 3, 4, 5, and 6 from top left to bottom right. Plots of 2D PCA and LDA dimensionality reduction on the Indian Pines and then Iris datasets









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1b) Discuss the analysis of results

Pines Dataset:

The HSI for the Indian Pines location had 202 layers of pixels for each pixel of ground truth, and only 150x150 pixels of ground truth. To a person, that's basically impossible to visualize the differences between each type of ground pixel. There's too many dimensions to the data to be understandable or visualizable. By performing dimensionality reduction and feature extraction we're able to see only the more important features and dimensions that are affecting the category a pixel is defined as. It unclutters the data so people don't have to see all the noise in the background and can instead view the distinction between classes based on the most important features. Reducing to only 2 dimensions here for display did overly restrict the distinction between classes, because there is a large amount of overlap in both the PCA and LDA plot. The classes have different trends, but it's difficult to separate which exactly is which, especially in the clumps of data. My takeaway here is that there is not a high level of data separability, because we were unable to cluster. For the Pines dataset I used K=10 for both PCA and LDA. That was the initial value in the demo video for running PCA, and it seemed to produce viable results so I kept it. The LDA seems to have clumped the different ground types better into clusters. I think because LDA is supervised, it was better able to handle the large amount of data and classifications. It's goal is to maximize feature separability, so it makes sense that it would separate the different classes into clusters better, whereas PCA might be a more accurate depiction of the similarities of the classes.

Iris Dataset:

The Iris dataset only has 4 features, so it's almost overkill to run dimensionality on it when you could probably classify the different classes by hand. However, it does enable you to display it in a very concise manner that's easy to understand. On the Iris dataset the clusters are almost entirely separate, so we can infer that there is high data separability and difference between the 3 classes. I chose K=2 for this dataset because that is the highest value allowed for LDA (the minimum of classes or features -1). I used that value for both PCA and LDA so there would be fewer differences in how they were run. It's hard to say which worked better on the Iris dataset because both gave very similar results. However, the LDA had fewer overlapping points between the Versicolor and Virginica so I would argue that it did better at dimensionality reduction.

2a) Supervised classification on the Iris and Indian Pines datasets

Figure 7: Classification accuracy relative to test size w/o dimensionality reduction on IRIS

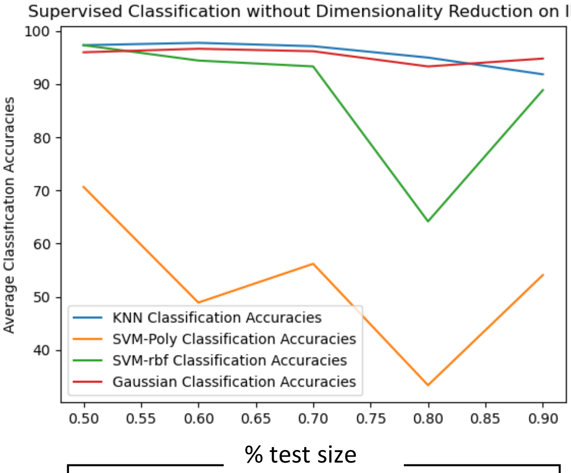


Figure 8: Training accuracy relative to test size w/o dimensionality reduction on IRIS

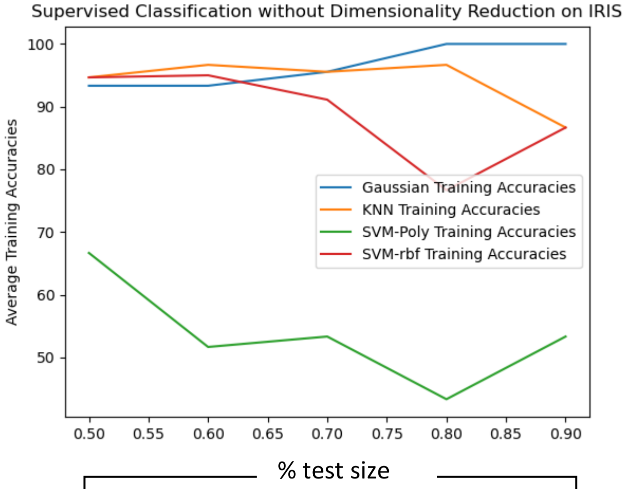


Figure 9: Classification accuracy relative to test size w/ PCA reduction on IRIS

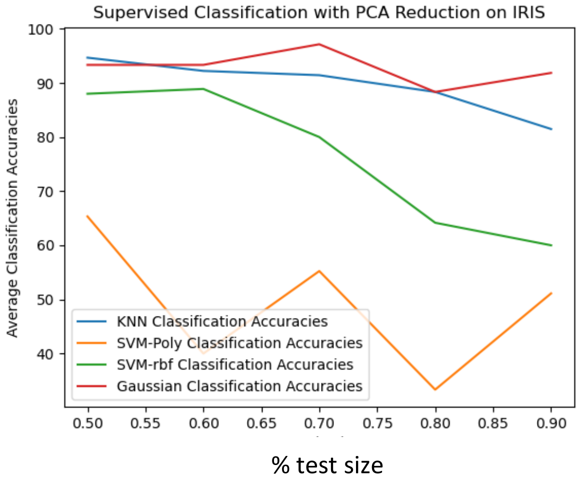
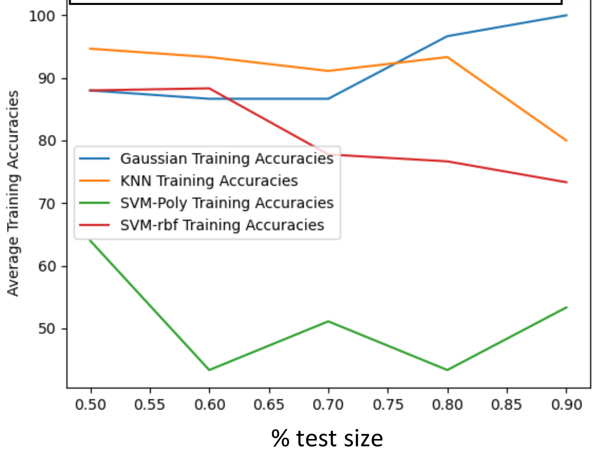


Figure 10: Training accuracy relative to test size w/ PCA reduction on IRIS



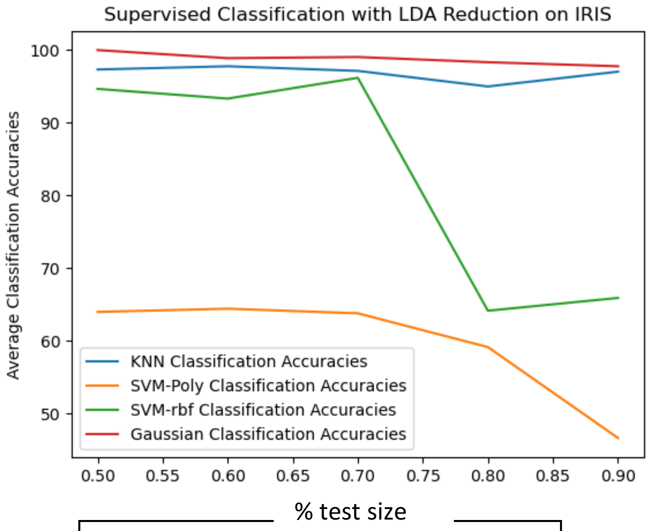


Figure 11: Classification accuracy relative to test size w/ LDA reduction on IRIS

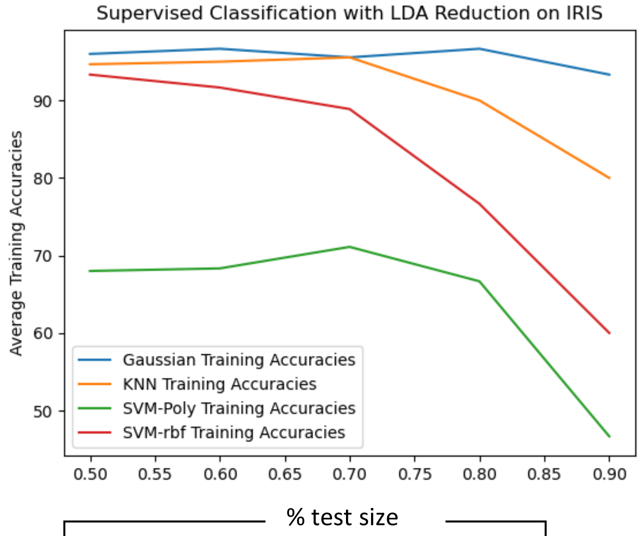


Figure 12: Training accuracy relative to test size w/ LDA reduction on IRIS

PINES)

Figure 13: Classification accuracy relative to test size w/o dimensionality reduction on PINES

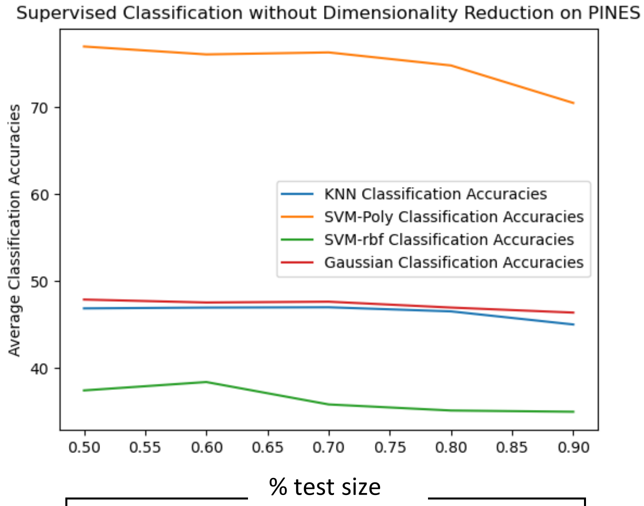


Figure 14: Training accuracy relative to test size w/o dimensionality reduction on PINES

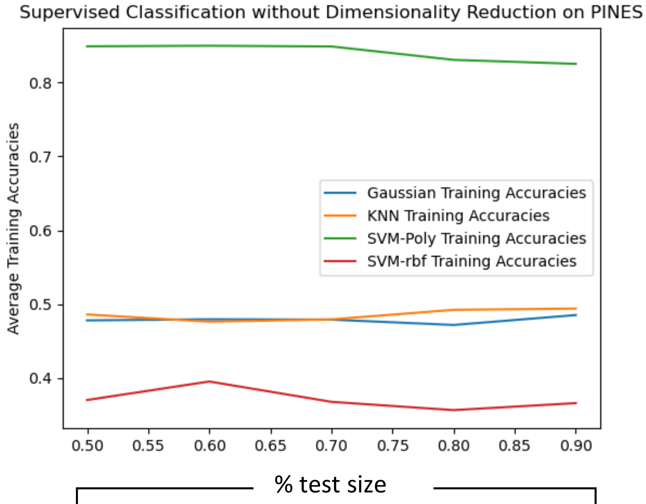


Figure 15: Classification accuracy relative to test size w/ PCA dimensionality reduction on PINES

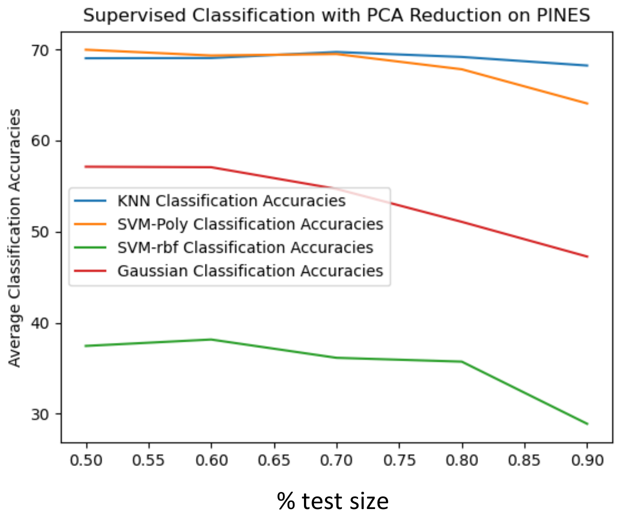
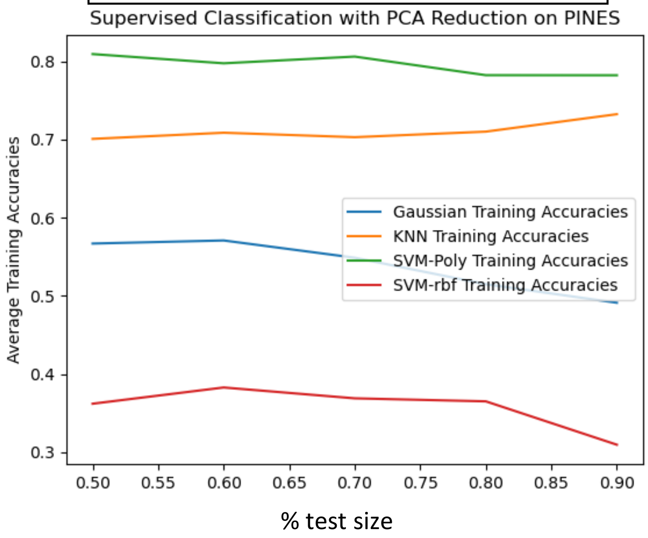


Figure 16: Training accuracy relative to test size w/ PCA dimensionality reduction on PINES



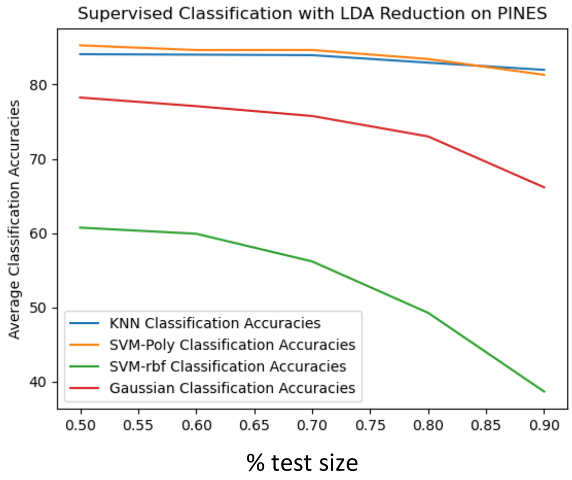


Figure 17: Classification accuracy relative to test size w/ LDA dimensionality reduction on PINES

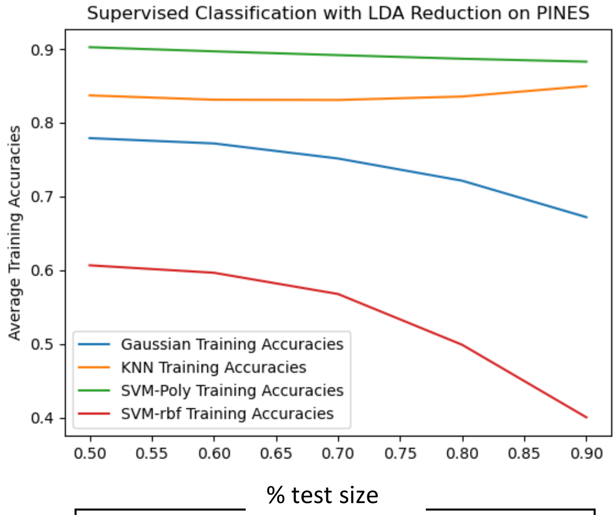


Figure 18: Training accuracy relative to test size w/ LDA dimensionality reduction on PINES

iii) Figure 19: tabularized class-wise classification accuracy charts for 30% training size over all methods without dimensionality reduction for the Iris dataset

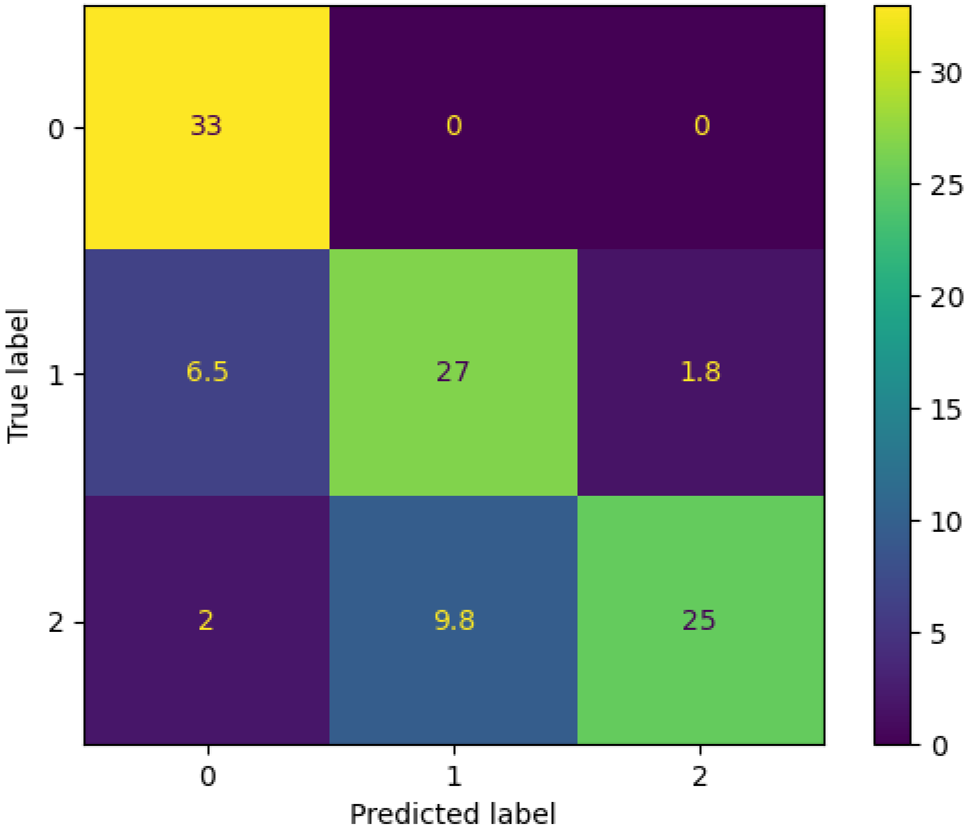
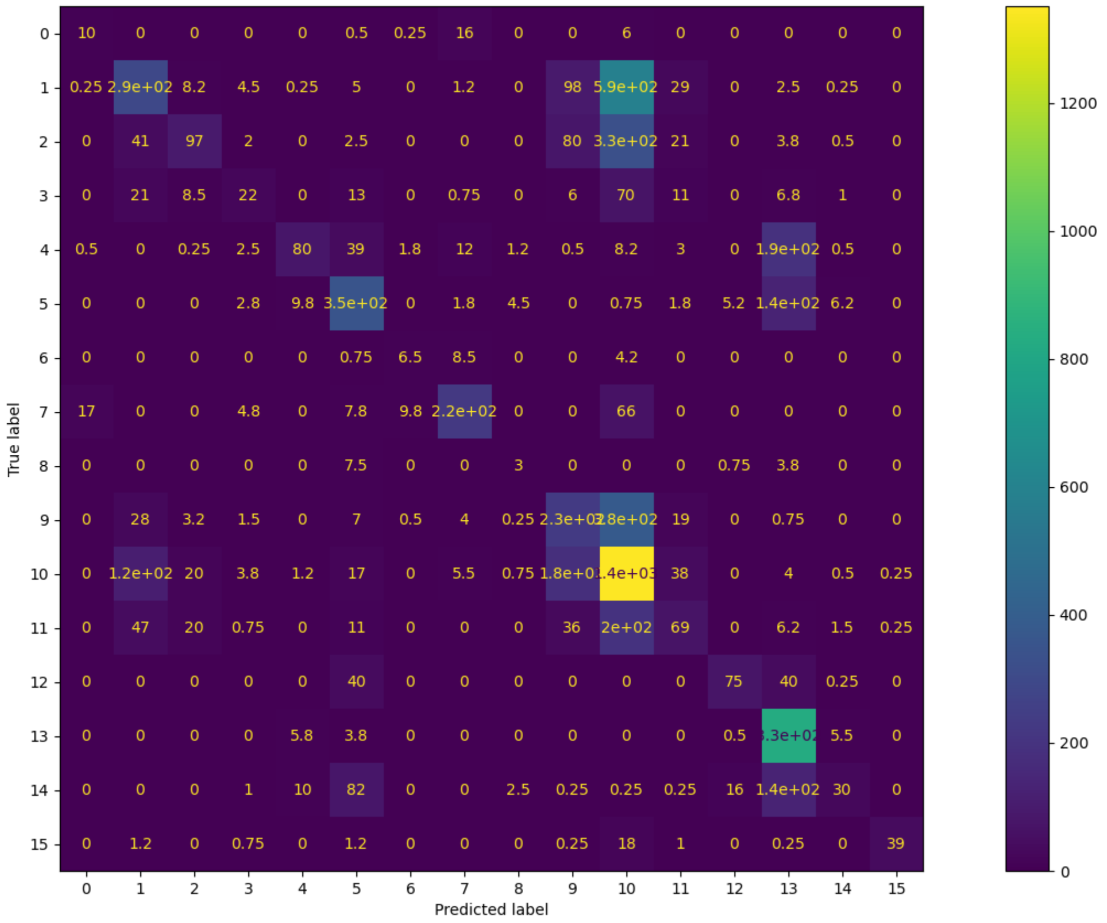


Figure 20: tabularized class-wise classification accuracy charts for 30% training size over all methods without dimensionality reduction for the Indian Pines dataset



2b) Discuss the analysis of results

Pines Dataset:

The highest achieved accuracy was with the SVM with a poly kernel on the dataset after using LDA. A very close second was the K-Nearest Neighbor after using LDA. K-Nearest Neighbor is a very strong model for machine learning, so I'm unsurprised that it performed well. However, because KNN does better with training data much larger than number of features, I think that as training size increases it might pull further ahead of the SVM (Varghese, 2018). It seems like there is enough data for the LDA to remove unimportant features and the polynomial kernel to simulate more effective ones and then train on that. The worst was the SVM with an rbf filter on every case. It's probable that if time were spent tuning the C and gamma parameters that SVM-rbf would have been more effective, as the parameters have a 'critical' effect on the model's performance according to sklearn's documentation. My quick research onto which kernel performs well on certain types of data did not return much. Many people stated that it's difficult to tell in advance and best to attempt multiple kernels to see which will work better for your specific problem.

Overall, the PCA and LDA had pretty drastic effects on the dataset. The 2 SVM's were relatively unaffected, and only increased or decreased within 10% accuracy after LDA or PCA was run, but KNN and Gaussian jumped at least 30% accuracy after LDA was run. However, LDA had a higher accuracy for every model. This means the earlier hypothesis that LDA was more effective on the Pines dataset was correct. The reason the LDA and PCA improve performance so much must be that there are more dimensions than are useful for a model on this size of data. Reducing the dimensions allows the models to pick up on more important features that correspond with classes. This makes sense because there are 202 layers for each pixel, but we found earlier that only 2 PC's had a strong correlation. Without PCA or LDA, 3 of the models didn't even improve more than 5% even as the training size increased from 10% to 50% of the data. With the LDA, there are distinct curves of improvement for both the SVM with rbf and Gaussian models.

Although the plots are not displayed, LDA and PCA also improve the confusion matrices created with a train size of 30%. The main diagonal skews lighter and there are fewer bright spots outside of correct choices. This implies that dimensionality reduction also has a positive effect on the sensitivity and specificity of a model if the dataset has too many dimensions and features compared to size.

Iris Dataset:

A lot of the discussion of the Iris dataset analysis hinges on the fact that it is a very small dataset with very few features, which makes it prone to overfitting. Running dimensionality reduction is useful if there is too much noise and a model will struggle to pick up on the important features. With a dataset that only has 4 features, dimensionality reduction will take away important and useful features, making it more difficult for supervised models to learn. Because of this, running the PCA before training models decreased model classification and training accuracy or left it the same in every single case on the 30% test size, and in most averages of all the models over each test size. Sensitivity and specificity were again not affected by running PCA. Another interesting point is the overfitting. The SVM with a poly kernel severely overfits the data at 30% test size, with a 94% training accuracy and a 51-55% validation accuracy. It's higher after running PCA. The SVM with an rbf kernel overfits as well but to less of an extreme. You can see it as well in the average accuracies from 20-40% training sizes, where the training accuracy is about 10% above the classification accuracy. These solutions might be overly complex for such a simple dataset. The K-Nearest Neighbors once again performs the best on the 30% training size, winning by 2% over the SVM with rbf kernel on PCA data and the Gaussian model on both the PCA and raw data. I was surprised by this because I figured for a simpler dataset the SVM's would work better. The RBF kernel was close without PCA, so the kernel must have a large effect on how an SVM works. Perhaps a simpler kernel like linear would produce better results. The Gaussian model was also a high performer, which makes sense with what I said earlier on the Pines dataset, that it would work better on a more evenly distributed dataset. Overall, it seems like the K-Nearest Neighbors model is the most effective model for datasets in this range.

Varghese: https://towardsdatascience.com/comparative-study-on-classic-machine-learning-algorithms-24f9ff6ab222

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Code Appendix:

```
import scipy.io as io
import matplotlib.pyplot as plt
import numpy as np
import pandas as pd
from sklearn.model_selection import train_test_split, StratifiedKFold,
cross_val_score
from sklearn import datasets
from sklearn.decomposition import PCA
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis
from sklearn.preprocessing import MinMaxScaler
from sklearn.neighbors import KNeighborsClassifier
from sklearn.svm import SVC
from sklearn.naive_bayes import GaussianNB
from sklearn.metrics import plot_confusion_matrix, ConfusionMatrixDisplay
from sklearn.pipeline import Pipeline


def pines_analysis(R_filepath, display=False):
    # Load in Indian Pines data from file and reshape/make into dataframes
    R_file = io.loadmat(R_filepath)
    gth = np.array(R_file['gth'])
    X = np.array(R_file['X'])
    R_rows = R_file['num_rows']
    R_cols = R_file['num_cols']
    R_bands = R_file['num_bands']
    # Store ground truth data
    gth = np.reshape(gth, (int(R_rows)*int(R_cols)))
    gth_mat = io.loadmat('data/indian_gth.mat')
    gth_mat = {i:j for i, j in gth_mat.items() if i[0] != "_"}
    gt = pd.DataFrame({i: pd.Series(j[0]) for i, j in gth_mat.items()})
    # Pre-process data
    scaler_model = MinMaxScaler()
    scaler_model.fit(X.astype(float))
    X = scaler_model.transform(X)
    # Give a heads up to the user about data information
    print('gt shape:', gt.shape)
    print('X shape:', X.shape)
    # Class types in order of the Pines dataset
    target_names = ["Alfalfa", "Corn-notill", "Corn-mintill", "Corn", "Grass-
pasture",
                    "Grass-trees", "Grass-pasture-mowed", "Hay-windrowed",
"Oats",
                    "Soybean-notill", "Soybean-mintill", "Soybean-clean",
"Wheat", "Woods",
                    "Buildings-Grass-Treess-Drives", "Stone-Steel-Towers"]

    # Starting PCA
    pca = PCA(n_components=10)
    principleComponents = pca.fit_transform(X)
    # Creating dataframes from PCA output
    principleDf = pd.DataFrame(data=principleComponents,
                               columns = ['PC-' + str(i+1) for i in range(10)])
    finalDf1 = pd.concat([principleDf, gt], axis=1)
    # Reshaping PCA output for plotting, adding PC titles to each column
    x1 = X.transpose()
    X_pca = np.matmul(x1, principleComponents)
    x_pca_df = pd.DataFrame(data=X_pca, columns=['PC-' + str(i+1) for i in
range(10)])
    X_pca_df = pd.concat([x_pca_df, gt], axis=1)

    # Starting LDA
    X = X.transpose()
    lda = LinearDiscriminantAnalysis(n_components=10)
    linear_discriminants = lda.fit(X, np.ravel(gt)).transform(X)
    # Making dataframes from LDA
    linearDf = pd.DataFrame(data=linear_discriminants,
                            columns = ['LD-' + str(i+1) for i in range(10)])
    finalDf2 = pd.concat([linearDf, gt], axis=1)
    # Reshaping output of LDA so it can be plotted, assigning LD's to each column
of data
    x2 = X.transpose()
    X_lda = np.matmul(x2, linear_discriminants)
    x_lda_df = pd.DataFrame(data=X_lda, columns=['LD-' + str(i+1) for i in
range(10)])
    X_lda_df = pd.concat([x_lda_df, gt], axis=1)

    if display:
        # Lists that will be re-used for each plot
        class_num = [i+1 for i in range(15)]
        colors = ["navy", "turquoise", "mediumslateblue", "gray", "lime", "pink",
"yellow",
                  "red", "black", "tomato", "mediumorchid", "darkolivegreen",
"darkorange",
                  "crimson", "gold", "peru", "mediumslateblue"]
        markerm = ['o', 'o', 'o', 'o', 'o', 'o', 'o', '+', '+', '+', '+', '+',
'+', '+', '*', '*']

        # Displaying Variance Ratio
        plt.figure()
        plt.bar([1,2,3,4,5,6,7,8,9,10],
list(pca.explained_variance_ratio_*100),label="Principal Components", color="b")
        plt.legend()
        plt.xlabel('Principal Components')
        pc = []
        for i in range(10):
            pc.append('PC' + str(i+1))
        plt.xticks([1,2,3,4,5,6,7,8,9,10],pc,fontsize=8,rotation=30)
        plt.ylabel('Variance Ratio')
        plt.title('Variance Ratio of INDIAN PINES Dataset')
        plt.show()

        # Displaying PCA
        fig = plt.figure(figsize=(10,10))
        ax = fig.add_subplot(1,1,1)
        ax.set_xlabel('PC-1', fontsize=15)
        ax.set_ylabel('PC-2', fontsize=15)
        ax.set_title('PCA on INDIAN PINES Dataset', fontsize=20)
        for target, color, m in zip(class_num, colors, markerm):
            indicesToKeep = X_pca_df['gth'] == target
            ax.scatter(X_pca_df.loc[indicesToKeep, 'PC-1'],
                       X_pca_df.loc[indicesToKeep, 'PC-2'],
                       c=color, marker=m, s=9)
        ax.legend()
        ax.grid()
        plt.show()
        # Displaying LDA
        fig = plt.figure(figsize=[10, 10])
        ax = fig.add_subplot(1,1,1)
        ax.set_xlabel('LD-1', fontsize=15)
        ax.set_ylabel('LD-2', fontsize=15)
        ax.set_title('LDA on INDIAN PINES Dataset', fontsize=20)
        for color, i, target_name in zip(colors, class_num, class_num):
            ax.scatter(linear_discriminants[gth==i, 0],
linear_discriminants[gth==i,1],
                        color=color, label=target_name)
        ax.legend()
        ax.grid()
        plt.show()


def iris_analysis(display=False):
    # Load iris dataset into data and targets
    iris = datasets.load_iris()
    X = iris.data
    y = iris.target
    target_names = iris.target_names

    # Run PCA on the iris dataset
    pca = PCA(n_components=2)
    X_r = pca.fit(X).transform(X)
    # Run LDA on the iris dataset
    lda = LinearDiscriminantAnalysis(n_components=2)
    X_r2 = lda.fit(X, y).transform(X)

    # Percentage of variance explained for each components
    print(
        "explained variance ratio (first two components): %s"
        % str(pca.explained_variance_ratio_)
    )
    # Plot figures if prompted
    if display:
        # Show the first 2 PC's
        plt.figure()
        plt.bar([1,2],list(pca.explained_variance_ratio_*100), label='Principal
Components', color='b')
        plt.legend()
        plt.xlabel("Principal Components")
        pc = []
        for i in range(2):
            pc.append('PC' + str(i+1))
        plt.xticks([1,2],pc,fontsize=8,rotation=25)
        plt.ylabel("Variance Ratio")
        plt.title("Variance Ratio of normal distributed data (IRIS)")
        # Display 2D PCA results
        plt.figure()
        colors = ["navy", "turquoise", "darkorange"]
        lw = 2
        for color, i, target_name in zip(colors, [0, 1, 2], target_names):
            # Show the PCA results for each datatype in the same color
            plt.scatter(
                X_r[y == i, 0], X_r[y == i, 1], color=color, alpha=0.8, lw=lw,
label=target_name
            )
        plt.legend(loc="best", shadow=False, scatterpoints=1)
        plt.title("PCA of IRIS dataset")
        # Display 2D LDA results
        plt.figure()
        for color, i, target_name in zip(colors, [0, 1, 2], target_names):
            # Show the LDA results for each datatype in the same color
            plt.scatter(
                X_r2[y == i, 0], X_r2[y == i, 1], alpha=0.8, color=color,
label=target_name
            )
        plt.legend(loc="best", shadow=False, scatterpoints=1)
        plt.title("LDA of IRIS dataset")
        # Show all the plots to screen
        plt.show()


def iris_classification(run_pca=False, run_lda=True):
    if run_pca and run_lda:
        print("Can't run both lda and pca.")
        return
    # Load IRIS dataset, run PCA, and run combinations of all test sizes and
model types
    # Display output to the user's screen

    # Load iris dataset into X and y variables
    iris = datasets.load_iris()
    X = iris.data
    y = iris.target
    plot_data = {}
    # Check for PCA flag and run dimensionality reduction if needed
    if run_pca:
        pca = PCA(n_components=2)
        X = pca.fit_transform(X)
    if run_lda:
        lda = LinearDiscriminantAnalysis(n_components=2)
        X = lda.fit(X, y).transform(X)

    test_sizes = [.9, .8, .7, .6, .5]
    confusion_matrices = []
    for test_size in test_sizes:
        # Split dataset based on test size
        X_train, X_validation, Y_train, Y_validation = train_test_split(X, y,
test_size=test_size,random_state=1,shuffle=True)
        # Re-make each model for the current test size
        models = [('KNN', KNeighborsClassifier()), ('SVM-Poly', SVC(gamma='auto',
kernel='poly')),
                  ('SVM-RBF', SVC(gamma='auto', kernel='rbf')), ('NB',
GaussianNB())]
        # Lists to hold average accuracies for later
        classification_accuracy = []
        training_accuracy = []
        for name, model in models:
            # Create a pipeline to preprocess data and run the model
            pipeline = Pipeline([("scaler", MinMaxScaler()), ("classifier", 
model)])
            # Fit to the training dataset
            pipeline.fit(X_train, Y_train)
            # Create a confusion matrix
            if test_size == .7:
                disp = plot_confusion_matrix(pipeline, X_validation, 
Y_validation, cmap=plt.cm.Blues)
                confusion_matrices.append(disp.confusion_matrix)
            # Calculate and store overall accuracy of the model
            classification_score = pipeline.score(X_validation, Y_validation)
            classification_accuracy.append(classification_score*100)
            # Calculate and store training accuracy of the model
            training_accuracy.append(pipeline.score(X_train, Y_train)*100)
            # Print model information to display
            data_line = "test size: " + str(test_size) + " model: " + str(name) + 
" training accuracy: " +\
                        str(pipeline.score(X_train, Y_train)*100) + " 
classification accuracy: " +\
                        str(classification_score*100)
            print(data_line)
        # Combine all the averages per test size
        plot_data[test_size] = [training_accuracy, classification_accuracy]
    confusion_matrices = np.array(confusion_matrices)
    avg_matrix = np.mean(confusion_matrices, axis=0)
    print("Confusion matrix:", avg_matrix)
    plt.figure()
    display_matrix = ConfusionMatrixDisplay(avg_matrix)
    display_matrix.plot()
    plt.show()
    # Display average overall accuracy and training accuracy to output for each 
test size
    training_accuracies = [plot_data[x][0] for x in plot_data]
    print("Training accuracies:", training_accuracies)
    classification_accuracies = [plot_data[x][1] for x in plot_data]
    print("Classification accuracies:", classification_accuracies)


def pines_classification(R_filepath, run_pca=False, run_lda=False):
    if run_pca and run_lda:
        print("Can't run both pca and lda")
        return
    # Runs combinations of model types/test sizes with or without PCA
dimensionality reduction on pines dataset
    # Loading in the pines dataset
    R_file = io.loadmat(R_filepath)
    gth = np.array(R_file['gth'])
    X = np.array(R_file['X']).transpose()
    R_rows = R_file['num_rows']
    R_cols = R_file['num_cols']
    R_bands = R_file['num_bands']
    gth = np.reshape(gth, (int(R_rows)*int(R_cols)))
    # Ugly but works. Remove all the data where there isn't a ground truth
    zeros = (gth == 0).nonzero()
    print(gth.shape)
    print(X.shape)
    print("zeros:", zeros)
    for i in range(len(zeros)):
        zeros_new = (gth == 0).nonzero()
        delete_index = zeros_new[0]
        gth = np.delete(gth, delete_index)
        X = np.delete(X, delete_index, axis=0)
    print(gth.shape)
    print(X.shape)
    if run_pca:
        # Run PCA on data and save back to the X variable
        pca = PCA(n_components=10)
        principleComponents = pca.fit_transform(X)
        x1 = X.transpose()
        X = np.matmul(x1, principleComponents)
        print("X:", principleComponents.shape)
        print("gth:", gth.shape)
        X = principleComponents
        print("Running with PCA dimensionality reduction")
    elif run_lda:
        lda = LinearDiscriminantAnalysis(n_components=10)
        linear_discriminants = lda.fit(X, np.ravel(gth)).transform(X)
        X = linear_discriminants
        print("X:", X.shape)
        print("gth:", gth.shape)
        print("Running with LDA reduction")
    else:
        # Display data info
        print("X:", X.shape)
        print("gth:", gth.shape)
        print("Running without dimensionality reduction")
    print("GTH max class:", gth.max())
    plot_data = {}
    test_sizes = [.9, .8, .7, .6, .5]
    confusion_matrices = []
    for test_size in test_sizes:
        # Splitting data by test size
        X_train, X_validation, Y_train, Y_validation = train_test_split(X, gth,
test_size=test_size,
                                                                        random_st
ate=1, shuffle=True)
        # Re-making each model to use on the current test size (cache size taken
from CPU cache size to go faster)
        models = [('NB', GaussianNB()), ('KNN', KNeighborsClassifier()), ('SVM-
Poly', SVC(gamma='auto', kernel='poly', cache_size=5200000)),
                  ('SVM-RBF', SVC(gamma='auto', kernel='rbf',
cache_size=5200000))]
        classification_accuracy = []
        training_accuracy = []
        for name, model in models:
            # Create a pipeline to preprocess data and run the model
            pipeline = Pipeline([("scaler", MinMaxScaler()), ("classifier",
model)])
            # Fit to the training dataset
            pipeline.fit(X_train, Y_train)
            if test_size == .7:
                # Make a confusion matrix
                disp = plot_confusion_matrix(pipeline, X_validation,
Y_validation, cmap=plt.cm.Blues)
                confusion_matrices.append(disp.confusion_matrix)
            # Overall model classification score vs training data score
            classification_score = pipeline.score(X_validation, Y_validation)
            train_score = pipeline.score(X_train, Y_train)
            # Add to a list to calculate the average later
            training_accuracy.append(train_score)
            classification_accuracy.append(classification_score*100)
            # Printing model information to output
            data_line = "test size: " + str(test_size) + " model: " + str(name) +
" training accuracy: " + str(train_score*100) + " classification accuracy: " +
str(classification_score*100)
            print(data_line)
        # Adding all model averages to a dictionary corresponding with test size
        plot_data[test_size] = [training_accuracy, classification_accuracy]
    # Average out all the display matrices and plot it
    confusion_matrices = np.array(confusion_matrices)
    avg_matrix = np.mean(confusion_matrices, axis=0)
    print("Confusion matrix:", avg_matrix)
    plt.figure()
    display_matrix = ConfusionMatrixDisplay(avg_matrix)
    display_matrix.plot()
    plt.show()
    # Displaying overall accuracies for each test size
    test_sizes = [x*100 for x in test_sizes]
    training_accuracies = [plot_data[x][0] for x in plot_data]
    print("Training accuracies:", training_accuracies)
    classification_accuracies = [plot_data[x][1] for x in plot_data]
    print("Classification accuracies:", classification_accuracies)


def plot_classification(iris, pines):
    # Plots the training/overall accuracies of each model at each test-size
    test_sizes = [.9, .8, .7, .6, .5]
    if pines:
        # Saved data from PINES classification output (Hard-coded to avoid re-
running models)
        # No reduction, PCA, LDA
        classification_accuracies = [[[45.018970189701896, 70.47154471544715,
34.99186991869919, 46.38482384823848], [46.52439024390244, 74.78048780487805,
35.13414634146341, 46.96341463414634], [46.99651567944251, 76.2787456445993,
35.83275261324042, 47.63763066202091], [46.959349593495936, 76.04878048780488,
38.40650406504065, 47.54471544715447], [46.868292682926835, 76.9560975609756,
37.44390243902439, 47.88292682926829]],
                                     [[68.21680216802169, 64.05420054200542,
28.899728997289976, 47.2520325203252], [69.15853658536585, 67.8048780487805,
35.71951219512195, 51.0609756097561], [69.70034843205575, 69.4773519163763,
36.139372822299656, 54.67595818815331], [69.04065040650407, 69.3170731707317,
38.146341463414636, 57.05691056910569], [69.01463414634146, 69.95121951219512,
37.44390243902439, 57.11219512195122]],
                                     [[81.97289972899729, 81.31165311653118,
38.68834688346883, 66.16802168021681], [82.9390243902439, 83.42682926829268,
49.28048780487805, 73.01219512195122], [83.94425087108014, 84.6411149825784,
56.19512195121952, 75.76306620209058], [84.01626016260163, 84.6341463414634,
59.91869918699187, 77.08943089430895], [84.0780487804878, 85.26829268292683,
60.74146341463415, 78.2439024390244]]]
        training_accuracies = [[[0.494140625, 0.8251953125, 0.3662109375,
0.4853515625], [0.4924353343094192, 0.8306490971205466, 0.35675939482674474,
0.4719375305026842], [0.47950553025374104, 0.8487312947299935,
0.36792452830188677, 0.47918022121014964], [0.4764576726030739,
0.8497194437667723, 0.3954623078799707, 0.47962917784825565],
[0.48614363778298203, 0.8489461358313818, 0.3704137392661983,
0.4781420765027322]],
                               [[0.732421875, 0.7822265625, 0.3095703125,
0.4912109375], [0.7101024890190337, 0.7823328452903856, 0.36505612493899464,
0.5148853099072719], [0.7029928432010409, 0.8061158100195186,
0.36890045543266103, 0.5487963565387117], [0.708709441327153, 0.797511588192242,
0.3827762868992437, 0.5708709441327153], [0.7008196721311475, 0.8093286494925839,
0.3620218579234973, 0.5669398907103825]],
                               [[0.849609375, 0.8828125, 0.400390625, 0.671875],
[0.8355295265983407, 0.8867740361151781, 0.4987798926305515, 0.72132747681796],
[0.8308392973324659, 0.8916720884840599, 0.5676642810670136, 0.7514638906961614],
[0.8311783361795559, 0.8968040985606246, 0.5964869480361064, 0.771895584288851],
[0.8370413739266198, 0.9024199843871975, 0.6065573770491803,
0.7790788446526151]]]
        for i, accuracies in \
                enumerate(zip(classification_accuracies, training_accuracies)):
            classification_accuracies_itr = accuracies[0]
            training_accuracies_itr = accuracies[1]
            KNN_accuracies = [x[0] for x in classification_accuracies_itr]
            KNN_train_accuracies = [x[0] for x in training_accuracies_itr]
            SVM_poly_accuracies = [x[1] for x in classification_accuracies_itr]
            SVM_poly_train_accuracies = [x[1] for x in training_accuracies_itr]
            SVM_rbf_accuracies = [x[2] for x in classification_accuracies_itr]
            SVM_rbf_train_accuracies = [x[2] for x in training_accuracies_itr]
            GNB_accuracies = [x[3] for x in classification_accuracies_itr]
            GNB_train_accuracies = [x[3] for x in training_accuracies_itr]
            plt.plot(test_sizes, KNN_accuracies, label="KNN Classification
Accuracies")
            plt.plot(test_sizes, SVM_poly_accuracies,label="SVM-Poly
Classification Accuracies")
            plt.plot(test_sizes, SVM_rbf_accuracies,label="SVM-rbf Classification
Accuracies")
            plt.plot(test_sizes, GNB_accuracies,label="Gaussian Classification
Accuracies")
            plt.xlabel("% test size")
            plt.ylabel("Average Classification Accuracies")
            if i == 0:
                plt.title("Supervised Classification without Dimensionality
Reduction on PINES")
            elif i == 1:
                plt.title("Supervised Classification with PCA Reduction on
PINES")
            elif i == 2:
                plt.title("Supervised Classification with LDA Reduction on
PINES")
            plt.legend()
            plt.show()
            plt.figure()
            plt.plot(test_sizes, GNB_train_accuracies, label="Gaussian Training 
Accuracies")
            plt.plot(test_sizes, KNN_train_accuracies, label="KNN Training 
Accuracies")
            plt.plot(test_sizes, SVM_poly_train_accuracies, label="SVM-Poly 
Training Accuracies")
            plt.plot(test_sizes, SVM_rbf_train_accuracies, label="SVM-rbf 
Training Accuracies")
            plt.xlabel("% test size")
            plt.ylabel("Average Training Accuracies")
            if i == 0:
                plt.title("Supervised Classification without Dimensionality 
Reduction on PINES")
            elif i == 1:
                plt.title("Supervised Classification with PCA Reduction on 
PINES")
            elif i == 2:
                plt.title("Supervised Classification with LDA Reduction on 
PINES")
            plt.legend()
            plt.show()
    if iris:
        # Saved data from IRIS classification output (Hard-coded to avoid re-
running models)
        # No reduction, PCA, LDA <- data order
        training_accuracies = [[[86.66666666666667, 53.333333333333336, 
86.66666666666667, 100.0],
                               [96.66666666666667, 43.333333333333336, 
76.66666666666667, 100.0],
                               [95.55555555555556, 53.333333333333336, 
91.11111111111111, 95.55555555555556],
                               [96.66666666666667, 51.66666666666667, 95.0, 
93.33333333333333],
                               [94.66666666666667, 66.66666666666666, 
94.66666666666667, 93.33333333333333]],
                               [[80.0, 53.333333333333336, 73.33333333333333, 
100.0],
                                [93.33333333333333, 43.333333333333336, 
76.66666666666667, 96.66666666666667],
                                [91.11111111111111, 51.11111111111111, 
77.77777777777779, 86.66666666666667],
                                [93.33333333333333, 43.333333333333336, 
88.33333333333333, 86.66666666666667],
                                [94.66666666666667, 64.0, 88.0, 88.0]],
                               [[80.0, 46.666666666666664, 60.0,
93.33333333333333],
                                [90.0, 66.66666666666666, 76.66666666666667,
96.66666666666667],
                                [95.55555555555556, 71.11111111111111,
88.88888888888889, 95.55555555555556],
                                [95.0, 68.33333333333333, 91.66666666666666,
96.66666666666667],
                                [94.66666666666667, 68.0, 93.33333333333333,
96.0]]]
        classification_accuracies = [[[91.85185185185185, 54.074074074074076,
88.88888888888889, 94.81481481481482],
                                     [95.0, 33.33333333333333, 64.16666666666667,
93.33333333333333],
                                     [97.14285714285714, 56.19047619047619,
93.33333333333333, 96.19047619047619],
                                     [97.77777777777777, 48.888888888888886,
94.44444444444444, 96.66666666666667],
                                     [97.33333333333334, 70.66666666666667,
97.33333333333334, 96.0]],
                                     [[81.48148148148148, 51.11111111111111,
60.0, 91.85185185185185],
                                      [88.33333333333333, 33.33333333333333,
64.16666666666667, 88.33333333333333],
                                      [91.42857142857143, 55.23809523809524,
80.0, 97.14285714285714],
                                      [92.22222222222223, 40.0,
88.88888888888889, 93.33333333333333],
                                      [94.66666666666667, 65.33333333333333,
88.0, 93.33333333333333]],
                                     [[97.03703703703704, 46.666666666666664,
65.92592592592592, 97.77777777777777],
                                      [95.0, 59.166666666666664,
64.16666666666667, 98.33333333333333],
                                      [97.14285714285714, 63.8095238095238,
96.19047619047619, 99.04761904761905],
                                      [97.77777777777777, 64.44444444444444,
93.33333333333333, 98.88888888888889],
                                      [97.33333333333334, 64.0,
94.66666666666667, 100.0]]]
        # It's ugly but it works. Iterate through the data and display each plot.
        # Order is KNN, SVM-Poly, SVM-rbf, Gaussian. This way I don't have to
rerun the
        # classification (slow) to display data (fast)
        for i, accuracies in \
                enumerate(zip(classification_accuracies, training_accuracies)):
            classification_accuracies_itr = accuracies[0]
            training_accuracies_itr = accuracies[1]
            KNN_accuracies = [x[0] for x in classification_accuracies_itr]
            KNN_train_accuracies = [x[0] for x in training_accuracies_itr]
            SVM_poly_accuracies = [x[1] for x in classification_accuracies_itr]
            SVM_poly_train_accuracies = [x[1] for x in training_accuracies_itr]
            SVM_rbf_accuracies = [x[2] for x in classification_accuracies_itr]
            SVM_rbf_train_accuracies = [x[2] for x in training_accuracies_itr]
            GNB_accuracies = [x[3] for x in classification_accuracies_itr]
            GNB_train_accuracies = [x[3] for x in training_accuracies_itr]
            plt.plot(test_sizes, KNN_accuracies, label="KNN Classification 
Accuracies")
            plt.plot(test_sizes, SVM_poly_accuracies,label="SVM-Poly 
Classification Accuracies")
            plt.plot(test_sizes, SVM_rbf_accuracies,label="SVM-rbf Classification 
Accuracies")
            plt.plot(test_sizes, GNB_accuracies,label="Gaussian Classification 
Accuracies")
            plt.xlabel("% test size")
            plt.ylabel("Average Classification Accuracies")
            if i == 0:
                plt.title("Supervised Classification without Dimensionality 
Reduction on IRIS")
            elif i == 1:
                plt.title("Supervised Classification with PCA Reduction on IRIS")
            elif i == 2:
                plt.title("Supervised Classification with LDA Reduction on IRIS")
            plt.legend()
            plt.show()
            plt.figure()
            plt.plot(test_sizes, GNB_train_accuracies, label="Gaussian Training 
Accuracies")
            plt.plot(test_sizes, KNN_train_accuracies, label="KNN Training 
Accuracies")
            plt.plot(test_sizes, SVM_poly_train_accuracies, label="SVM-Poly 
Training Accuracies")
            plt.plot(test_sizes, SVM_rbf_train_accuracies, label="SVM-rbf 
Training Accuracies")
            plt.xlabel("% test size")
            plt.ylabel("Average Training Accuracies")
            if i == 0:
                plt.title("Supervised Classification without Dimensionality 
Reduction on IRIS")
            elif i == 1:
                plt.title("Supervised Classification with PCA Reduction on IRIS")
            elif i == 2:
                plt.title("Supervised Classification with LDA Reduction on IRIS")
            plt.legend()
            plt.show()


def main():
    # Driver for pines and iris data analysis/classification
    filepath = "data/indianR.mat"
    iris_analysis(display=True)
    pines_analysis(filepath, display=True)
    iris_classification(run_pca=True, run_lda=False)
    iris_classification(run_pca=False, run_lda=True)
    iris_classification(run_pca=False, run_lda=False)
    pines_classification(filepath, run_pca=False, run_lda=False)
    pines_classification(filepath, run_pca=True, run_lda=False)
    pines_classification(filepath, run_pca=False, run_lda=True)
    plot_classification(iris=True, pines=True)


if __name__ == "__main__":
    main()
```