In [1]: # Define the directory paths for control and parkinson folders
 control_folder = "/Users/JOSEPHSPC04292016/Desktop/BE 175/Final Project/
 parkinson_folder = "/Users/JOSEPHSPC04292016/Desktop/BE 175/Final Project/

So to take it step by step, this first cell takes in the folder paths and outputs two master arrays that hold information on the std. deviation of pressure and the condition(control or parkinson) of each patient(or file)

```
In [2]: import numpy as np
        def average std deviation(arr):
            # Calculate the standard deviation of the array
            std_deviation = np.std(arr)
            return std deviation
        def calculate distance from center(x values, y values, result array):
            # Calculate the midpoint of x and y ranges
            x_{midpoint} = (np_{max}(x_{values}) + np_{min}(x_{values})) / 2
            y midpoint = (np.max(y values) + np.min(y values)) / 2
            # Calculate distances from center for each point
            for x, y in zip(x_values, y_values):
                distance = np.sqrt((x - x_midpoint)**2 + (y - y_midpoint)**2)
                result_array.append(distance)
        def read data(file path, x array, y array, x1, y1, x2, y2, time 0, time 1
            with open(file path, 'r') as file:
                for line in file:
                    data = line.strip().split(';')
                    if data[-1] == '0': # Check if the last element is '0'
                         x array.append(int(data[0]))
                         y array.append(int(data[1]))
                         time 0.append(int(data[-2]))
                         grip 0.append(int(data[3]))
                    if data[-1] == '1': # Check if the last element is '1'
                         x1.append(int(data[0]))
                         v1.append(int(data[1]))
                         time 1.append(int(data[-2]))
                         grip 1.append(int(data[3]))
                    if data[-1] == '2': # Check if the last element is '2'
                         x2.append(int(data[0]))
                        y2.append(int(data[1]))
                        time 2.append(int(data[-2]))
                         grip 2.append(int(data[3]))
        def masterfunction( file path , fileID ):
            x_val_0 = []
            y val 0 = []
            x val 1 = []
            y_val_1 = []
            x_val_2 = []
            y_val_2 = []
            time 0 = []
            time 1 = []
            time 2 = []
            grip_0 = []
```

```
grip 1 = []
         grip 2 = []
         read_data(file_path, x_val_0, y_val_0, x_val_1, y_val_1, x_val_2, y_val_1, x_val_2, y_val_1, x_val_2, y_val_2, y_val_2, y_val_2, y_val_2, y_val_2, y_val_3, y_val_4, y_val_4, y_val_5, y_val_6, 
         # now we have filled in all of our data into the respective arrays
         if fileID == "0":
                  radius 0 = []
                  calculate_distance_from_center(x_val_0, y_val_0, radius_0)
                  result neg slop prop = 0 #calculate slope proportions(time 0, rad
                  result avg grip deviation = average std deviation(grip 0)
         if fileID == "1":
                  radius 1 = []
                  calculate_distance_from_center(x_val_1, y_val_1, radius_1)
                  result neg slop prop = 0 #calculate slope proportions(time 1, rad
                  result avg grip deviation = average std deviation(grip 1)
         return result neg slop prop, result avg grip deviation
import os
# Define an empty master 2D array to hold patient information <code>BUILDING</code> I<code>l</code>
master arrayID0 = []
# Function to determine the value of the third column based on folder name
def determine label(folder name):
         if folder name == "control":
                  return 0
         elif folder name == "parkinson":
                  return 1
         else:
                  return None
# Iterate through the control folder
for filename in os.listdir(control folder):
         file path = os.path.join(control folder, filename)
         if os.path.isfile(file path):
                  result_neg_slop_prop, result_avg_grip_deviation = masterfunction
                  label = determine label("control")
                 master_arrayID0.append([result_neg_slop_prop, result_avg_grip_dev
# Iterate through the parkinson folder
for filename in os.listdir(parkinson folder):
         file path = os.path.join(parkinson folder, filename)
         if os.path.isfile(file_path):
                  result neg slop prop, result avg grip deviation = masterfunction
                  label = determine_label("parkinson")
                  master_arrayID0.append([result_neg_slop_prop, result_avg_grip_dev
# Print the master 2D array
```

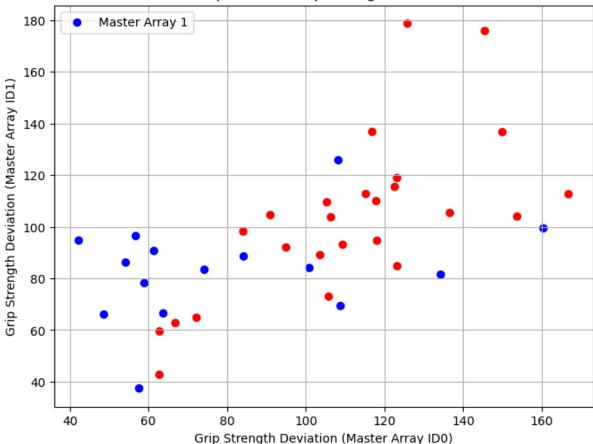
```
master arrayID1 = []
# Function to determine the value of the third column based on folder na
def determine label(folder name):
    if folder_name == "control":
        return 0
    elif folder name == "parkinson":
        return 1
    else:
        return None
# Iterate through the control folder
for filename in os.listdir(control folder):
    file path = os.path.join(control folder, filename)
    if os.path.isfile(file_path):
        result neg slop prop, result avg grip deviation = masterfunction
        label = determine label("control")
        master_arrayID1.append([result_neg_slop_prop, result_avg_grip_dev
# Iterate through the parkinson folder
for filename in os.listdir(parkinson folder):
    file path = os.path.join(parkinson folder, filename)
    if os.path.isfile(file path):
        result_neg_slop_prop, result_avg_grip_deviation = masterfunction
        label = determine_label("parkinson")
        master arrayID1.append([result neg slop prop, result avg grip de
# Print the master 2D array
print("Master 2D Array:")
# for row in master_arrayID1:
     print(row)
# print("Master 2D Array:")
# for row in master_arrayID0:
     print(row)
```

Master 2D Array:

then with the two "master arrays" corresponding to each test ID 0 (dynamic or spiral test) it will then look to plot the std. dev of pressure of each test ID against each other, while labeling which patients are control or parkinson's by the color

```
In [3]: import numpy as np
        import matplotlib.pyplot as plt
        from sklearn.svm import SVC
        # Assuming master arrayID0 and master arrayID1 are defined
        master_array_1 = master_arrayID0
        master array 2 = master arrayID1
        # Extract grip strength deviation from master arrays
        grip deviation 1 = np.array([row[1] for row in master array 1]).reshape(
        grip deviation 2 = np.array([row[1] for row in master array 2]).reshape(
        # Flatten grip_deviation_2 to avoid DataConversionWarning
        grip deviation 2 = grip deviation 2.ravel()
        # Extract labels from master arrays
        labels 1 = [row[2]  for row in master array 1]
        labels 2 = [row[2]  for row in master array 2]
        # Define colors based on labels
        colors_1 = ['blue' if label == 0 else 'red' for label in labels_1]
        colors_2 = ['green' if label == 0 else 'blue' for label in labels_2]
        # Plot data
        plt.figure(figsize=(8, 6))
        plt.scatter(grip_deviation_1, grip_deviation_2, c=colors_1, marker='o',
        plt.title('Comparison of Grip Strength Deviation')
        plt.xlabel('Grip Strength Deviation (Master Array ID0)')
        plt.ylabel('Grip Strength Deviation (Master Array ID1)')
        plt.legend()
        plt.grid(True)
        plt.show()
        print(colors_1)
```

Comparison of Grip Strength Deviation



['blue', 'blue', 'blue', 'blue', 'blue', 'blue', 'blue', 'blue', 'blue', 'blue', 'red', 'red'

these next two cells look to parse the arrays regarding color and the std. deviations, into a more usable form that the SVM function can take in, essentially just reformatting!

```
In [4]: # color_ar = ['blue', 'blue', 'bl
```

```
In [5]: import numpy as np
        import matplotlib.pyplot as plt
        # Assuming grip_deviation_1 and grip_deviation_2 are defined
        # Convert grip deviation arrays to one-dimensional numpy arrays
        grip_deviation_1 = np.ravel(grip_deviation_1)
        grip deviation 2 = np.ravel(grip deviation 2)
        # Combine grip deviations into one big 2D array
        combined array = np.column stack((grip deviation 1, grip deviation 2))
        # Plot the graph
        # plt.scatter(combined_array[:, 0], combined_array[:, 1])
        # plt.xlabel('Grip Strength Deviation (ID 0)')
        # plt.ylabel('Grip Strength Deviation (ID 1)')
        # plt.title('Comparison of Grip Strength Deviation')
        # plt.grid(True)
        # plt.show()
        print(combined array)
```

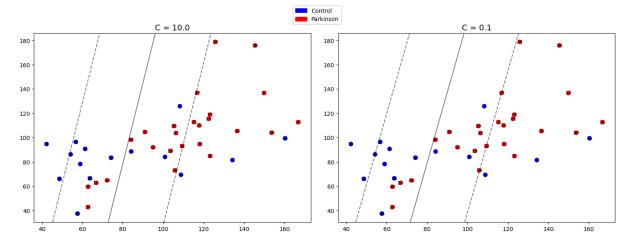
```
[[ 56.77315768
                96.37497372]
[100.91022406
               84.0334577 ]
[134.303481
                81.44286085]
[ 84.20098324
               88.48953288]
[108.82030568
                69.305926681
[ 61.403805
                90.62500651]
[ 54.22182406
               86.13772141]
[108.2692326
               125.74136469l
[ 42.27846714
               94.64909324]
[ 58.96029062
                78.16058026]
74.22848566
               83.350049431
48.68896221
                65.986860021
[160.40326366
               99.36571537]
[ 63.77263137
               66.44717921
[ 57.62499538
               37.38036058]
[117.8877146
               109.93085098]
66.85199151
               62.733168221
[123.19680632 118.86393949]
[103.63480362
               89.02435569]
[105.82783018
               72.9508759 ]
[ 72.23328176 64.77232856]
[122.60438284 115.41738226]
[109.39284744
               93.02392928]
[118.10510402
                94.577373021
[ 84.09743316
               98.141353
[115.26093716 112.67288449]
[136.62203951 105.34091362]
[116.88445617 136.72627941]
[125.83459999 178.64248242]
[105.36797685 109.47161584]
[ 62.83494336
               59.480056481
[106.38200878 103.68640994]
94.99210611
               91.975903491
[ 90.99283576 104.51501638]
[ 62.78287367
               42.683027251
[123.24003119 84.72805978]
[166.79567206 112.58531665]
[149.96443175 136.62902596]
[145.50412279 175.77991856]
[153.71023929 103.93404364]]
```

Lastly we are throwing our data into the SVM model with soft margins and then creating a simple function that uses the parameters of our decision boundary to predict if someone has parkinson, with a confidence interval that is based on how far from the decision boundary it is

```
In [6]: | from sklearn.datasets import make_blobs
        from sklearn.svm import SVC
        import numpy as np
        import matplotlib.pyplot as plt
        import matplotlib.patches as mpatches
        # Assuming combined_array and numerical_array are defined somewhere
        X, y = combined array, numerical array
        def plot_svc_decision_function(model, ax=None, plot_support=True):
            """Plot the decision function for a 2D SVC"""
            if ax is None:
                ax = plt.qca()
            xlim = ax.get xlim()
            ylim = ax.get_ylim()
            # create grid to evaluate model
            x = np.linspace(xlim[0], xlim[1], 30)
            y = np.linspace(ylim[0], ylim[1], 30)
            Y, X = np.meshgrid(y, x)
            xy = np.vstack([X.ravel(), Y.ravel()]).T
            P = model.decision_function(xy).reshape(X.shape)
            # plot decision boundary and margins
            ax.contour(X, Y, P, colors='k',
                       levels=[-1, 0, 1], alpha=0.5,
                       linestyles=['--', '-', '--'])
            # plot support vectors
            if plot support:
                ax.scatter(model.support_vectors_[:, 0],
                           model.support_vectors_[:, 1],
                            s=300, linewidth=1, facecolors='none')
            ax.set_xlim(xlim)
            ax.set_ylim(ylim)
        fig, ax = plt.subplots(1, 2, figsize=(16, 6))
        fig.subplots_adjust(left=0.0625, right=0.95, wspace=0.1)
        for axi, C in zip(ax, [10.0, 0.1]):
            model = SVC(kernel='linear', C=C).fit(X, y)
            # Change yellow points to red and red points to blue
            colors = ['blue' if label == 0 else 'red' for label in y]
            axi.scatter(X[:, 0], X[:, 1], c=colors, s=50)
            plot svc decision function(model, axi)
            axi.scatter(model.support_vectors_[:, 0],
                        model.support_vectors_[:, 1],
                        s=300, lw=1, facecolors='none')
            # Label each point with its index
            for i, (x, y_val) in enumerate(zip(X[:, 0], X[:, 1])):
                axi.text(x, y_val, i, color='black', fontsize=8, ha='center', va
            axi.set_title('C = \{0:.1f\}'.format(C), size=14)
        # Create legend
        legend elements = [
```

```
mpatches.Patch(color='blue', label='Control'),
   mpatches.Patch(color='red', label='Parkinson')
]

fig.legend(handles=legend_elements, loc='upper center')
plt.show()
```



```
In [9]: def predict_parkinson_with_confidence(model, x_coord, y_coord):
            """Predict whether a new point belongs to Parkinson's class or not."
            # Reshape the coordinates into a 2D array
            new point = np.array([[x coord, y coord]])
            # Use the decision function to get the signed distance to the hyperp
            distance to hyperplane = model.decision function(new point)
            # Compute confidence based on the signed distance
            confidence = np.abs(distance to hyperplane)
            # Use the trained model to predict the class of the new point
            prediction = model.predict(new point)
            return prediction[0], confidence[0]
        # Example usage:
        new x = 80.5 # Example x coordinate of the new point
        new_y = 100.0 # Example y coordinate of the new point
        # Assuming 'model' is your trained SVM model
        prediction, confidence = predict_parkinson_with_confidence(model, new_x,
        print("Prediction for point ({}, {}): {}, Confidence: {:.2f}".format(new
```

Prediction for point (80.5, 100.0): Control, Confidence: 0.11

| In | [| 1: | |
|----|---|----|--|
| | | | |
| In | [| 1: | |