## CO542- NEURAL NETWORKS AND FUZZY SYSTEMS SELF ORGANIZING MAPS (SOM)

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## **CODE**

```
import pandas as pd
    from matplotlib.lines import Line2D
    from sklearn.preprocessing import MinMaxScaler
    from minisom import MiniSom
    import matplotlib.pyplot as plt
    import matplotlib.gridspec as gridspec
    # 1. Load the data set as a pandas' data frame and generate the feature matrix by selecting the
    # appropriate features in the data set.
    diabetes_data = pd.read_csv('/content/drive/MyDrive/Colab Notebooks/diabetes.csv')
    x_col = [col for col in diabetes_data.columns if col not in ['Outcome']]
    y_col = 'Outcome
    features = diabetes_data[x_col]
    features_val = features.values
    target = diabetes data[y col]
    target_val = target.values
    # print(target_val)
    # 2. Use sklearn.preprocessing.MinMaxScaler normalize the data between 0 and 1.
    minMaxScalar = MinMaxScaler()
    features_scaled = minMaxScalar.fit_transform(features_val)
    # print(features_scaled)
    # 3. Initialize the weights using MiniSom.pca_weights_init function (Also identify the usage of
    # random_weights_init method and mention an advantage of using pca_weights_init).
    som = MiniSom(6, 6, 8, sigma=0.3, learning_rate=0.5)
                                                                    # initialization of 6x6 SOM
                                                                    # Initialize the weights
    som.pca_weights_init(features_scaled)
    # 4. Identify the difference between Minisom.train_batch and Minisom.train_random methods available
    # minisom and use one of the models to train your self-organizing map.
    som.train_random(features_scaled, 5000)
                                                                    # trains the SOM with 5000 iterations
```

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# 6. Use Minisom.distance map function to visualize the results obtained from the training process and
           # use appropriate markers to indicate individual samples matched into each cell (according to the
           # classes; patient who has diabetes/ do not have diabetes define two markers).
           plt.figure(figsize=(8, 7))
           plt.pcolor(som.distance_map().T, cmap='viridis')
           plt.colorbar()
           markers = ['o', 'x']
           colors = ['C0', 'C1']
            for id, x in enumerate(features_scaled):
                                                                                          # getting the winner
                     w = som.winner(x)
                      \# place a marker on the winning position for the sample x
                     plt.plot(w[0] + 0.5, w[1] + 0.5,
                                              markers[target_val[id] - 1],
                                              markerfacecolor='None',
                                              markeredgecolor=colors[target_val[id] - 1],
                                              markersize=12.
                                              markeredgewidth=2)
            legend\_elements = [Line2D([0], [0], marker=markers[0], color=colors[0], label='Has Diabetes', legend\_elements = [Line2D([0], [0], marker=markers[0], color=colors[0], label='Has Diabetes', label='H
                                                                                markerfacecolor='w', markersize=12, linestyle='None', markeredgewidth=2),
                                                              Line2D([0], [0], marker=markers[1], color=colors[1], label='Do not have Diabetes',
                                                                                markerfacecolor='w', markersize=12, linestyle='None', markeredgewidth=2)]
            plt.legend(handles=legend_elements, bbox_to_anchor=(0.05, 1.1), loc='upper left',
                                         borderaxespad=0., ncol=3, fontsize=12)
            plt.show()
```

```
# 8. Visualize the proportion of samples per class falling in a specific neuron
# matplotlib.gridspec.GridSpec and matplotlib.patches.Patcha
labels_map = som.labels_map(features_scaled, target_val)
fig = plt.figure(figsize=(6, 6))
the_grid = gridspec.GridSpec(6, 6, fig)
for position in labels_map.keys():
    label_fracs = [labels_map[position][t] for t in target.unique()]
    plt.subplot(the_grid[6-1-position[1], position[0]], aspect=1)
    patches, texts = plt.pie(label_fracs)

plt.legend(target.unique(), bbox_to_anchor=(0, 0), ncol=3, loc='upper left', borderaxespad=0.)
plt.show()
```

Usage of random\_weights\_init method:
 It initializes the weights of the Self-Organizing Maps by picking random samples from the data.

an advantage of using pca\_weights\_init method:

It does not depend on the random processes and converges the training process faster.

- 4. train\_random method is the random training, where the model is trained by picking random samples from the data train\_batch is the batch training, where the model is trained by picking the samples in the order they are stored.
- 5. Each cell in the distance map is the normalized sum of Euclidean distances between a neuron and its neighbors.

6.

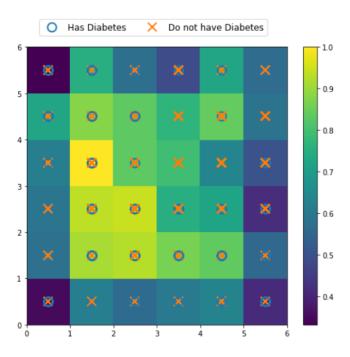


Figure 1: Results Obtained from the Training Process

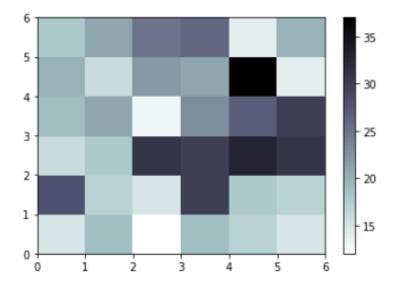


Figure 2: Activation Response

8.

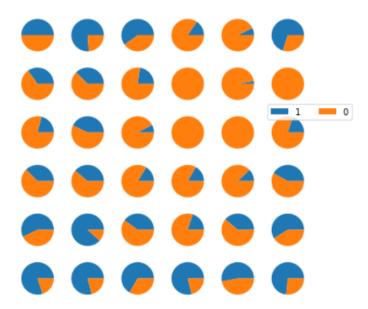


Figure 3: Proportion of Samples per Class Falling in a Specific Neuron