

## **Modified Kohonen Map Codes**

Note : Kindly install the signal processing toolbox in matlab for using the dtw similarity measure function.

The modified Kohonen Map algorithm code contains of the following modules:

1. Neurons.m - Main file that performs the clustering
2. FNInitialization.m - Function that samples points according to the proposed technique.
3. OneDTrain.m - Function to train the kohonen map.

Note : The FNInitialization.m and OneDTrain.m files are called within the Neurons.m file. One only needs to run Neurons.m to perform clustering.

To run the code on any data set of the UCR time series archive -

[https://www.cs.ucr.edu/~eamonn/time\\_series\\_data\\_2018/](https://www.cs.ucr.edu/~eamonn/time_series_data_2018/), please paste the above two files in the same directory as the data set and run Neurons.m. There is no need to change anything. The UCR archive contains many different types of datasets, each type consists of two sets : train and test. This is done so that one can use the archive for classification as well. However, since we are only doing clustering, the data is run on all the train sets. Pick any one dataset, go to its directory and paste the programmes in the zipped file.

To change the number of clusters required :

- 1) In the Neurons.m file, change num\_centroids to the desired number of clusters.

The following code files are various validation measures that can be run to quantify the clustering performance:

1. CHIndex.m - To calculate the Calinski-Harasbasz index
2. InterGroupVariance.m - To calculate the InterGroupVariance
3. RandIndex.m - To calculate the rand index of the clustering result.

To call each of these functions, run the following lines in the MATLAB terminal:

InterGroupVariance(norm\_train,labels), CHIndex(labels,norm\_train) and  
[randindex,~,~] = RandIndex(labels,norm\_train).

For comparison, a hierarchical clustering program is also programmed and placed in the zip file. To perform hierarchical clustering, paste the following module in the dataset directory and run it:

1) Hierarchical.m

The same metrics can be used in this case, note that this time the commands to run them are as follows:

InterGroupVariance(norm\_train,T), CHIndex(labels,T) and  
[randindex,~,~] = RandIndex(labels,T).

As an example, along with the zip file for codes, another zip file consisting of a dataset and all these codes is included. You can unzip the latter and run either Neurons.m or Hierarchical.m to perform kohonen and hierarchical clustering respectively.