**READ ME**

ERROR HISTOGRAM

* Run\_ErrorHistogram.m is the parent code which calls all other functions for further processing.

Feature Extraction Steps

* **GT\_Histogram\_Frontal\_Face\_Malignant** - Call this function to extract the features from ground truth ROI of IR Frontal Facial image (Malignant subjects).
* **GT\_Histogram\_Frontal\_Face\_Precancer** - Call this function to extract the features from ground truth ROI of IR Frontal Facial image (Non Malignant subjects).
* **GT\_Histogram\_Frontal\_Face\_Normal** - Call this function to extract the features from ground truth ROI of IR Frontal Facial image (Normal subjects).
* **GT\_Front\_FeatureConcate**- Call this function to concatenate all the subject specific features in a single Matrix.
* **GT\_Histogram\_Frontal\_Face\_Normal\_AgeAdjust** - Call this function to extract the features from ground truth ROI of IR Frontal Facial image (Normal subjects with age greater than 30).
* **GT\_Histogram\_Profile\_Face\_Malignant** - Call this function to extract the features from ground truth ROI of IR Profile Facial image (Malignant subjects).
* **GT\_Histogram\_Profile\_Face\_Precancer** - Call this function to extract the features from ground truth ROI of IR Profile Facial image (Non Malignant subjects).
* **GT\_Histogram\_Profile\_Face\_Normal** - Call this function to extract the features from ground truth ROI of IR Profile Facial image (Normal subjects).
* **GT\_Histogram\_Profile\_Face\_Normal\_AgeAdjust** - Call this function to extract the features from ground truth ROI of IR Profile Facial image (Normal subjects with age greater than 30).
* **GT\_Profile\_FeatureConcate** - Call this function to concatenate all the subject specific features in a single Matrix. **GT\_Profile\_FeatureConcate\_AgeAdjust** - Call this function to concatenate all the subject specific features in a single Matrix.

Storing Extracted Features

Features are stored in the folder **Error Histogram**

**Path:** SPIE\_2016\ErrorHistogram

Classification Steps

* **GT\_MN\_kmeans\_fuzzy:** Call this function to classify the extracted features of Malignant versus Normal using Cluster Prototype Classifier

Subroutines called-

**find\_optimum\_clust\_fcm ( )** - Used to find the optimum number of c lusters required for the data set by fuzzy c means clustering.

**find\_optimum\_clust\_kmeans ( )** - Used to find the optimum number of clusters required for the data set by K means clustering.

**fcm ( )** - Performs fuzzy C means clustering.-->MATLAB INBUILT

**Kmeans ( )** – Performs Kmeans clustering. .-->MATLAB INBUILT

**classification ( )** – Used to find the accuracy of the Data set by

comparing true labels and predicted labels.

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**Kmeans ( )** – Performs Kmeans clustering. -->MATLAB INBUILT

**classification ( )** – Used to find the accuracy of the Data set by

comparing true labels and predicted labels.

Storing Classification Results

Classification results are stored inside the folder **Error Histogram Results as .mat files**

**Path:** SPIE\_2016\SPIE 2016 Classification\Error Histogram Results