**READ ME**

* **Run\_Haralick- This** is the parent code which calls all other functions for further processing.

Feature Extraction Steps

* **GT\_Malignant\_Texture\_Frontal\_Face\_thermal**- Call this function to extract the features from ground truth ROI of IR Frontal Facial image (Malignant subjects).
* **GT\_Precancer\_Texture\_Frontal\_Face\_thermal**- Call this function to extract the features from ground truth ROI of IR Frontal Facial image (Non Malignant subjects).
* **GT\_Normal\_Texture\_Frontal\_Face\_thermal**- Call this function to extract the features from ground truth ROI of IR Frontal Facial image (Normal subjects).
* **GT\_Front\_HaralickFeatureConcate**- Call this function to concatenate all the subject specific features in a single Matrix.
* **GT\_MN\_pvalue\_AUC\_FrontalFace:** This function calculates the significant features for malignant versus normal for frontal setting
* **GT\_PN\_pvalue\_AUC\_FrontalFace: :** This function calculates the significant features for precancerous versus normal for frontal setting
* **AgeAdjust\_GT\_Normal\_Texture\_Frontal\_Face\_thermal**- Call this function to extract the features from ground truth ROI of IR Frontal Facial image (Normal subjects with age greater than 30).

* **GT\_Front\_HaralickFeatureConcate\_AgeAdjust** - Call this function to concatenate all the age adjusted subject specific features in a single Matrix.
* **AgeAdjust\_GT\_MN\_pvalue\_AUC\_FrontalFace:** This function calculates the significant features for malignant versus age adjusted normal subjects for frontal setting
* **AgeAdjust\_GT\_PN\_pvalue\_AUC\_FrontalFace:** This function calculates the significant features for precancerous versus age adjusted normal subjects for frontal setting
* **GT\_Malignant\_Texture\_Profile\_Face\_thermal**- Call this function to extract the features from ground truth ROI of IR Profile Facial image (Malignant subjects).
* **GT\_Precancer\_Texture\_Profile\_Face\_thermal** - Call this function to extract the features from ground truth ROI of IR Profile Facial image (Non Malignant subjects).
* **GT\_Normal\_Texture\_Profile\_Face\_thermal** - Call this function to extract the features from ground truth ROI of IR Profile Facial image (Normal subjects).
* **GT\_Profile\_HaralickFeatureConcate**- Call this function to concatenate all the subject specific features in a single Matrix for Profile setting.
* **GT\_MN\_pvalue\_AUC\_ ProfileFace:** This function calculates the significant features for malignant versus normal for profile setting
* **GT\_PN\_pvalue\_AUC\_ ProfileFace: :** This function calculates the significant features for precancerous versus normal for Profile setting.
* **AgeAdjust\_GT\_Normal\_Texture\_Profile\_Face\_thermal**- 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\_HaralickFeatureConcate\_AgeAdjust** - Call this function to concatenate all the age adjusted subject specific features in a single Matrix for profile setting.
* **AgeAdjust\_GT\_MN\_pvalue\_AUC\_ProfileFace:** This function calculates the significant features for malignant versus age adjusted normal subjects for Profile setting
* **AgeAdjust\_GT\_PN\_pvalue\_AUC\_ProfileFace:** This function calculates the significant features for precancerous versus age adjusted normal subjects for Profile setting
* **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 **HaralickFeatures**

**Path:** HaralickTexture\HaralickFeatures

Significant Features are stored in the folder **SignifantFeaturesPath:** HaralickTexture\HaralickFeatures\ \SignifantFeatures

Classification Steps

* **kmeans\_fuzzy\_MN** **::** 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

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

comparing true labels and predicted labels.

* **kmeans\_fuzzy\_PN** **:** Call this function to classify the extracted features of Precancerous versus Normal using Cluster Prototype Classifier

Subroutines called-

**find\_optimum\_clust\_fcm ( )** - Used to find the optimum number of clusters 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

**classificationND ( )** – 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 **Haralick Results as .mat files**

**Path:** HaralickTexture\Classification\Haralick Results