Radiogenomics Analysis Report

27/09/2021 20:22:45

------------------------------Model inputs------------------------------

Mode:Train

Model:multiTaskLASSO

Params:default

No. of imaging features provided: 36

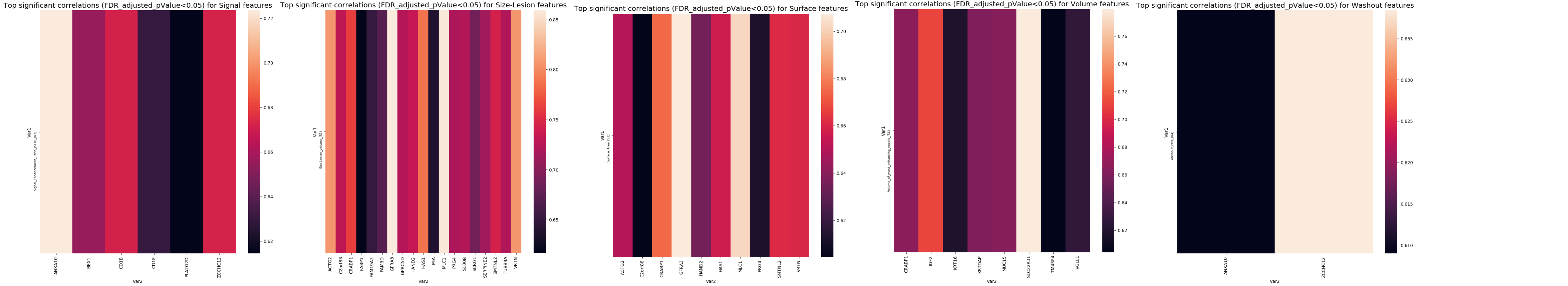**No. of gene features provided:976**

SampleID check results: 'The SampleIDs match for imaging and gene features'

No. of samples: 89

performing Stand_scaler normalization for imaging features

performing Stand_scaler for gene features

--------------------------Multivariate Correlations (pearson based)----------------------

Top significant correlations (FDR_adjusted_pValue<0.05) for Signal features

Top significant correlations (FDR_adjusted_pValue<0.05) for Size-Lesion features

Top significant correlations (FDR_adjusted_pValue<0.05) for Surface features

Top significant correlations (FDR_adjusted_pValue<0.05) for Volume features

Top significant correlations (FDR_adjusted_pValue<0.05) for Washout features

--------------------------------Features with highly significant correlations----------------------------------

Below is the list of imaging features

['Signal_Enhancement_Ratio_(SER)_(K7)', 'Size-Lesion_volume_(S1)', 'Surface_Area_(S3)', 'Volume_of_most_enhancing_voxels_(S4)', 'Washout_rate_(K4)']

Below is the list of gene features

['ACTG2', 'ANXA10', 'BEX1', 'C2orf88', 'CD1B', 'CD1E', 'CRABP1', 'FABP1', 'FAM19A3', 'FAM3D', 'GFRA3', 'GPRC5D', 'HAND2', 'HAS1', 'IGF2', 'KRT16', 'KRTDAP', 'MIA', 'MLC1', 'MUC15', 'PLA2G2D', 'PRG4', 'S100B', 'SCRG1', 'SERPINE2', 'SLC22A31', 'SMTNL2', 'TM4SF4', 'TUBB4A', 'VGLL1', 'VRTN', 'ZCCHC12']

Number of imaging features

5

Number of gene features

32

-------------------------------Number of Samples for Training and Testing--------------------------------

No. of samples for training:71

No. of samples for test:18

--------------------------Model Summary----------------------

Model Type : multiTaskLASSO

Cross Validation Metrics:

Parameters: cv=3 scoring:neg_mean_squared_error

Cross validation score:1.23177137897

Model Parameters:

normalize:False

warm_start:False

selection:cyclic

fit_intercept:True

max_iter:1000

random_state:None

tol:0.0001

copy_X:True

alpha:1.0

----------------Model evaluation for Train data-------------------

Min Square Error for the Model

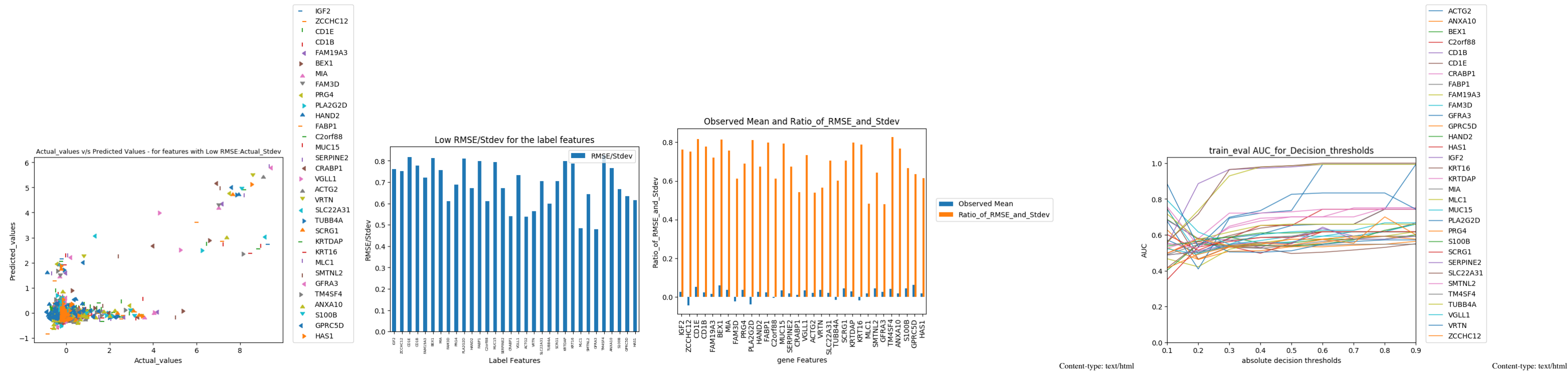**MSE of train_eval set:0.572509296261**

No. of features showing LOW 'RMSE/Stdev' (<=1.0): 32

All such features with their Low 'RMSE/Stdev' values could be found in output file: train_eval_multiTaskLASSO_Labels_with_Low_Ratio.csv

No. of features showing HIGH 'RMSE/Stdev' (>1.0): 0

All such features with their High 'RMSE/Stdev' values could be found in output file: train_eval_multiTaskLASSO_Labels_with_High_Ratio.csv

Model evaluation for Train data for label features showing Low 'RMSE/Stdev' (<=1.0)

Actual_values v/s Predicted Values - for features with Low RMSE:Actual_Stdev

Low RMSE/Stdev for the label features

Observed Mean and Ratio_of_RMSE_and_Stdev

train_eval AUC_for_Decision_thresholds

----------------Model evaluation for Test data-------------------

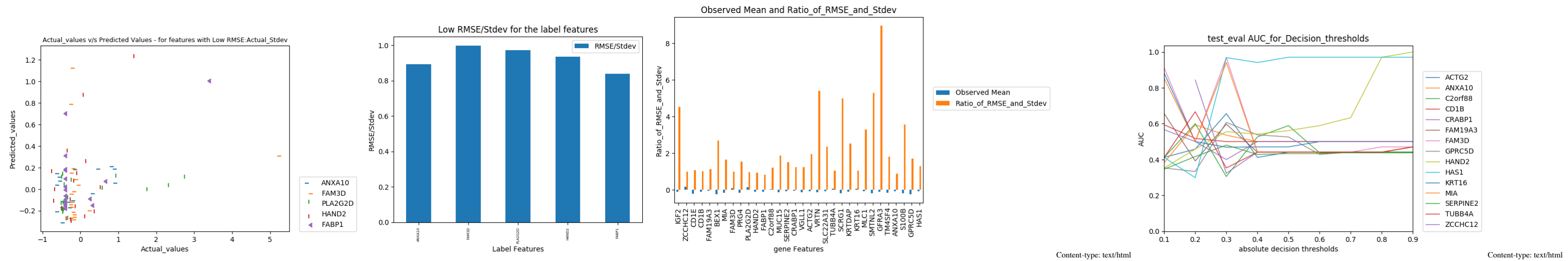**Min Square Error for the Model**

MSE of test_eval set:0.4174060082

No. of features showing LOW 'RMSE/Stdev' (<=1.0): 5

All such features with their Low 'RMSE/Stdev' values could be found in output file: test_eval_multiTaskLASSO_Labels_with_Low_Ratio.csv

No. of features showing HIGH 'RMSE/Stdev' (>1.0): 27

All such features with their High 'RMSE/Stdev' values could be found in output file: test_eval_multiTaskLASSO_Labels_with_High_Ratio.csv

Model evaluation for Test data for label features showing Low 'RMSE/Stdev' (<=1.0)

Actual_values v/s Predicted Values - for features with Low RMSE:Actual_Stdev

Low RMSE/Stdev for the label features

Observed Mean and Ratio_of_RMSE_and_Stdev

test_eval AUC_for_Decision_thresholds