Radiogenomics Analysis Report

22/09/2021 17:01:46 ----Model inputs-----Mode:Train

No. of imaging features provided: 540

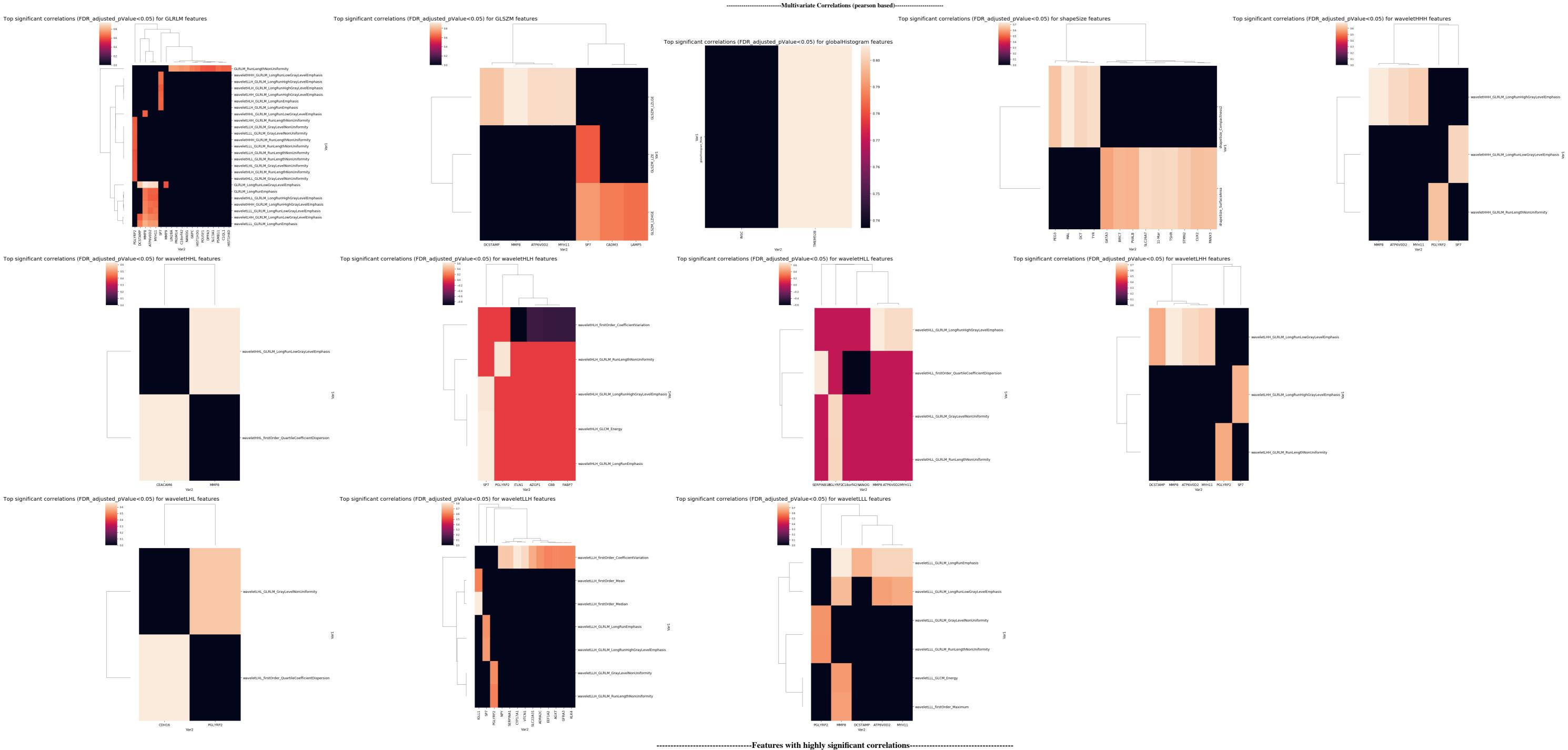
Model:multiTaskLinearModel

Params:default

No. of gene features provided:976 ${\bf Sample ID \ check \ results: \ 'The \ Sample IDs \ match \ for \ imaging \ and \ gene \ features'}$

 $performing \ Stand_scaler \ normalization \ for \ imaging \ features$

performing Stand_scaler for gene features



Below is the list of imaging features

[GLRLM_LongRunEmphasis', 'GLRLM_LongRunEmphasis', 'GLRLM_LongRunLowGrayLevelEmphasis', 'waveletHHL_GLRLM_LongRunLowGrayLevelEmphasis', 'waveletHHL_GLRLM_LongRunHighGrayLevelEmphasis', 'waveletLHL_GLRLM_LongRunHighGrayLevelEmphasis', 'waveletLHL_GLRLM_LongRunHighGrayLevelEmphasis',

Below is the list of gene features

['11-Mar', 'ADRA2C', 'AGXT', 'APR6V0D2', 'AZGPI', 'BIRC7', 'C18orf42', 'C1QL1', 'C8B', 'CADM3', 'CPI1AI', 'BISTIH4D', 'IGLL1', 'NNCG', 'NPY', 'PANX3', 'PEG3', 'PQLYP2', 'POUSFI', 'PNMI4', 'PSMBII', 'PVALB', 'SERPINAI', 'SLC22A3I', 'SLC2A3I', 'SLC2A3I', 'SLC3A1', 'SLC3A1', 'SLC3A1', 'NNCG', '

Number of imaging features

Number of gene features

-----Number of Samples for Training and Testing------No. of samples for training:84

 ${\bf Model\ Type: multiTask Linear Model}$

Cross validation score: 1.21075627758

Model Parameters:

No. of samples for test:22

warm_start:False

normalize:False

selection:cyclic fit_intercept:True

11_ratio:0.5

max_iter:1000 random_state:None

copy_X:True

----Model Summary-----

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

MSE of train_eval set:0.571045581713

Min Square Error for the Model

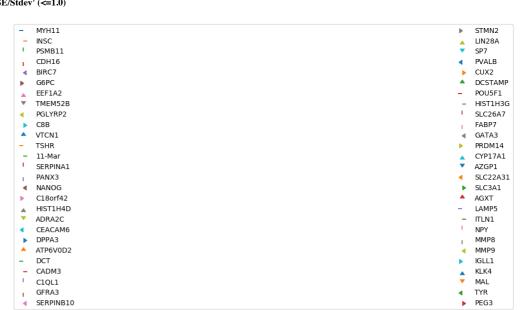
No. of features showing LOW 'RMSE/Stdev' (<=1.0): 54

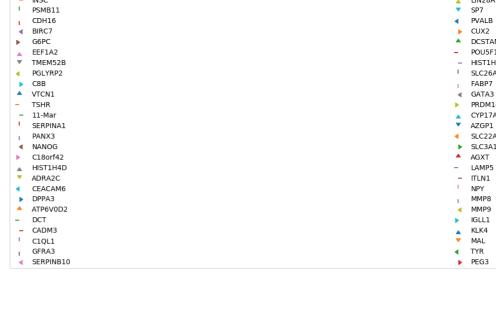
All such features with their Low 'RMSE/Stdev' values could be found in output file: train_eval_multiTaskLinearModel_Labels_with_Low_Ratio.csv

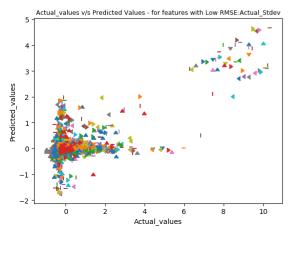
No. of features showing HIGH 'RMSE/Stdev' (>1.0): 0

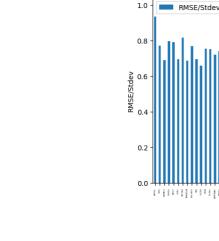
 $All such features with their High \ 'RMSE/Stdev' \ values could be found in output file: train_eval_multiTaskLinearModel_Labels_with_High_Ratio.csv$

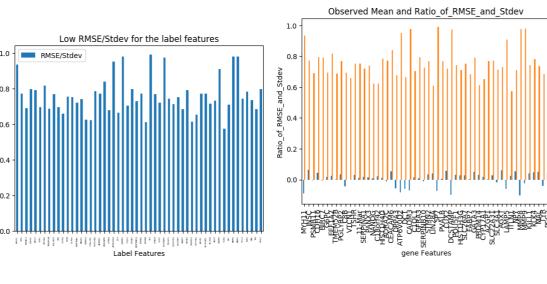
Model evaluation for Train data for label features showing Low 'RMSE/Stdev' (<=1.0)

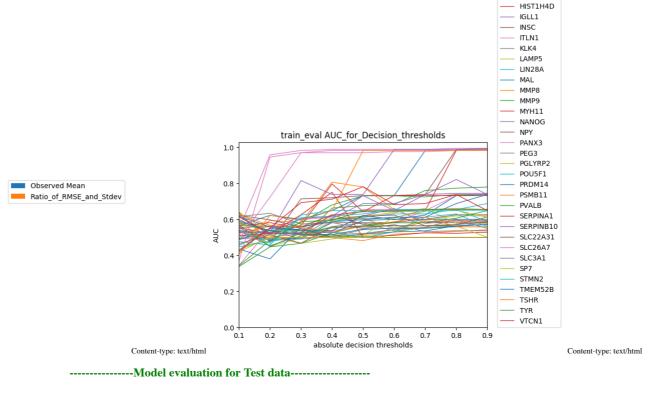












— 11-Mar
— ADRA2C
— AGXT
— ATP6V0D2
— AZGP1
— BIRC7
— C18orf42
— C1QL1
— C8B
— CADM3
— CDH16
— CEACAM6
— CUX2
— CYP17A1
— DCSTAMP
— DCT
— DPPA3
— EEF1A2
— FABP7
— G6PC
— GATA3
— GFRA3
— HIST1H3G

Min Square Error for the Model MSE of test_eval set:0.850476820968

No. of features showing LOW 'RMSE/Stdev' (<=1.0): 8

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

No. of features showing HIGH 'RMSE/Stdev' (>1.0): 46

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

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

