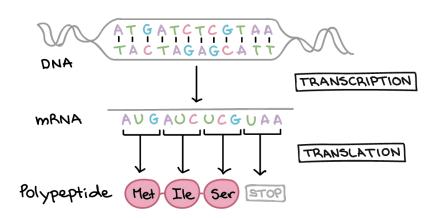
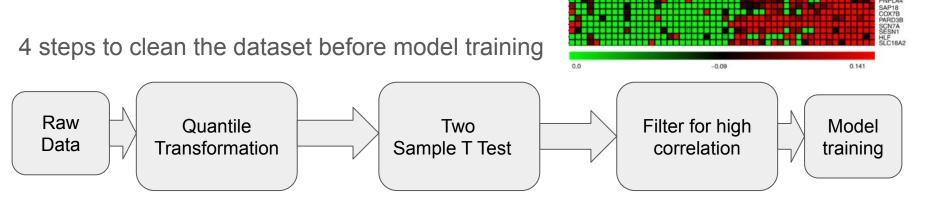
Mid Project Bootcamp

Predicting if a Patient has Cancer from Gene Expression Set

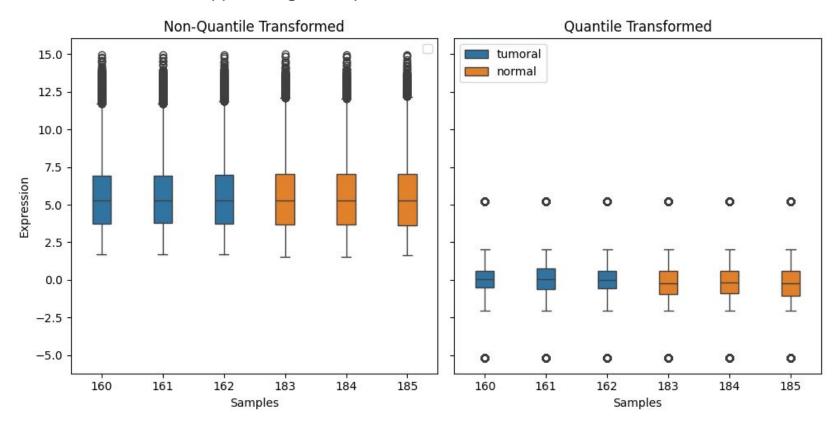
Introduction to Gene Profiling





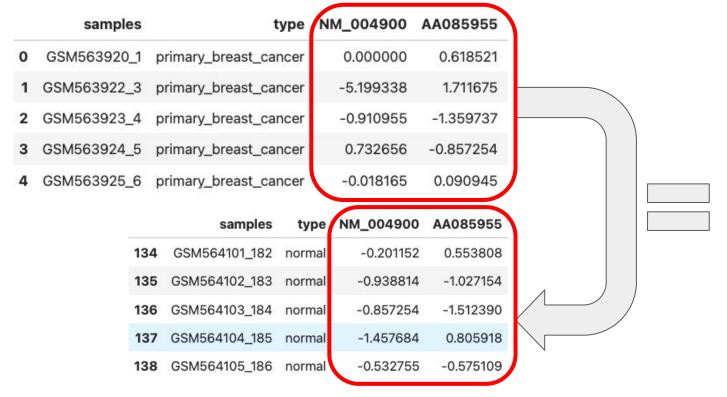
Quantile Transformation

Quantile transformation is applied to gene expression data to normalize its distribution



Two Sample T Test

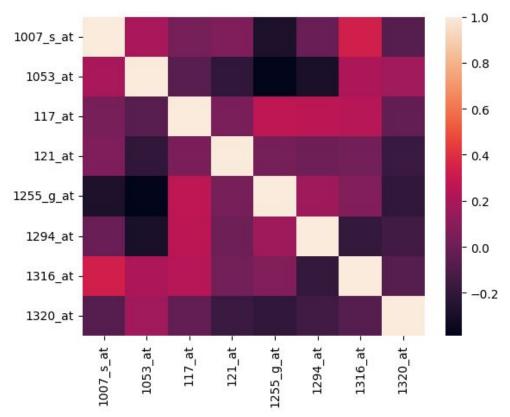
A two-sample t-test is employed to assess whether there is a significant difference in the mean expression levels between tumoral and normal genes.



Filter for Multi correlation coefficients between Genes

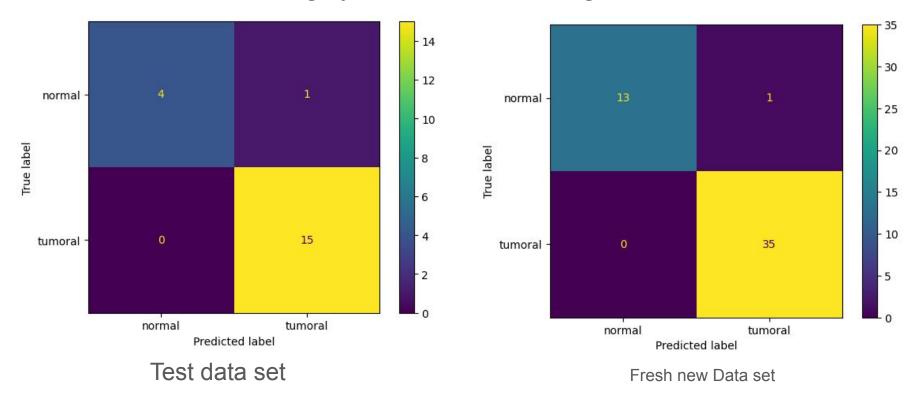
Filtering genes with high correlation is a crucial step to reduce overfitting in the

final model.



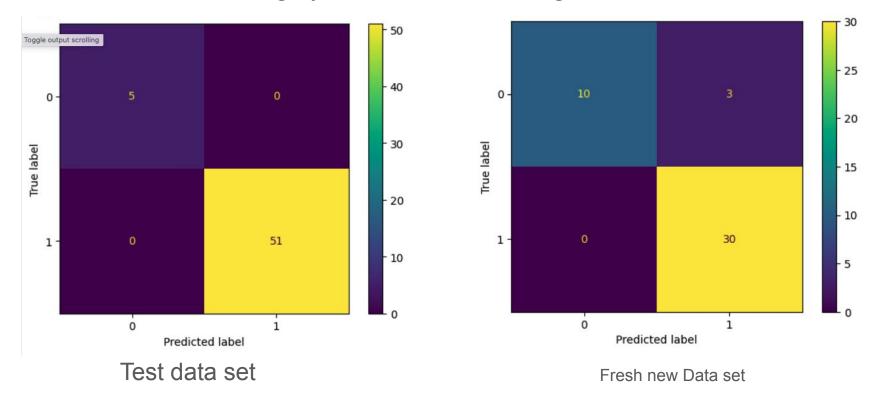
Logistic Model for Predicting Prostate Cancer

A logistic regression model was employed to predict whether a sample belongs to the normal or tumoral category based on the filtered gene set.



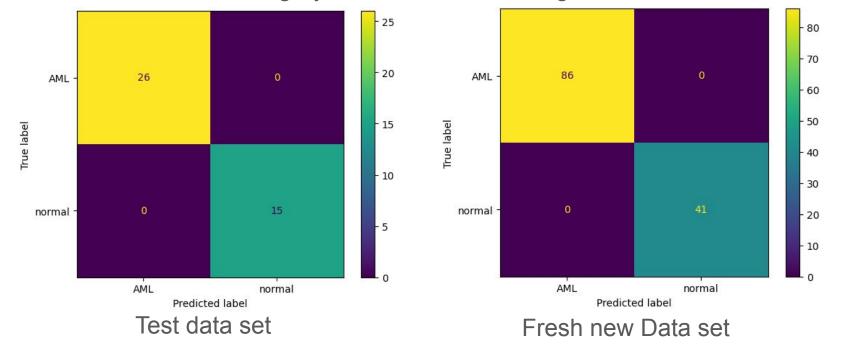
Logistic Model for Predicting Breast Cancer

A logistic regression model was employed to predict whether a sample belongs to the normal or tumoral category based on the filtered gene set.



Logistic Model for Predicting Leukemia AML-type Cancer

A logistic regression model was employed to predict whether a sample belongs to the normal or tumoral category based on the filtered gene set.



Thank you