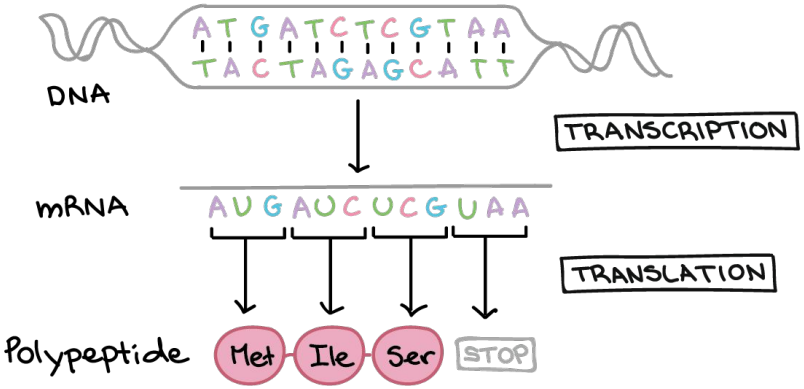
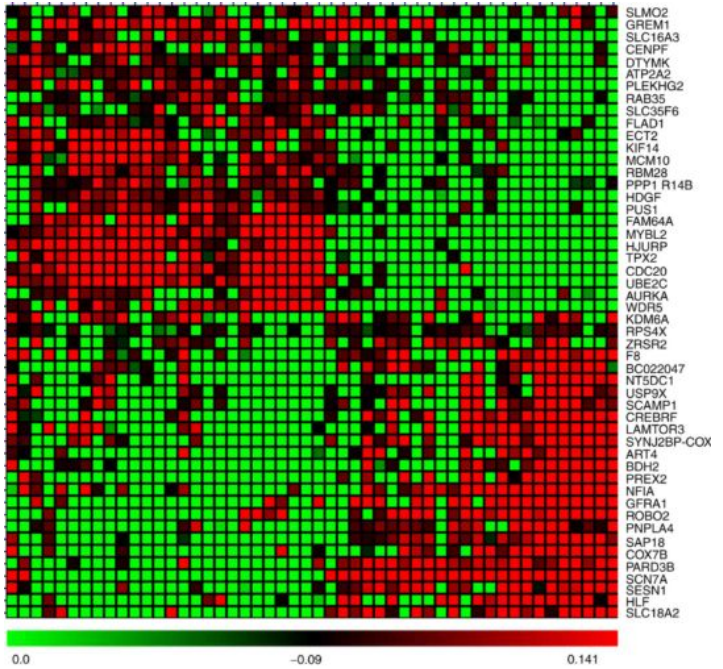
# Mid Project Bootcamp

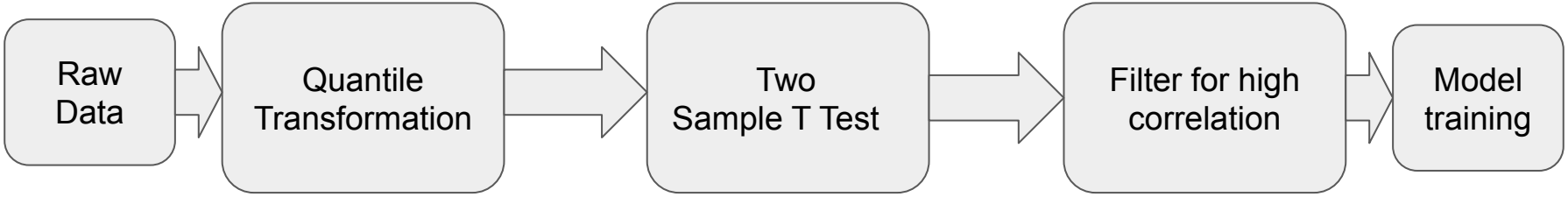
Predicting if a Patient has Cancer from Gene Expression Set

# Introduction to Gene Profiling



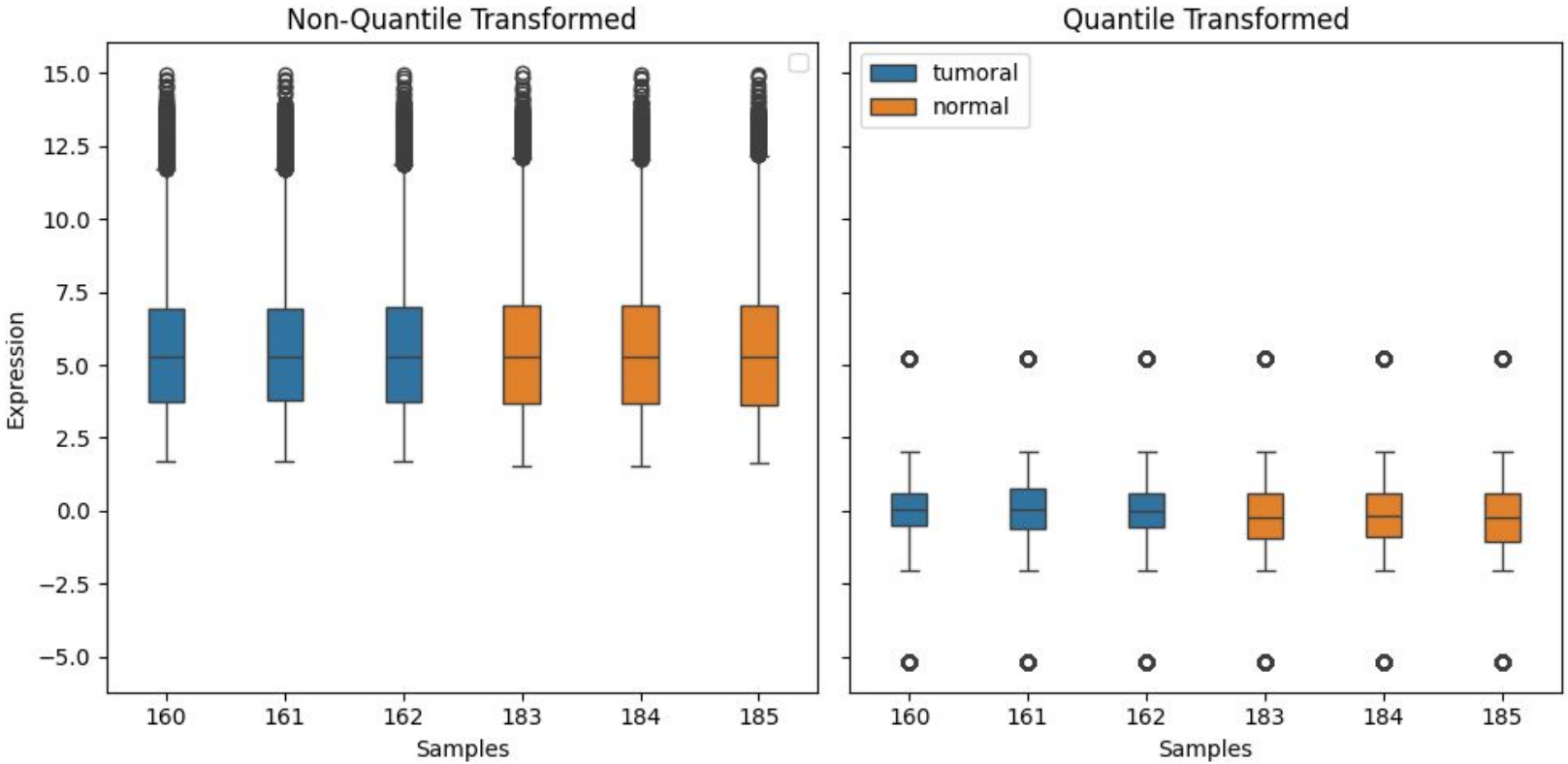




4 steps to clean the dataset before model training



# Quantile Transformation

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

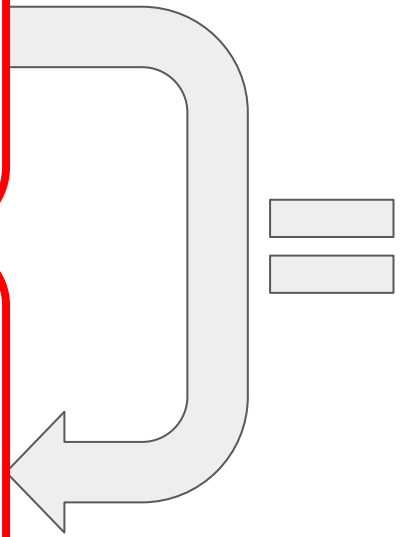


# Two Sample T Test

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.

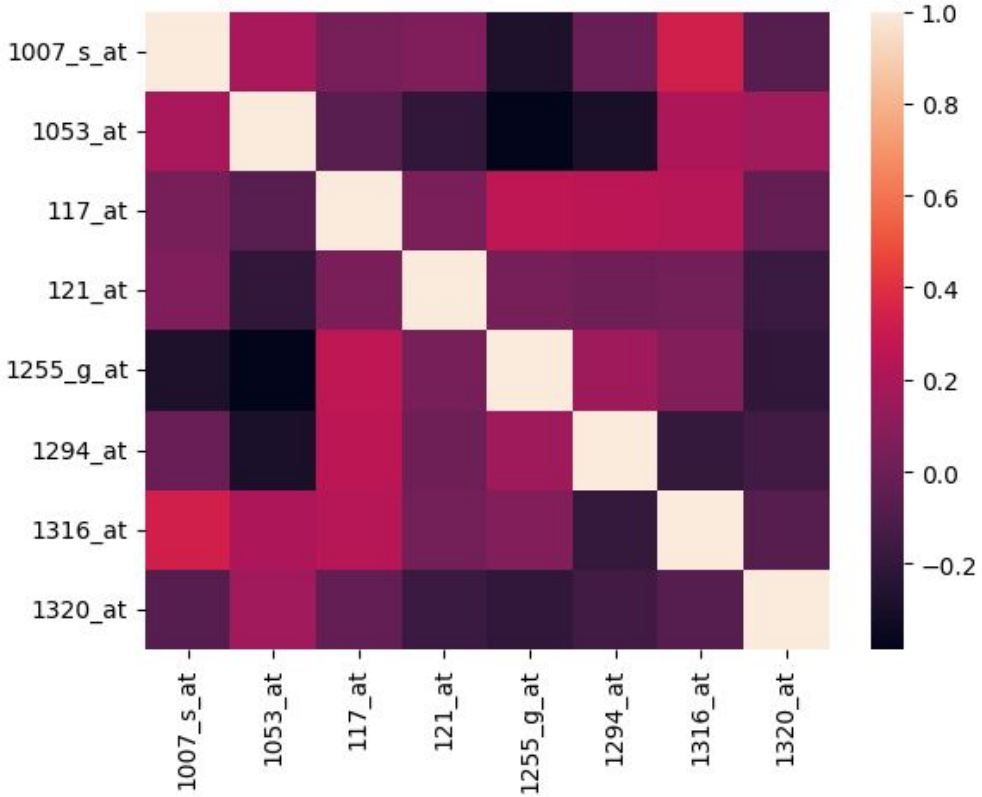
| | samples | type | NM_004900 | AA085955 |
|---|---|---|---|---|
| 0 | GSM563920_1 | primary_breast_cancer | 0.000000 | 0.618521 |
| 1 | GSM563922_3 | primary_breast_cancer | -5.199338 | 1.711675 |
| 2 | GSM563923_4 | primary_breast_cancer | -0.910955 | -1.359737 |
| 3 | GSM563924_5 | primary_breast_cancer | 0.732656 | -0.857254 |
| 4 | GSM563925_6 | primary_breast_cancer | -0.018165 | 0.090945 |

| | samples | type | NM_004900 | AA085955 |
|---|---|---|---|---|
| 134 | GSM564101_182 | normal | -0.201152 | 0.553808 |
| 135 | GSM564102_183 | normal | -0.938814 | -1.027154 |
| 136 | GSM564103_184 | normal | -0.857254 | -1.512390 |
| 137 | GSM564104_185 | normal | -1.457684 | 0.805918 |
| 138 | GSM564105_186 | normal | -0.532755 | -0.575109 |



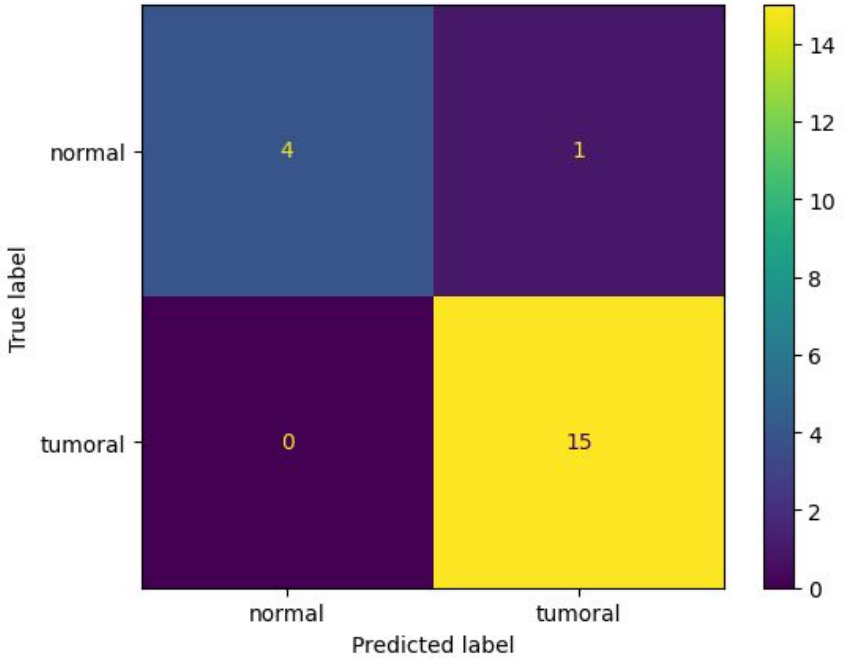
# Filter for Multi correlation coefficients between Genes

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

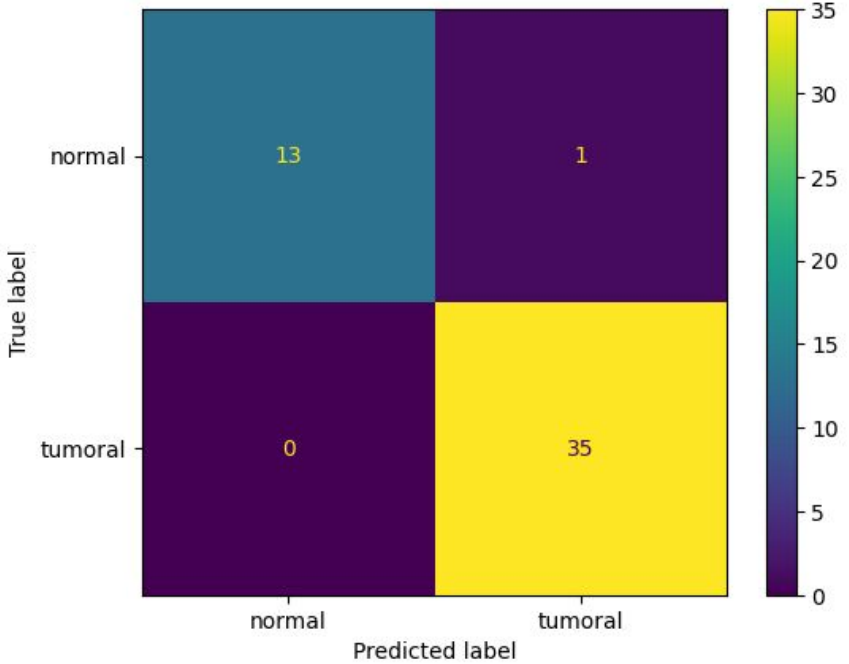


# Logistic Model for Predicting Prostate Cancer

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



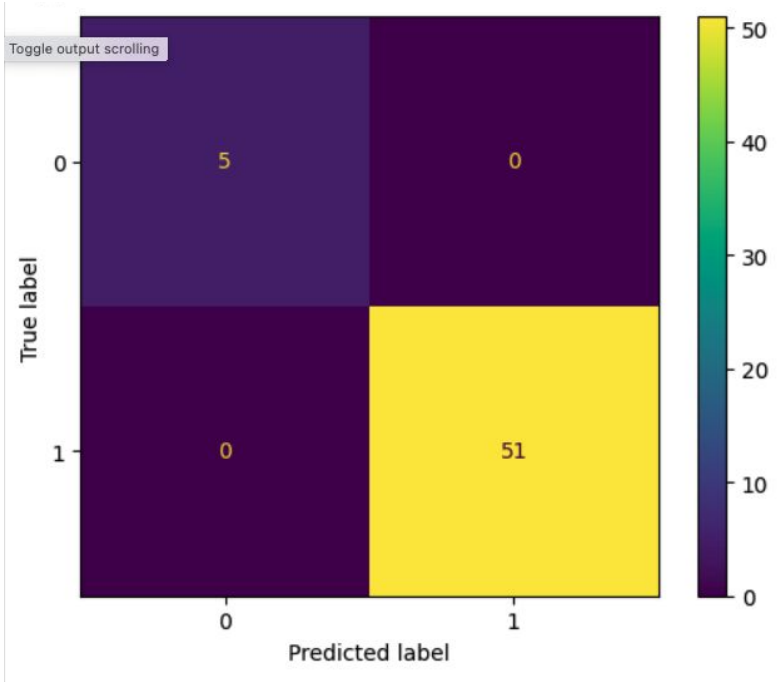

Test data set



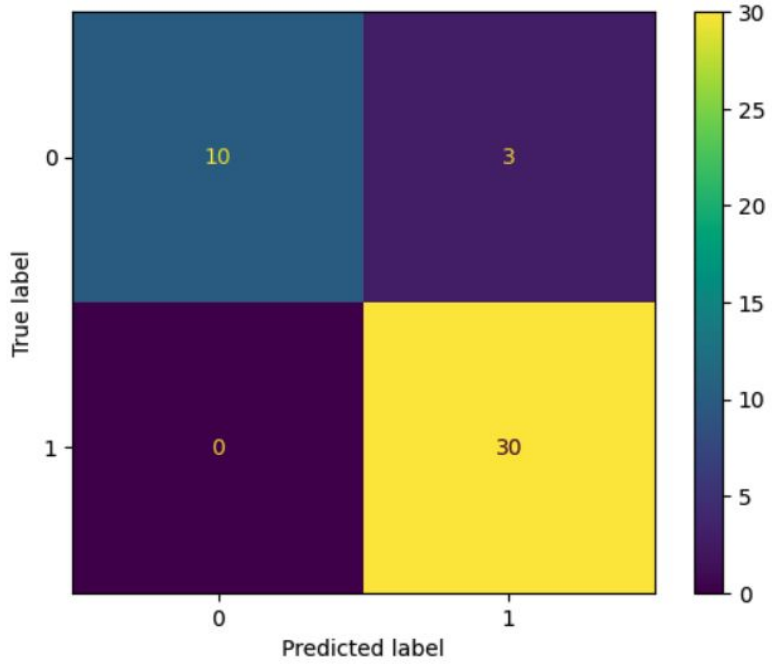

Fresh new Data set

# 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.




Test data set




Fresh new Data set