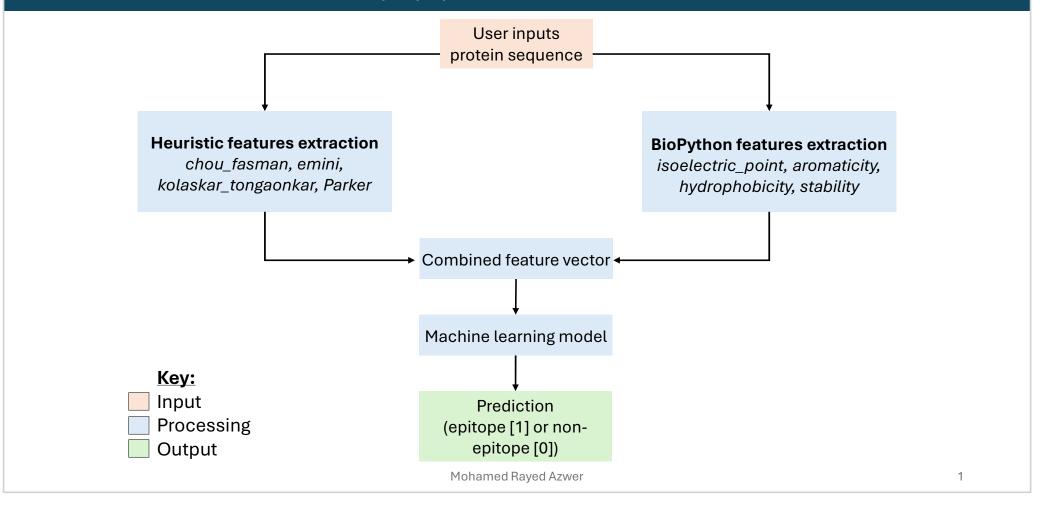
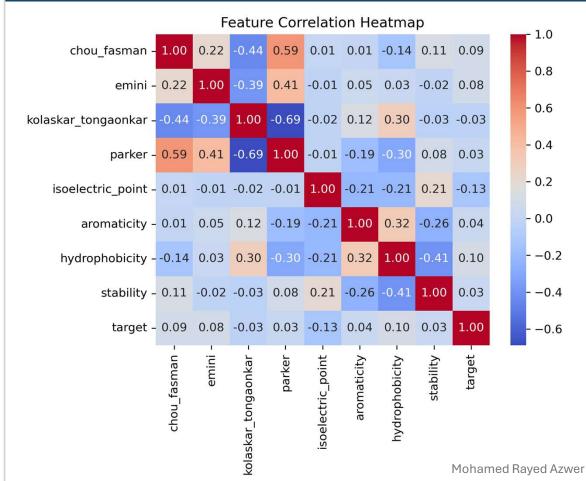
Machine Learning Pipeline

B-Cell epitope prediction for COVID-19 / SARS



Correlation Heatmap

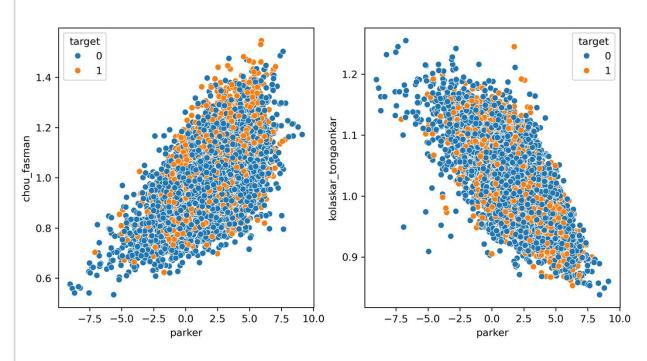


Parker hydrophilicity and Chou-Fasman show moderate positive scores а correlation (+0.59), suggesting regions that are hydrophilic tend to also favour beta-turn structures

hydrophilicity and Kolaskar-**Parker Tongaonkar** scores show a **strong negative** correlation (-0.69), suggesting that highly hydrophilic regions are less likely to be predicted antigenic as Kolaskarbv Tongaonkar.

Comparative Feature Relationship

Parker vs Chou-Fasman and Kolaskar-Tongaonkar

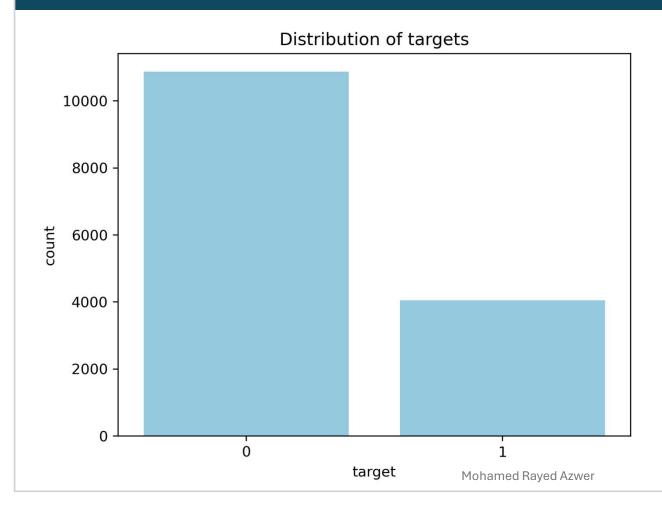


The scatter plots show how hydrophilicity (Parker) interacts with two other feature scores.

Parker and Chou–Fasman showed a positive trend, meaning hydrophilic residues often coincide with regions having a higher Chou–Fasman beta-turn propensity, which represents the probability of a peptide forming flexible, surface-exposed structures.

Parker and Kolaskar–Tongaonkar displayed a <u>negative correlation</u>, suggesting these two heuristics capture distinct physicochemical aspects of epitope behaviour.

Training Dataset Class Distribution For Epitope Prediction



The dataset used in this machine learning model for training was **unbalanced** between targets, 0 (non-epitope), and 1 (epitope)

To ensure a fair evaluation, stratified train-test splitting was employed

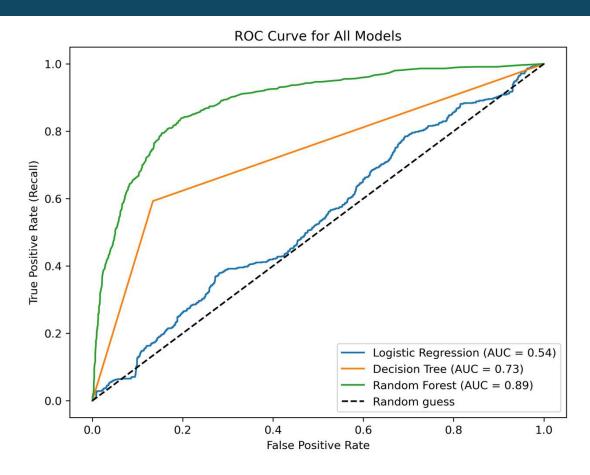
target

0 10865

1 4042

Name: count, dtype: int64

ROC Curve Analysis of Classifiers for Epitope Prediction



Three classifiers were evaluated in the machine learning pipeline: Logistic Regression, Decision Tree, and Random Forest.

Amongst them, the **Random Forest** model performed best, achieving an Area Under the ROC Curve (AUC) of 0.89, indicating strong predictive ability.

In contrast, Logistic Regression showed the weakest performance with an AUC of 0.54, which is roughly equivalent to random guessing.