**Project Report**

**Predictive analysing of biological responses with molecular functions using the classification approach in machine learning**

**Team: Source Forge**

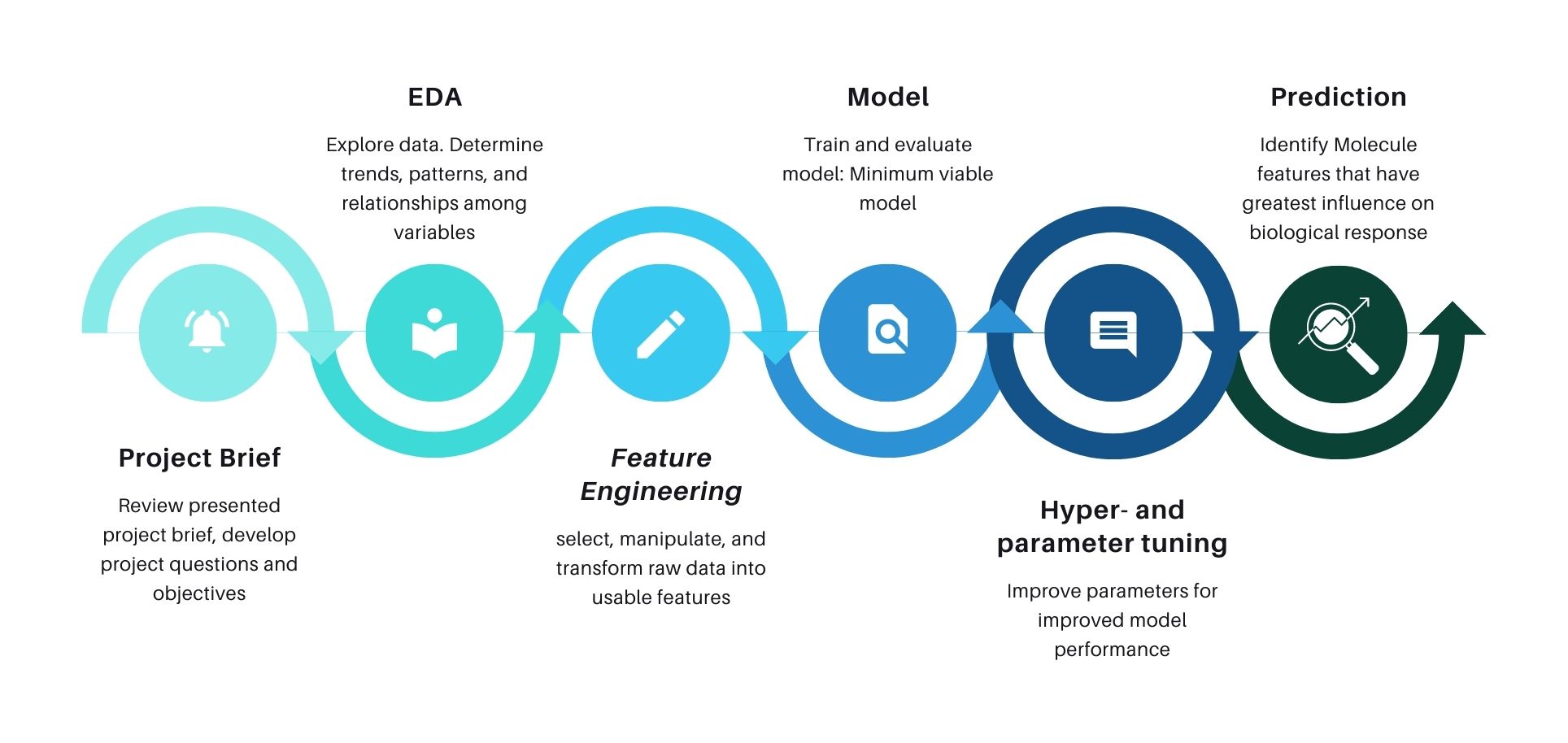
**Introduction**

At the molecular level, many biological responses in organismal systems take place. An accurate understanding of the life sciences depends on an understanding of molecular functions. The catalytic and binding activities that take place at the molecular level are demonstrated by molecular functions. Furthermore, it is well known that living cells can sense mechanical pressure and convert it into biological reactions. Through the development of models and predictive analyses, the machine learning technique is a systematic procedure that seeks to understand the molecular basis of biological activity. The last ten years have seen significant advancements in the field of molecular biology, with significant implications for biotechnology and human health. The classification approach in machine learning, which has until now eluded researchers, offers quick and easy ways to analyse chemical and biological interactions in cells.

**Aim and Objectives**

This project's goal is to develop a strong model that can associate molecular data to a real biological response and predict each molecule's biological activity following supervised machine learning, given a novel test dataset that the model has never seen before.

## **Flow Process**



**Project Brief:** A formal introduction and brief overview of the project plan, asking the right questions and implementing strategies for the data extraction and exploration

**Exploratory Data Analysis (EDA):** Exploring the features of the dataset to determine trends, patterns and relationships among variables to generate insights and informed decision

**Feature Engineering:** This comprises selecting, transforming, and manipulating raw data into usable features. This is an effective technique or procedure because it improves predictive models by highlighting trends and isolating relevant information.

**Modelling**: This includes developing the model, training and testing it, and selecting the most suitable model for the project.

**Hyper and Parameter Tuning:** This entails optimizing the model's parameters for improved performance. This is by far the most crucial component of the process since it involves direct control of the behaviour of the training algorithm and has a substantial impact on the overall performance of the model being trained.

**Prediction**: This is where the project's goal of finding molecular properties that have the greatest influence on biological response is met.

**Model deployment:** The validated and final model should be deployed to the web at this point so that anybody can make live predictions.

## **Data Source**

The dataset used to solve this classification problem was obtained from Kaggle's database, which can be found here. [‘https://www.kaggle.com/c/bioresponse’]

**Data Preparation**

Since this problem involves binary classification, it is expected that the dataset will contain a target feature (a sample can only consist of one of two things) that involves using a range of features (pieces of information in a given dataset) about a molecular function to predict whether or not a biological response occurred. The dataset had 2501 rows and 1777 columns, with 1 target column labelled "Activity" and 1775 columns labelled "D1- D1775" (known as descriptors). Because the dataset had already been standardized, it was only natural to obtain dummies to understand what happened during the normalization. "Here it was discovered that one hot encoding was performed," because the dataset had been normalized. And it was only natural to conduct some exploration to check for imbalance. For this, the plot below which in this case is the activity variable, was analyzed. And it was discovered that there were 317 observations and the class approximation was balanced.

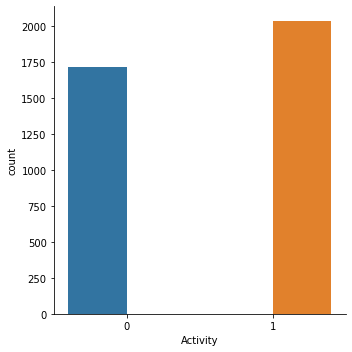
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Figure . Description of the feature distribution

The plot below describes the distribution of features. It tells us that certain values are distributed almost equally in each variable, while others are distributed unevenly. This leads to the assumption that the dataset may contain outliers because the majority of these values will be far from the mean. Moreover, this can also be seen with a box plot and kinetic density estimator (KDE), which will tell us whether the data is right or left-skewed.

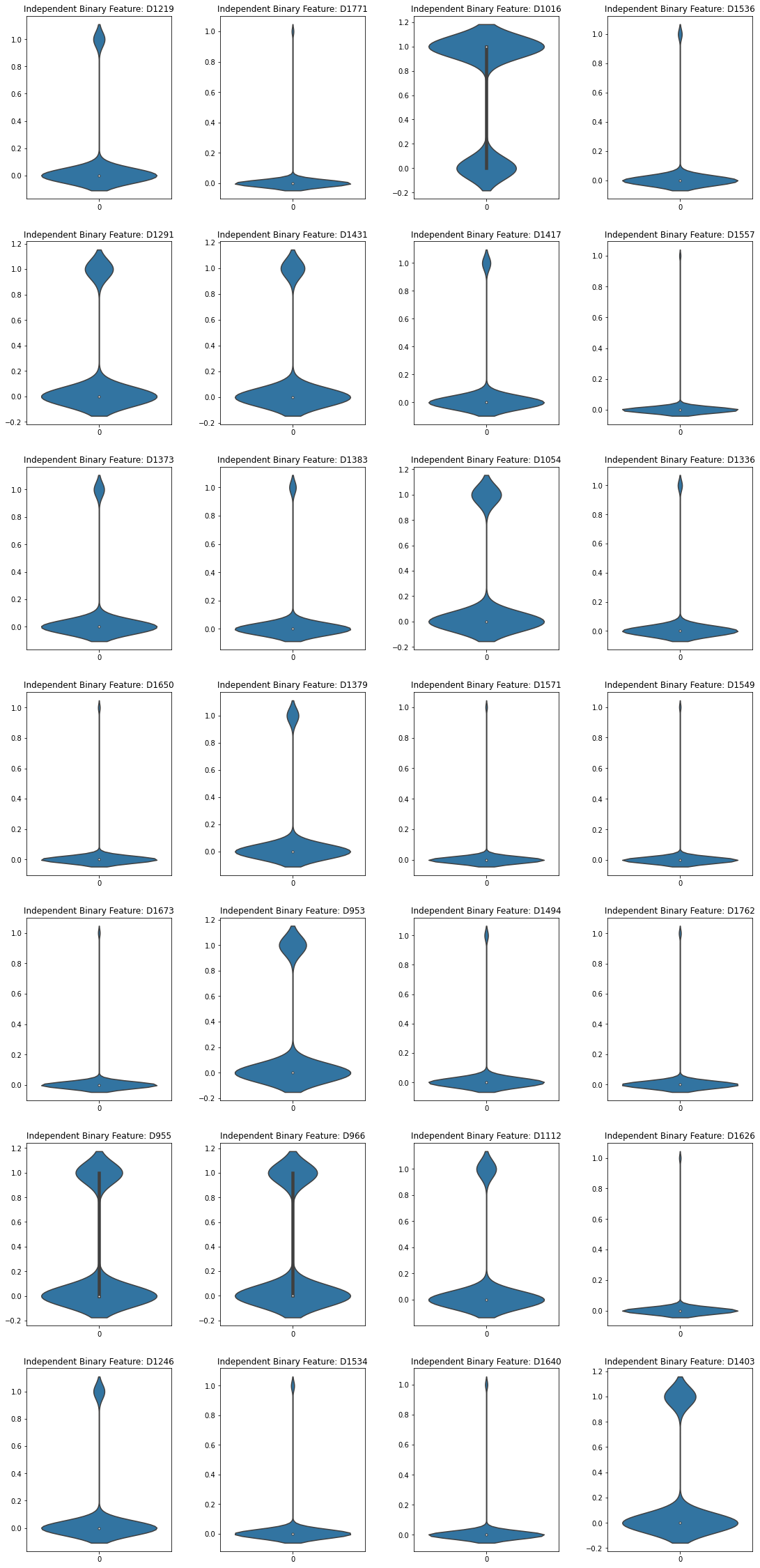


Figure . Description of the dataset skewness through KDE

## **Minimum Viable Model**

"A Minimum Viable Model (MVM), and the process that surrounds it, strives to maximize the early understanding of an ML/AI problem domain in a real-world setting while limiting investment of time and resources," according to (Jeff Bienkowski, 2019). The main question, though, is what this can achieve for us in this project.

This is a planning process in which we attempt to visually evaluate the performance characteristics of the models that can handle the classification problem, as well as the quantity and quality of the data. For example, the various models will be tested, and the various hyperparameters will be tuned to get the best accuracy score. Further to that, a comparison of the models will be performed to determine which has the best score before it is selected as the most suitable model for the dataset, thereby achieving the project's goal.

**Naïve Bayes**

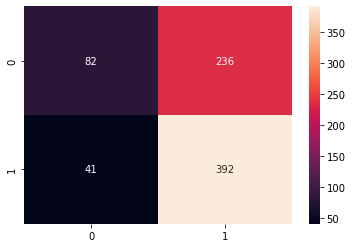


Figure . Naïve Bayes model

The Naïve Bayes model had an accuracy score of 63% (0.6311584553928096), and a log loss error of 12.739586905970421, which should be better. The confusion matrix of the Nave Bayes shows the actual value and predicted value. The Naïve Bayes model did not perform well, with a predicted value of 236 of false positive of classifying the molecule description to the actual value of 0, when it wasn't 0, and a false negative Type II error of 41, predicting 41 values of classification of 1.

On submission of the generated CSV to Kaggle, the score was (lower is better):

* Public score: 13.11529
* Private score: 12.34188

The leading score was 0.37355. It is observed that the model performs better on test data than on validation data. Better models or more feature engineering and hyperparameter tuning was employed to improve the score.

## **Logistics Regression**

The confusion matrix predicts 99 for the False Positive values (Type I Error) of the classified binary of the target value of "0," with a False Negative of 89 for the classification binary of 1. Overall, the model predicted 219 and 344 correct True Positive and True Negative values for the values of 0 and 1, with a log loss error of 8.646297100384551, 84%, which is pretty good.

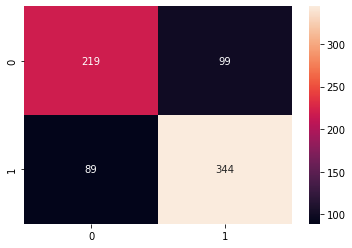


Figure . Logistics Regression

## **K-Nearest Neighbors**

The confusion matrix of the K-Nearest Neighbors model predicts values of 113 and 98 for the false Positive and False Negative (Type I and II Error) of the classification binary values of 0 and 1, respectively, indicating that the model correctly predicted the binary values of 0 and 1 with scores of 219 and 344, with a log loss error of 9.704090777411139 and an accuracy score of 74 % (0.7496671105193076)

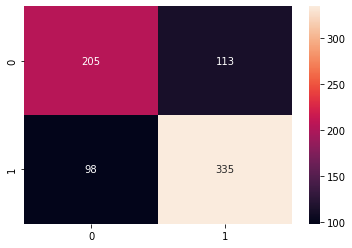


Figure . K-nearest neighbours

## **Support Vector Machine**

Although the Support Vector Machine model outperforms the preceding models in terms of accuracy and prediction, its classified binary value prediction is 223 and 334 for True Positive and Negative, respectively, and 95 and 99 for False Positive and False Negative (Type I & II Error). Surprisingly, its accuracy score is 0.7416777629826897, which is only 74%.

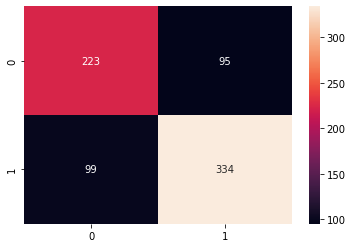


Figure . Support vector machine

## **Decision Tree Classifier**

The Decision Tree Classifier indicates the anticipated values of 219 and 320 respectively for the True Positive and Negative of the target features, whereas its faulty predictions are 99 and 113 respectively; which are the False Negative and Positive (Type I & II Error) (Type I & II Error) with an accuracy score of 0.7177097203728362, which is 71%.

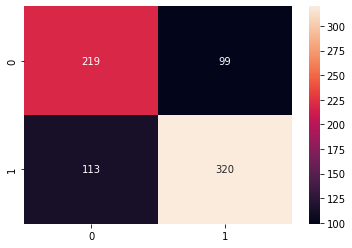


Figure . Decision Tree Classifier

## **Random Tree Classifier**

The Random Tree Classifier model has an accurate prediction of 249 and 361 appropriate predictions of the categorized binary values of 0 and 1. However, a lower score of False Negative and Positive (Type I & II Errors), where the model predicts incorrect values for the target feature demonstrated an accuracy score of 0.8122503328894807, which is 81%.

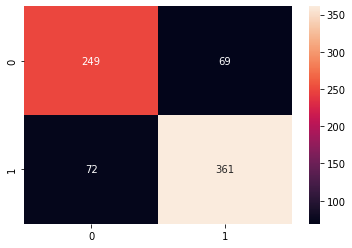


Figure . Random Tree Classifier

So, after looking at the various models and their various performance measurements, it was observed that the Random Tree classifier has the best-predicted outcome, whereas logistics regression has the highest accuracy score. This was evaluated after tuning the hyper-parameter to get the best out of the model scores.

## **The relationship between Internal and External Scores and the time taken to derive the outcome**

The graph below was displayed to show the link between the internal scores and external scores (i.e., the scores from the Kaggle competition on this dataset) and the time spent to derive these scores, as a result of the Kaggle competition. It takes longer to derive the log loss scores of the Nave Bayes model, which in this case is the performance measurement, although internally within the SourceGroup Project phase Bagging Decision Tree required the most time to derive the log loss score. However, internally SourceGroup had better scores.

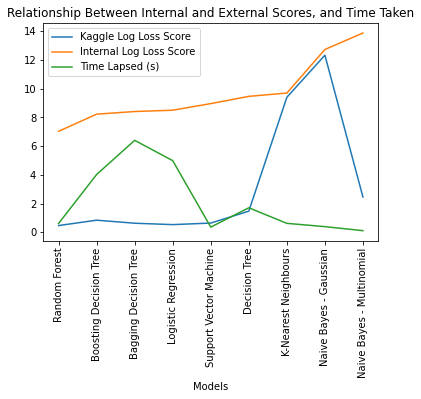


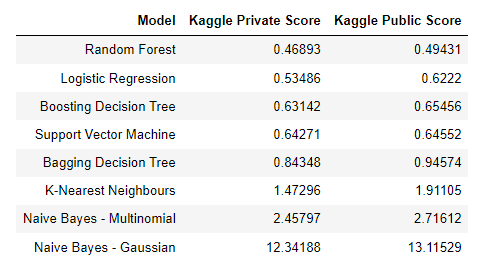
Figure . Relationship between internal and external scores versus the time taken

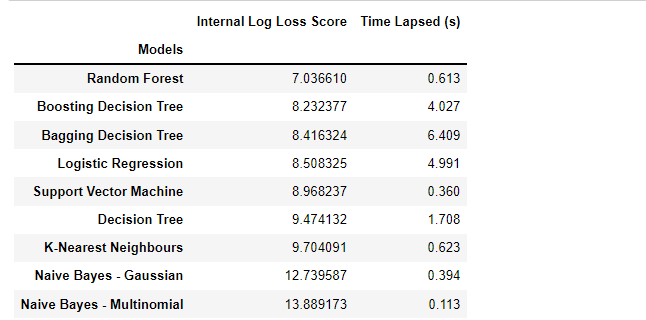
## **Result**

To clarify the results of this experiment, the table below clearly shows the results of the various models for both the Kaggle scores (public and internal). This is the log loss score on submission to Kaggle, as shown below, from best to worst performing (lower is better).

To summarize the findings, it was still thought to be a good option to also perform more feature engineering methods such as Elastic Net regularization, which had an intercept of 0.53366666666666, as the score and intercepts for both options were the same, it can be concluded that the binary columns do not need to be excluded from the regularization process. Also, comparing the scores of the regularization with the model scores for untuned data, it was evident that regularization is marginally beneficial, as it would arrive at number 5 in the table shown above for Kaggle scores. It had:

* Private score of 0.68822
* Public score of 0.69185





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## **Conclusion and Recommendations**

Large biomedical and patient datasets' potential can be unlocked by machine learning, which will contribute to the realisation of a future with improved health care. To find patterns that would be challenging or impossible for even highly skilled individuals to recognise, machine learning makes use of complex algorithms that operate on massive, heterogeneous data sets. Machine learning techniques have completely changed how data is classified, clustered, separated, and novel elements are identified. The classification of biologically complex data is being greatly accelerated by machine learning techniques.

Based on the findings in these analyses, it is highly recommended that a novel and better dataset can be utilized to develop better models for improved predictions to about a 95 per cent accuracy rate. This may open the door to future research on the subject, which would be extremely beneficial to the scientific research community.

# **Team Members**

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