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# TPOT-MLP-SVM: Hybrid Model of Multilayer Perceptron with Support Vector Machines Based on Genetic Programming for Predictive Analysis

Samaila Abdullahi, Saratha Sathasivam*

School of Mathematical Sciences, Universiti Sains Malaysia (USM), 11800 USM, Penang Malaysia

* Corresponding author: saratha@usm.my

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## ABSTRACT

*In recent years, hybrid machine learning models have gained significant attention due to their ability to leverage the strengths of multiple algorithms, improving predictive accuracy and robustness. Despite the performance of the conventional model, there is a need for improvement to achieve a better and more effective model. This paper presents a novel hybrid model, TPOT-MLP-SVM, which combines the Multilayer Perceptron (MLP) neural network and Support Vector Machines (SVM) within the framework of Genetic Programming (GP). The proposed model utilizes TPOT (Tree-based Pipeline Optimization Tool), an automated machine learning (AutoML) tool that applies genetic programming to optimize machine learning pipelines. By integrating MLP for its powerful capacity to model complex nonlinear relationships and SVM for its robust classification capabilities, the TPOT-MLP-SVM model seeks to hybridize the complementary advantages of both techniques. The utilization of genetic programming, the model automatically fine-tunes and selects optimal feature transformations, hyperparameters, and model configurations. The performance of the TPOT-MLP-SVM model is evaluated by real datasets, demonstrating its superiority in predictive accuracy compared to traditional standalone MLP and SVM models. When compared to traditional approaches that rely solely on MLP or SVM, the TPOT-MLP-SVM model consistently outperforms in terms of predictive accuracy, precision, sensitivity, specificity, f1-score, and ROC-AUC. Overall, TPOT-MLP-SVM has the potential to serve as a tool for predictive analysis, as it outperformed conventional models which were guided by genetic programming for early medical diagnosis in healthcare.*

**Keywords:** Machine Learning; Multilayer perceptron; Support vector machines; TPOT-Genetic Programming; Ensemble learning.

## 1 INTRODUCTION

The field of artificial intelligence has significantly developed with the advanced methods in machine learning that hybridize different supervised learning algorithms and meta models for better performance. Artificial intelligence (AI) is the process of mimicking human intelligence using machines that are programmed to learn and retrieve information like the human brain. Due to the advancement in the field of machine learning to properly predict and classify certain predictive problems, Automated machine learning (AutoML) was developed to achieve more reliable and accurate performance which optimizes machine learning pipelines to select the best pipelines combination using genetic programming. Machine learning is a computationally robust analysis-driven system that has extensively advanced due to its capability to handle complex tasks. The TPOT-MLP-SVM hybrid model is a novel predictive analysis approach that leverages the strengths of Multilayer Perceptron (MLP) and Support Vector Machines (SVM) with Genetic Programming (GP) for improved performance in complex datasets. This model combines MLP's learning from non-linear relationships with SVM's robustness in classification tasks, optimizing the model architecture and hyperparameters using Genetic Programming. Compared to traditional models, the TPOT-MLP-SVM approach offers optimization efficiency, better predictive accuracy, and flexibility for a wide range of problems. This evolutionary approach leads to more robust and scalable predictive models, making it more effective than traditional models.

Machine learning (ML) is regarded as one of the modern methods for predicting, recognizing, and making decisions without the intervention of humans [1]. According to [2] machine learning is a computational method for automated learning from historical data that improves the performance of the output for more accurate predictions. Machine learning algorithms learn data without depending on a predetermined equation [3]. The multilayer perceptron (MLP) is one of the most used artificial neural networks (ANNs) that consists of multiple layers of nodes and fully connected neurons with nonlinear activation functions. Machine learning tasks such as classification, regression, and pattern recognition consistently utilize MLPs. Multilayer Perceptron consists of an input layer, hidden layers, and an output layer [4]. MLP has been demonstrated to be highly effective when applied to nonlinear problems.

Support vector machines (SVMs) are robust classifiers that have been successfully applied to a wide variety of pattern recognition challenges. Also, it has been shown to be effective in the field of handwriting recognition [5]. Support Vector Machines (SVMs) have become widely used in domains such as computational biology, economics, and text categorization to solve classification and regression issues. This is because of several factors, including the ability to train and predict on large datasets using novel mathematical optimization approaches, to model non-linear distributions kernel functions where use separate all the data points, and, most importantly, the using computational learning theory [6]. It has proven support vector machines are very effective in numerous classification scenarios such as digit recognition and text mining [7]. SVM with RBF performed better than other kernel functions in terms of accuracy [8]. In [9] propose a new method for predicting financial hardship using an SVM ensemble with kernel, and the findings demonstrate that the SVM ensemble approach outperforms individual classifiers when utilized alongside feature selection strategies.

The ensemble learning algorithm refers to the learning ability of several base models and hybridizes their performance to produce the final evaluation of the model. The significance of the ensemble learning model is to improve robustness, stability, and accuracy of predictions. According to [10] The computational effort and configuration noises for VLSI circuit variants can be reduced with the help of the developed hybrid model. The main aims of the ensemble learning algorithm are to combine a set of diverse predicted models to achieve an optimal model that produces accurate and reliable prediction results [11]. Based on statistical metrics, ensemble-learning algorithms outperform individual classifiers in terms of prediction accuracy [12]. The aims of this research are as follows: (1) To develop a hybrid Model of Multilayer Perceptron with Support Vector Machines Based on Genetic Programming for Predictive Analysis. (2) To utilize genetic programming (GP) for hyperparameter optimization to improve model performance. (3) To integrate the ensemble learning algorithm and meta-model to achieve optimal model. and lastly, (4) to evaluate the proposed hybridized model with conventional models based on accuracy, precision, sensitivity, specificity, F1-score, and ROC-AUC. The proposed model has improved in performance, robustness, and ability to predict more accurately. The results obtained demonstrate that the proposed model has outperformed the conventional models based on accuracy, precision, and the ROC-AUC curve.

## 2 MATERIAL AND METHODS

### 2.1 Multilayer Perceptron Algorithm

A multilayer perceptron (MLP) is a type of neural network algorithm that employs the back-propagation method for supervised learning [13]. Figure 1 shows that the MLPs are fully connected with five layers architecture, including input, hidden, and output layer, in which each layer is connected to all other layers in the structure.

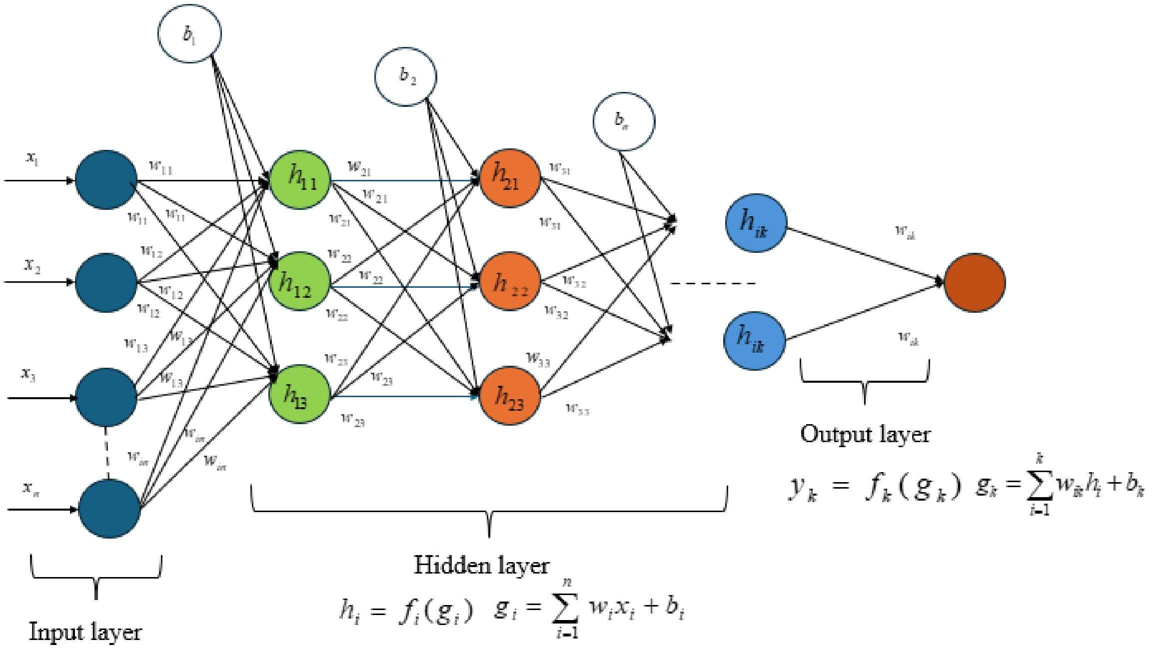


Figure 1: Multilayer perceptron Architecture

Figure 1 demonstrates the architecture multilayer perceptron. $x_i, h_i$ and $y_k$ represent the node expression in the input layer, hidden layer, and output layer, respectively. Equation (1) shows how the hidden layer values are calculated and pass through the output layer.

$$h_i = f_i(g_i)$$

subject to

$$g_i = \sum_{i=1}^{n} w_i x_i + b_i \tag{1}$$

where $h_i$ is the hidden layer, $f_i$ activation function , $w_i$ weight, $b_i$ bias, and $g_i$ weighted sum from the input to the hidden layer.

$$y_k = \begin{cases} 1, \sum_{i=1} w_k x_k + b_k > 0 \\ 0, \sum_{i=1} w_k x_k + b_k \le 0 \end{cases} \tag{2}$$

where $y_k$ represent the output value, $x_i$ input features , $w_i$ weight, and $b_i$ bias.

## 2.2 Support Vector Machines Algorithm

Support vector machines (SVMs) are also a supervised learning algorithm used for classification and regression. Support vector machines create decision boundaries that separate data points into higher dimensional space. The main goal is to maximize the hyperplane that separates the data points. The margin is the distance between the hyperplane and the support vectors. When samples are not linearly separable, the kernel function was applied to estimate the input space into higher dimensional space [14]. The support vector machine (SVM) is a notable and popular classification technique with adequate generalization capabilities, with few local minima, and less dependence on a selected few parameter [15]. The idea of SVM classifiers can be defined as follows, supposing there are features for the training set $(x_i, y_i)$ where $i = 1, 2, 3, ..., n$ and $x_i = (x_1, x_2, ..., x_n) \in R^n$ is $n$-dimensional feature space and $y_i \{-1, +1\}, \forall i \in \{1, 2, 3, ..., n\}$. If the prediction is close to the positive class, then $y_i$ is +1, and if the prediction is close to the negative class, then $y_i$ is -1. The hyperplane that separates the class labels can be defined as $\alpha_i x_i + \omega = 0$ , where $\alpha$ is the weight, $x$ is the input features, and $\omega$ is the bias. The corrected classified input features satisfy the prediction function as:

$$y_i (\alpha_i x_i + \omega) \ge 1 \tag{3}$$

The generalized function that separates the hyperplane and makes predictions is given as:

$$h(x_i) = \begin{cases} +1 \quad if \quad y_i (\alpha_i x_i + \omega) \ge 1 \\ -1 \quad if \quad y_i (\alpha_i x_i + \omega) \le -1 \end{cases} \tag{4}$$

Therefore, our goal is to increase the distance between the hyperplanes while keeping the data out of the margins. The margin that separates hyperplane and support vectors is given as:

$$\min_{\alpha,\omega} \frac{1}{2}\|\alpha\|^2$$

Subject to

$$y_i(\alpha_i x_i + \omega) \geq 1 \tag{5}$$

For nonlinear problems, support vector machines use the kernel technique to solve the nonlinear problem and transform data points into higher dimensional space. The idea of applying a kernel is to transform non-separated data into $n$-dimensional space that will linearly separate higher dimensional space. The prediction function of kernel SVM can be given as:

$$h(x_i) = \sum_{i=1}^{n} \alpha_i y_i k(x_i, x_j) + \omega \tag{6}$$

where $k(x_i, x_j)$ kernel function, $\alpha$ is the optimal weight, $x$ is features vector, $y$ is feature class label, and $\omega$ is the bias. The cost function that minimizes the error to evaluate how well the model performed in classifying data points is given as:

$$j(\alpha,\omega) = \lambda \frac{1}{2}\|\alpha\|^2 + \frac{1}{2}\sum_{i=1}^{n} \max(0, 1 - y_i(h(x))) \tag{7}$$

Parameters $c$ and $\gamma$ are yet to be determined. Hence, it is still needed to apply hyperparameter optimization to generate the best parameter values. Parameters $c$ and $\gamma$ are yet to be determined. Hence, it is still needed to apply hyperparameter optimization to generate the best parameter values.

## 2.3 TPOT-Genetic programming

Tree-based pipeline optimization tool (TPOT) is an automated machine learning tool that utilizes genetic programming to optimize machine learning pipelines. It dives into a wide range of pipeline configurations to find the best parameter combination for a given dataset. It also automates data preprocessing and hyperparameter optimization. Genetic programming executes an intelligent search across machine learning pipelines using supervised learning algorithm to enhance model performance [16]. TPOT evaluates the complexity of the pipeline while optimizing its accuracy [17]. Figure 2 represents the implementation stages of the tree-based pipeline optimization via genetic programming.

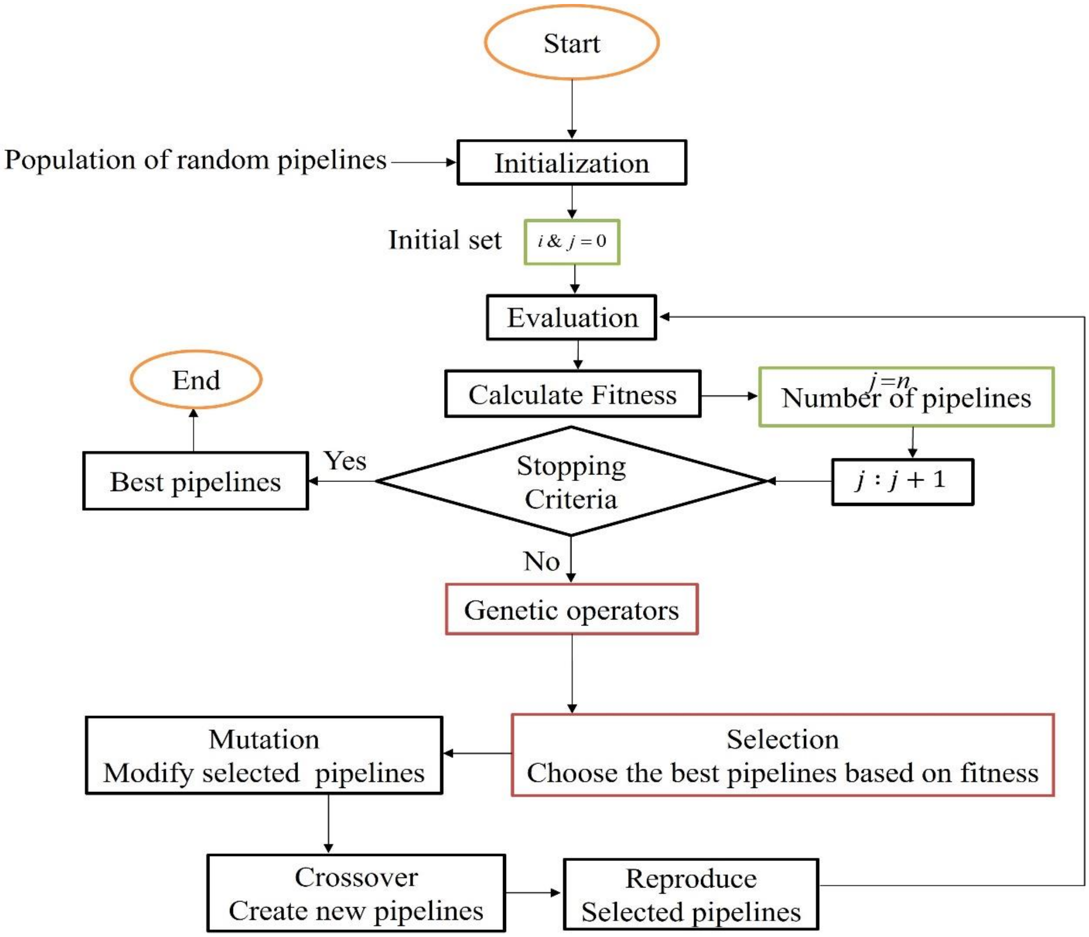


Figure 2: TPOT Architecture using genetic programming

## 2.4 Ensemble Learning Algorithm

Ensemble learning is a machine learning technique that aims to improve predictive probabilities by hybridizing multiple homogenous base learning algorithms to achieve more accurate and reliable results. The hybrid model will improve the model's performance compared to the individual learning algorithm. Most problems in machine learning now use ensemble techniques as the gold standard. These techniques train many models and combine their predictions to boost the performance of a single model's predictions [18]. The term "output fusion" is used to describe the procedure of combining the predictive probabilities of many "base models" into a single probability. The ensemble methods are subdivided into sequential and parallel ensemble methods. Ensemble learning is a machine learning technique that aims to improve predictive probabilities by hybridizing multiple homogenous base learning algorithms to achieve more accurate and reliable results.

## 2.5 Proposed Hybrid Model Using TPOT-Genetic Programming

Machine learning is one of the notable fields in artificial intelligence. It was proven that knowledge extraction can be achieved using predictive analysis. To improve predictive analysis, we employed an ensemble learning and genetic programming for parameter optimization.in this section we use real dataset to evaluate the effectiveness and robustness of TPOT-MLP-SVM and compare with conventional model of MLP-SVM, SVM and MLP. The real dataset will slip into 80% and 20% for training and testing. We apply preprocessing techniques using exploratory data analysis (EDA), principal component analysis (PCA) and Normalization to clean the dataset from unwanted features and noise for improving model performance. The Ensemble learning algorithm was utilized to hybridize and improve model performance as compared with individual models. Pursuing that, the below figure 3 represents the hybridized model of TPOT-MLP-SVM that will learn the relationship between the features of the real dataset predict optimal model.

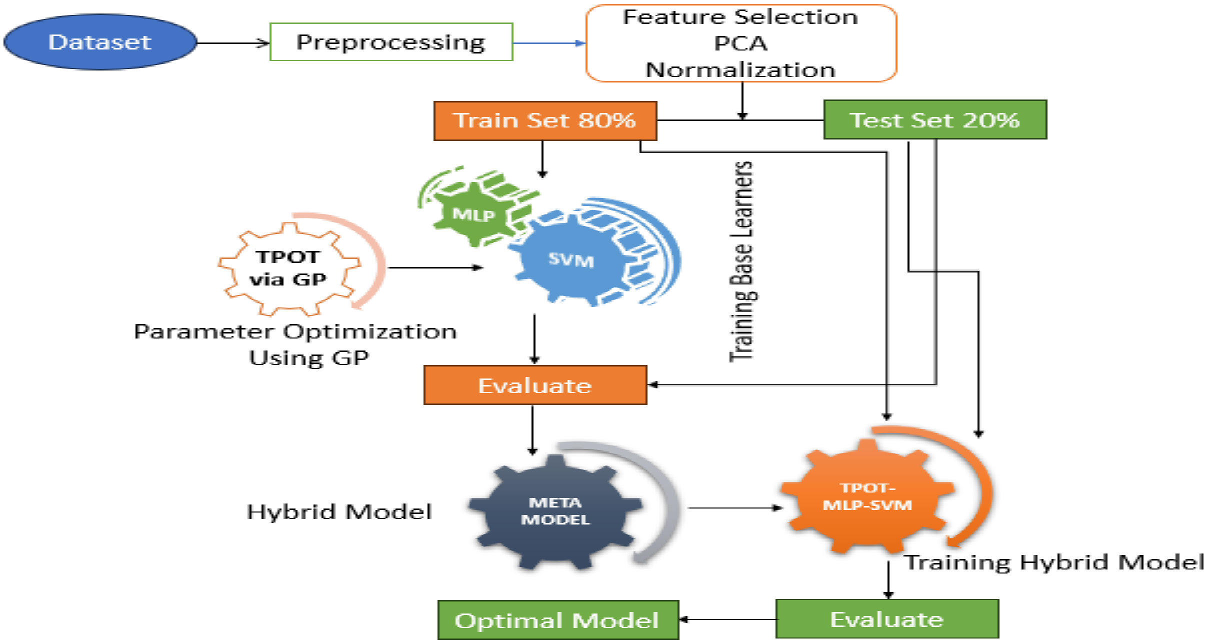


Figure 3: Architecture of the proposed hybrid model using genetic programming

The hybridized model aims to improve the model performance to obtain the best optimal model by combining predictive probabilities performance of base leaners as input features to the meta-model for predicting the final model performance. The effectiveness and robustness of the hybrid model was achieved by stacking TPOT-MLP-SVM. The standard performance evaluation metrics for predictive analysis were used to evaluate the model performance.

## 2.6 Implementation Setup

Anaconda Navigator via Jupiter Notebook version 6.5.2 software was used to perform the hybridized model of TPOT-MLP-SVM using real datasets. In this paperwork, we hybridized two base learning algorithms using ensemble machine learning algorithms due to its stability and effectiveness to achieve batter accuracy than single learning algorithms. The hybridized model architecture of multilayer perceptron (MLP) and support vector machines (SVMs) are base learning algorithms and the meta model that merges the predictions of the base model and predict the outcome as shown in Figure 3. This part of our proposed work will evaluate the performance of each phase using the standard classification performance metric. The training phase involves finding the best parameter using TPOT-Genetic programming and stratified cross validation. While the testing phase provides an optimal model within the desired parameter value and meta model. The performance evaluation metrics involved in this phase are Precision, Sensitivity, Specificity, f1-score, Accuracy, and ROC_AUC curve.

## 2.7 Performance evaluation metric

The performance of our proposed model is analyzed after executing a series of coding using Python programming techniques. The performance evaluation metric is very vital in classification models to have better understanding of how well the model performed. Several performance evaluation metrics have been used to explore and analyze different levels of model performance. In this paperwork, we employ the standard performance evaluation metrics for classification algorithm, which include accuracy, precision, sensitivity, specificity, F1-score, and the ROC-AUC curve. The metrics used are as follows:

The accuracy is the friction of correctly classified features to the total number of correctly identified features. The accuracy is constrained to be between [0, 1], where [1] indicates that all features in the class were accurately predicted and [0] indicates that no features were successfully predicted [14]. The model accuracy is given as:

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \tag{8}$$

The precision is the percentage of correctly classified features compared to all features assigned to that class. The precision is constrained to be between [0, 1], where [1] indicates that all features in the class were accurately predicted and [0] indicates that no features were successfully predicted [19]. The precision is given as:

$$Precision = \frac{TP}{TP + FP} \tag{9}$$

The sensitivity, also known as the true positive rate (TPR), is the percentage of positively classified features that are correctly classified, and all features belong to the positive class. The recall is constrained to be between [0, 1], where [1] indicates that all features in the class were accurately predicted and [0] indicates that no features were successfully predicted [19]. The sensitivity is given as:

$$Sensetivity = \frac{TP}{TP + FN} \tag{10}$$

The F1 score is constrained to be between [0, 1], where [1] indicates that all features in the class were accurately predicted and [0] indicates that no features were successfully predicted [20].

$$F1 - Score = 2 * \frac{precision * recall}{precision + recall} \tag{11}$$

ROC-AUC curve is the predictive probability curve generated by TRP and FPR using different threshold values to measure the capability of learning model to distinguish between class labels. When the roc-auc is greater than 0.5 then there is a possibility of learning model to classify correctly. The rou-auc is constrained to be between [0, 1], where [1] indicates that all features in the class were accurately predicted and [0] indicates that no features were successfully predicted [21]. The ROC-AUC is given as:

$$ROC - AUC = \frac{TPR}{FPR} \tag{12}$$

True positive (TP), true negative (TN) and true positive rate (TPR) are used to identify correct classification in the confusion matrix, while false positive (FP), false negative (FN) and false positive rate (FPR) are also used to identify misclassification of the sample features.

## 3 RESULTS AND DISCUSSION

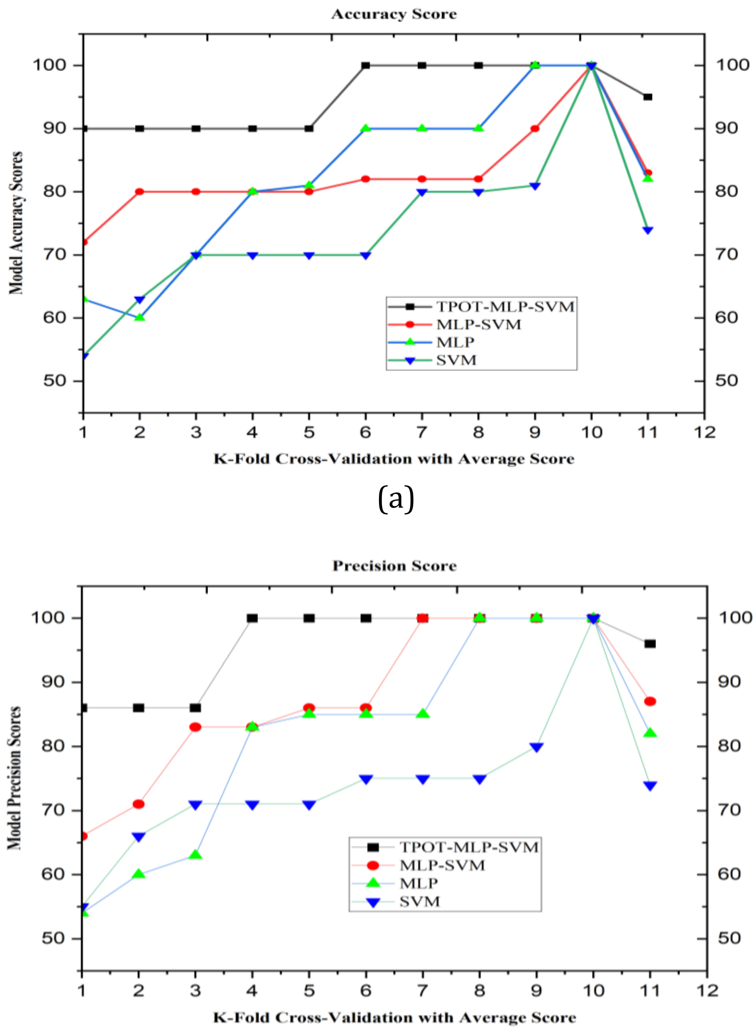
This research work proposed a hybridized TPOT-MLP-SVM model for predictive analysis and compared it with the conventional models. We used real datasets to evaluate the performance of our proposed model. The result of the proposed model was compared with conventional model of MLP-SVM, MLP and SVM that uses default parameters without applying cross-validation and hyperparameter optimization approach in building the predictive model. The architecture of the proposed model is shown in Figure 3, The findings are analyzed based on the criteria used to evaluate the proposed and conventional models. The proposed model of TPOT-MLP-SVM was developed and validated using CBC Covid-19 dataset to predict patients with COVID-19 using patients' clinical information. A data set of 103 hospitalized patients was obtained from Kaggle database of machine learning repository. the dataset was collected between 12 April and 31 August 2020 at Dhaka Medical College Hospital, Bangladesh which is approved by the Hospital Ethical Committee.

The dataset contained 13 features with 103 observations out of which 59.22% were recovered and 40.78% were not recovered. Preprocessing techniques were used to have clean and vital information from the dataset after which 11 features were used for the analysis. The CBC dataset was used to evaluate the performance of our proposed model and compare it with the conventional model based on accuracy, precision, sensitivity, specificity, F1-score, and the ROC-AUC curve. The dataset is divided into a standard ratio of 80:20 for use in machine learning models, where 80% of the dataset will be used for training, validation, and 20% for testing the model's performance [22]. The results of our proposed and classical models are shown in Table 1 and Figure 4 & 5 respectively. The proposed model has achieved better evaluation metrics during training, validation, and testing for the final prediction. The capability of the model to appropriately distinguish between recovered and unrecovered features on the target output determines its accuracy.

Table 1: Averaging performance analysis for Complete Blood Count (CBC) COVID-19 Dataset using 10k-fold cross validation.

| Models | Accuracy | Precision | Recall | F1-Score |
|---|---|---|---|---|
| TPOT-MLP-SVM | 0.96 | 0.96 | 0.97 | 0.95 |
| MLP-SVM | 0.87 | 0.87 | 0.92 | 0.85 |
| MLP | 0.91 | 0.82 | 0.90 | 0.82 |
| SVM | 0.80 | 0.74 | 0.88 | 0.74 |

Table 1 demonstrates the average results of the performance metrics of standalone model and hybrid model performance for the predictive analysis using k-fold cross-validation. The utilization TPOT (Tree-based Pipeline Optimization Tool) through genetic programming approach in this model are meant for hyperparameter optimization. The results are for testing accuracy, precision, sensitivity, and F1-Score of TPOT-MLP-SVM, MLP-SVM, MLP, and SVM models. The proposed model outperformed when compared to the other three models for the whole evaluation metric because it's have been proving that hybrid model integrated with AutoML has better performance than standalone model. The proposed model achieved low misclassification error of 4% follow by MLP with 9% which outperformed MLP-SVM by achieving 13% error while SVM attained 20% misclassification error.

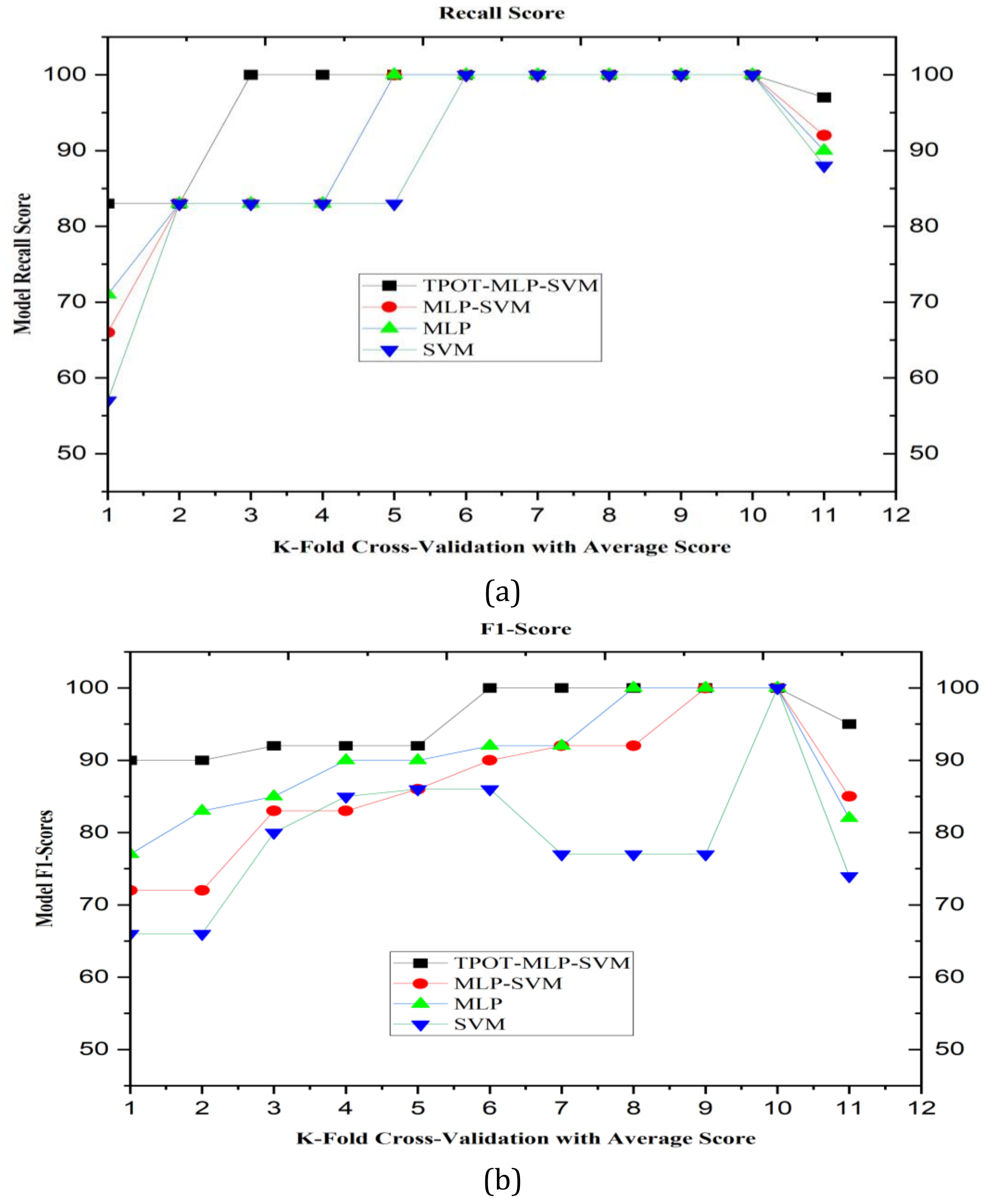


(a)

(b)

Figure 4: Performance Evaluation Metrics for the Proposed and conventional models on CBC COVID-19 dataset using k-fold cross validation (a) Accuracy (b) Precision

Figure 4(a) and (b) represent the Accuracy and precision for TPOT-MLP-SVM, MLP-SVM, MLP and SVM models. The proposed hybrid model outperformed the three models. The results illustrate that the Accuracy values for MLP-SVM, MLP and SVM are lower compared to TPOT-MLP-SVM model which achieved 96% compared to the other models that achieved 87%, 91%, and 80%, by taking the averages of k-fold cross-validation. Accuracy measures the overall correctness of a predictive model by evaluating how many predictions were correct out of the total predictions made. In comparison with existing models according to [23] utilized machine learning to predict complete blood count covid-19 using DT, SVM and KNN which achieved 91%, 90% and 90%, The proposed approach outperformed all three models in terms of accuracy because it utilized individual models. The precisions using k-fold cross-validation for TPOT-MLP-SVM, MLP-SVM, MLP and SVM models. Our proposed model achieved 96% precision outperforming MLP-SVM, MLP and SVM models and follow by MLP-SVM with 87% and MLP attained 8% while SVM attained 94% precision score and when comparing with the existing model according to [24] proposed gradient boosting to predict complete blood count covid-19 and the method attained 89.8% precision score lower than our proposed model The precision measures how well the model identifies all actual positives when precision is high the model will perform better.



(a)

(b)

Figure 5: Performance Evaluation Metrics for the Proposed and conventional models on CBC COVID-19 dataset using k-fold cross validation (a) Recall and (b) F1-Scores.

Figure 5(a) and (b) represent the graphical score of recall and F1-score using k-fold cross-validation for TPOT-MLP-SVM, MLP-SVM, MLP and SVM models. The proposed model outperformed MLP-SVM, MLP and SVM models which have low recall compared to TPOT-MLP-SVM with 97% recall score followed by MLP-SVM with 92% score while MLP attained 90% and SVM score low recall of 88%. This shows that our proposed model is more robust and more effective than conventional models. When comparing with existing models in [25]proposed learning approach to predict CBC Covid-19 dataset to detect patient with covid-19 utilizing MLP, SVM and XGBoost learning algorithms and approach attained 95% F1-scores each for all the algorithms which demonstrate that the proposed model correlated with the existing in terms of F1-score. The proposed model outperformed MLP-SVM, MLP and SVM models which low F1-score compared to TPOT-MLP-SVM with 95% recall score followed by MLP-SVM with 85% score while MLP attained 82% and SVM score lower of 74%. This shows that our proposed model is more robust and more effective than conventional models. Compared with existing models in [26] proposed learning approach to predict CBC Covid-19 dataset to detect patient with covid-19 utilizing MLP, SVM and XGBoost learning algorithms and approach attained 95% F1-scores each for all the algorithms which demonstrate that the proposed model correlated with the existing in terms of F1-score. Therefore, the proposed model has proven its robustness, effectiveness and capability to predict all classes correctly compared to other hybrid models. However, by utilizing genetic programming approach for hyperparameter optimization with k-fold cross validation techniques, the predictive analysis model has been improved and was able to achieve 97% correct predictive scores.

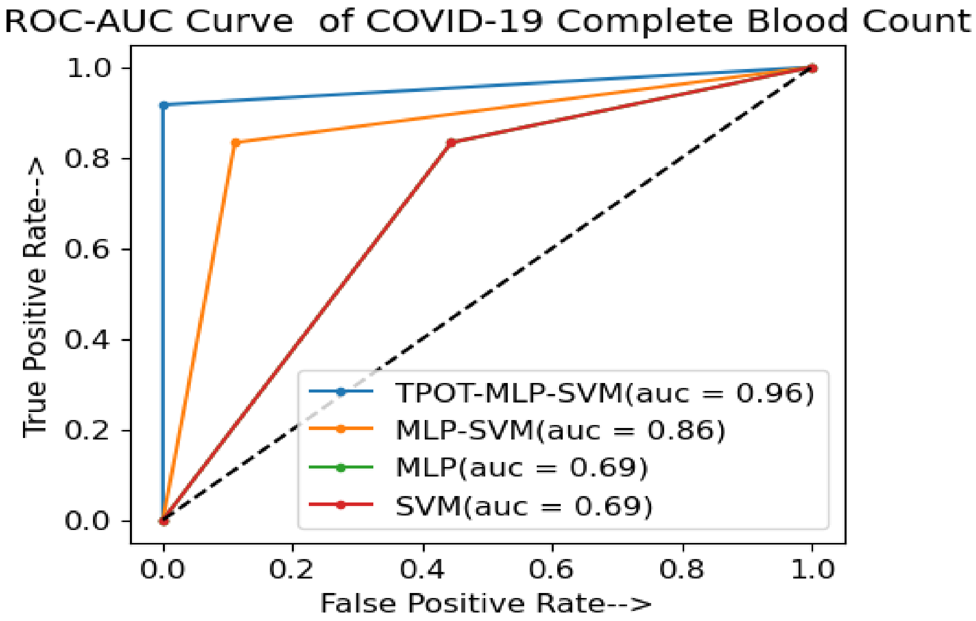


Figure 5: ROC-AUC Curve Metric of the proposed and conventional Models.

Figure 5 Receiver Operating Characteristics Area The under-the-curve (ROC-AUC) curve is plotted to determine the quality of the classification models. the auc-auc curve with different threshold values. The rou-auc for TPOT-MLP-SVM outperformed the conventional model. The result demonstrates that the roc-auc values score by MLP-SVM, MLP, and SVM are lower compared to the TPOT-MLP-SVM which score highest rou-auc score. The rou-auc of proposed model has effectively detected the recovered and unrecovered patients with COVID-19 cases. The better the score of rou-auc, the more effectively the model can predict between the classes.

## 4 CONCLUSION

In this paperwork, we present a workable strategy for creating the perfect prototype. This research used hybridized learning models TPOT-MLP-SVM for predictive analysis. The results demonstrate that all four models did better than expected to meet the required objectives. When the hybridized model makes use of genetic programming and k-fold cross validation, it outperforms the other conventional models. The application of genetic programming in the training phase demonstrates that the predictive analysis process is more effective at diversifying the input features and searching for the best parameter that will achieve higher accuracy. The contribution of k-fold cross-validation is that it is designed to train all datasets to address issues of overfitting and underfitting during the training phase to determine optimal solutions. The effectiveness and robustness of the model were then successfully compared to other approaches. In this research, the result achieved by TPOT-MLP-SVM outperforms the MLP-SVM, MLP and SVM models using performance assessment measures. To enhance the robustness and effectiveness of the machine learning models, we hybridized the outputs of the base models as inputs to the proposed model using an ensemble learning algorithm. The TPOT-MLP-SVM architecture's stability and efficacy provide insight into possible dynamics for use in real-world problems. For instance, considering the data mining techniques, the proposed model extracted the best features for categorizing the recovered occurrence based on the total blood count associated with COVID-19. Our model achieves good performance and accuracy. Regardless of its better performance, the proposed method has limitations that must be recognized. When there are many outputs in the target class, the proposal must be modified to fit the predictive analysis. In future, this approach can be improved further by applying other ensembles learning algorithms, metaheuristic algorithms, and hyperparameter optimization techniques can be used to improve the predict complete blood count covid-19 dataset more efficiently.

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