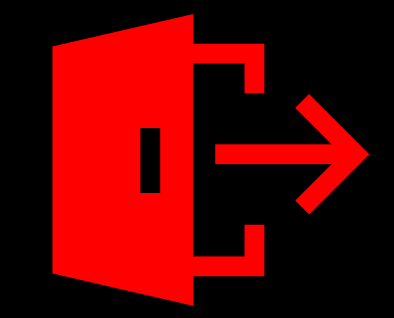


Gradient Boosting-based Prediction of Interactome Genes in Periodontitis With Cardiovascular Disease

AMIT PAWAR¹, PRADEEP KUMAR²

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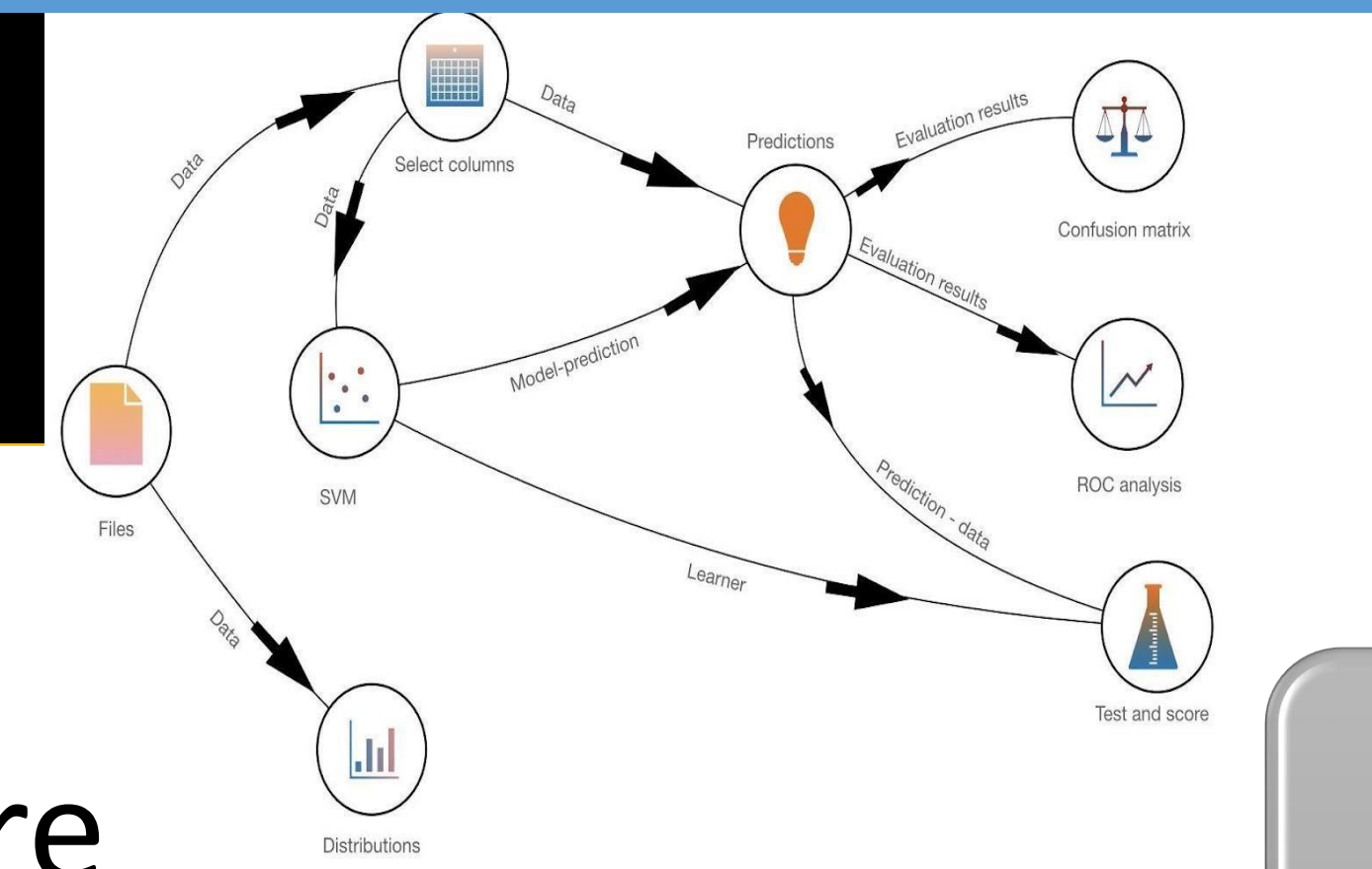
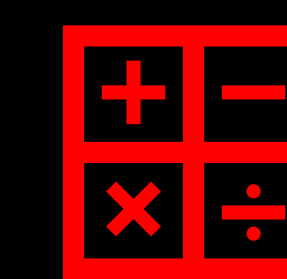


Introduction

This research delves into the intersection of machine learning and cardiovascular medicine, leveraging advanced techniques to explore the complex relationship between periodontitis and cardiovascular disease. The study aims to predict genes associated with both conditions, offering insights into genetic intricacies for early detection and personalized interventions. This interdisciplinary approach not only holds promise for precision medicine but also fosters collaboration between medical and computational fields, contributing to a deeper understanding of the connections within cardiovascular health and periodontal disease.

To develop machine learning algorithm to interactome genes in periodontitis with cardio vascular disease

1) To develop a data-driven prediction model for PD with cardiovascular disease using an advanced ML model. 2) To identify novel risk factors for prediction.



MATERIALS AND METHODS



The Gene Expression Omnibus (GEO) database

Gene expression datasets for periodontitis

Top 250 differential gene expression genes were identified using GEO2R TOOL

Gradient boosting was used to predict the hub genes

Gene ontology analysis were done using enrichr

Using gene mania , interactome was built for DEGS and hub genes were identified .

Transcriptomics data labeled, and separated into 80%training and 20%testing portions using Random Forest, neural networks, SVM.

Accuracy was predicted. Confusion matrix and ROC curve was generated.

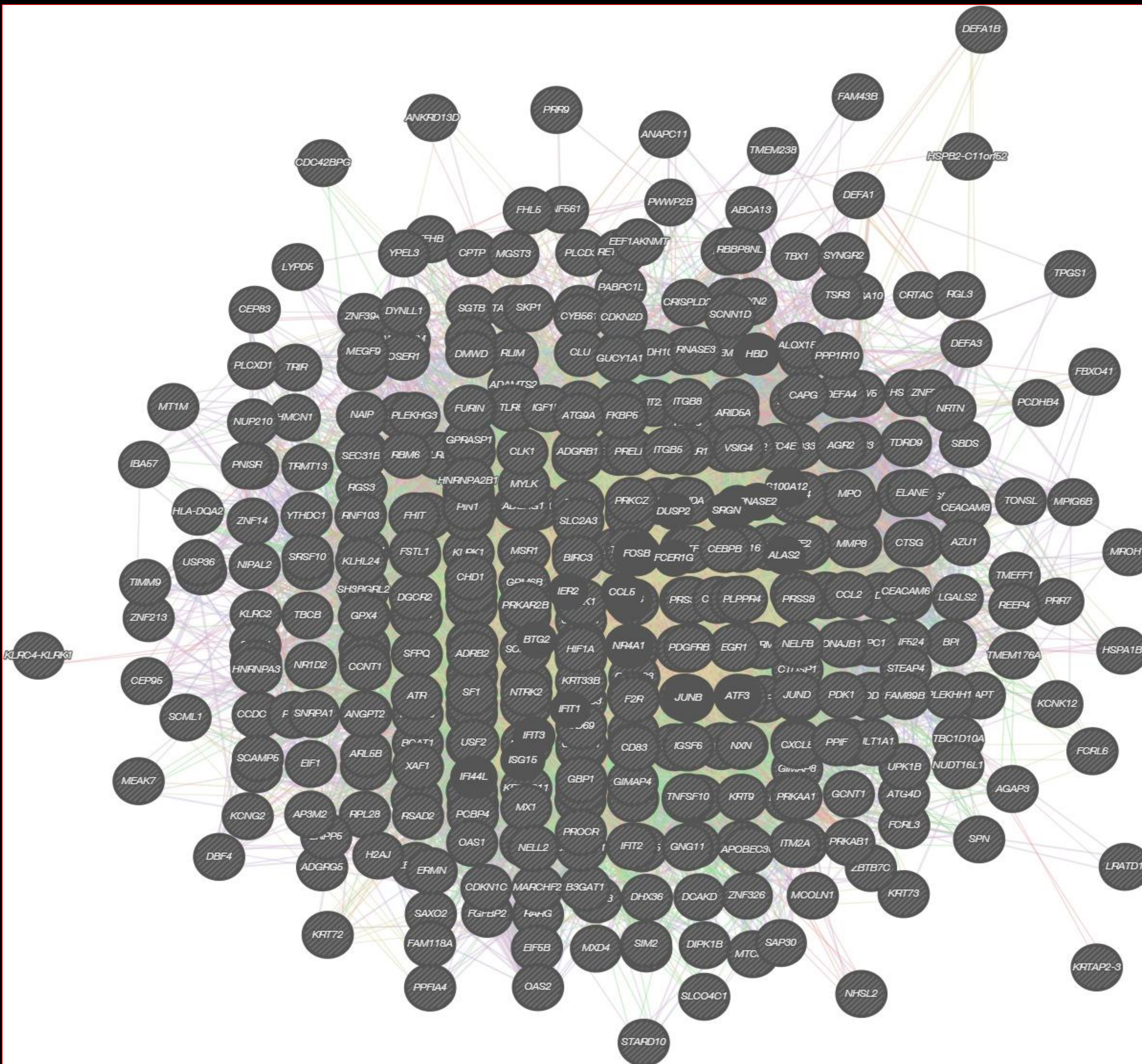
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RESULTS



MODEL	AUC	CA	F1	Precision	Recall	LogLoss	Specificity
Random Forest	1.000	1.000	1.000	1.000	1.000	0.097	0.498
Neural Network	1.000	1.000	1.000	1.000	1.000	0.021	1.000
SVM	0.938	1.000	1.000	1.000	1.000	0.387	1.000

Table 1: Model performance of all algorithms

		Predicted		Σ
		hub	non hub	
Actual	hub	97.5 %	11.1 %	81
	non hub	2.5 %	88.9 %	18
Σ		81	18	99

Table 2: Confusion Matrix with Decision Tree Model

		Predicted		Σ
		hub	non hub	
Actual	hub	100.0 %	0.0 %	81
	non hub	0.0 %	100.0 %	18
Σ		81	18	99

Table 3: Confusion matrix with Neural Network

		Predicted		Σ
		hub	non hub	
Actual	hub	97.5 %	11.1 %	81
	non hub	2.5 %	88.9 %	18
Σ		81	18	99

Table 4: Confusion matrix with Random Forest Model

After employing advanced machine learning techniques to investigate the intricate link between periodontitis and cardiovascular disease, this research has successfully identified potential genes associated with both conditions. The predictive models developed in this study offer valuable insights into the genetic factors underlying the complex relationship between periodontal health and cardiovascular well-being. The top differentially expressed genes for periodontitis and CVD and hub genes were identified as ***JUNB***, ***NR4A***, ***ZFP36***, ***ATF3***, and ***FOSB***.

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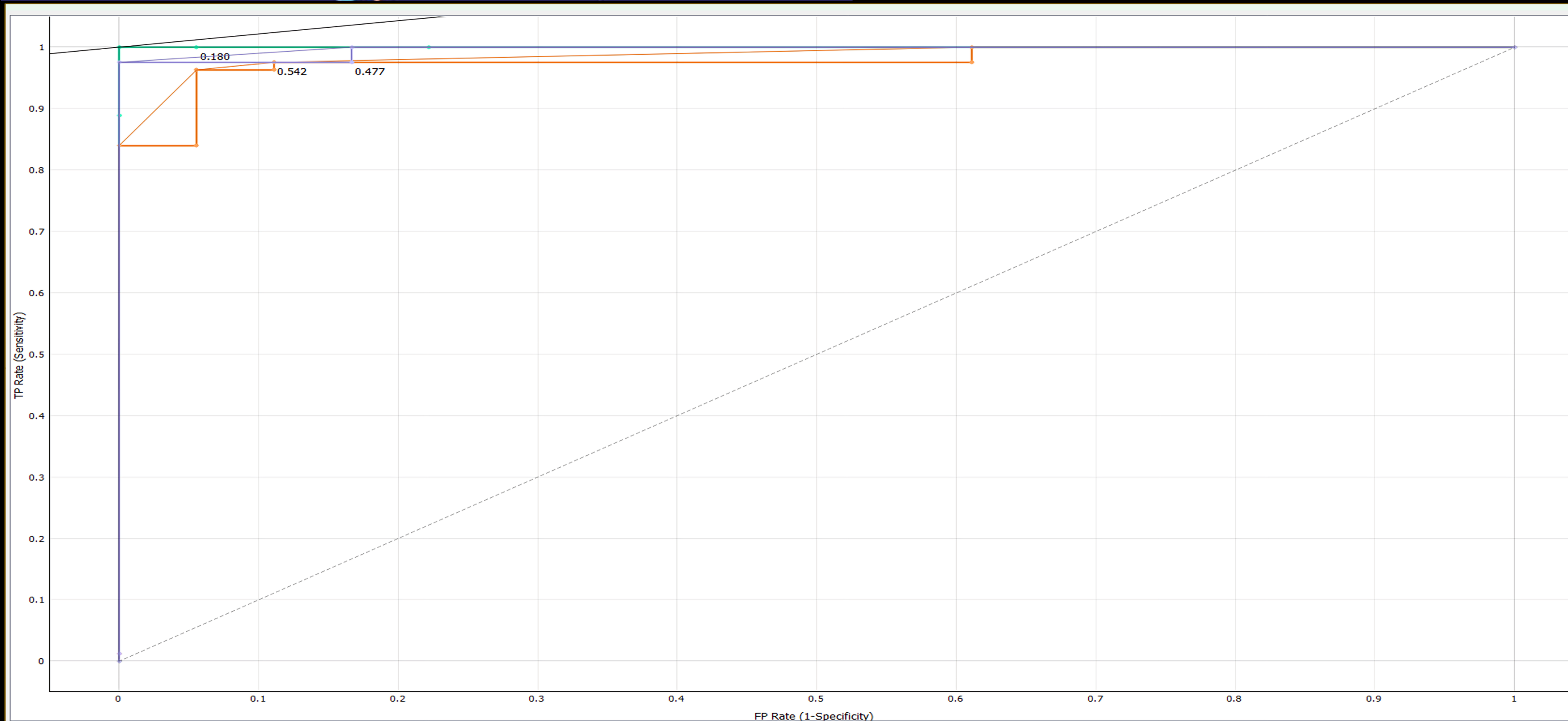


Figure 4 shows the ROC curve for HUB GENE, indicating a good prediction accuracy model.

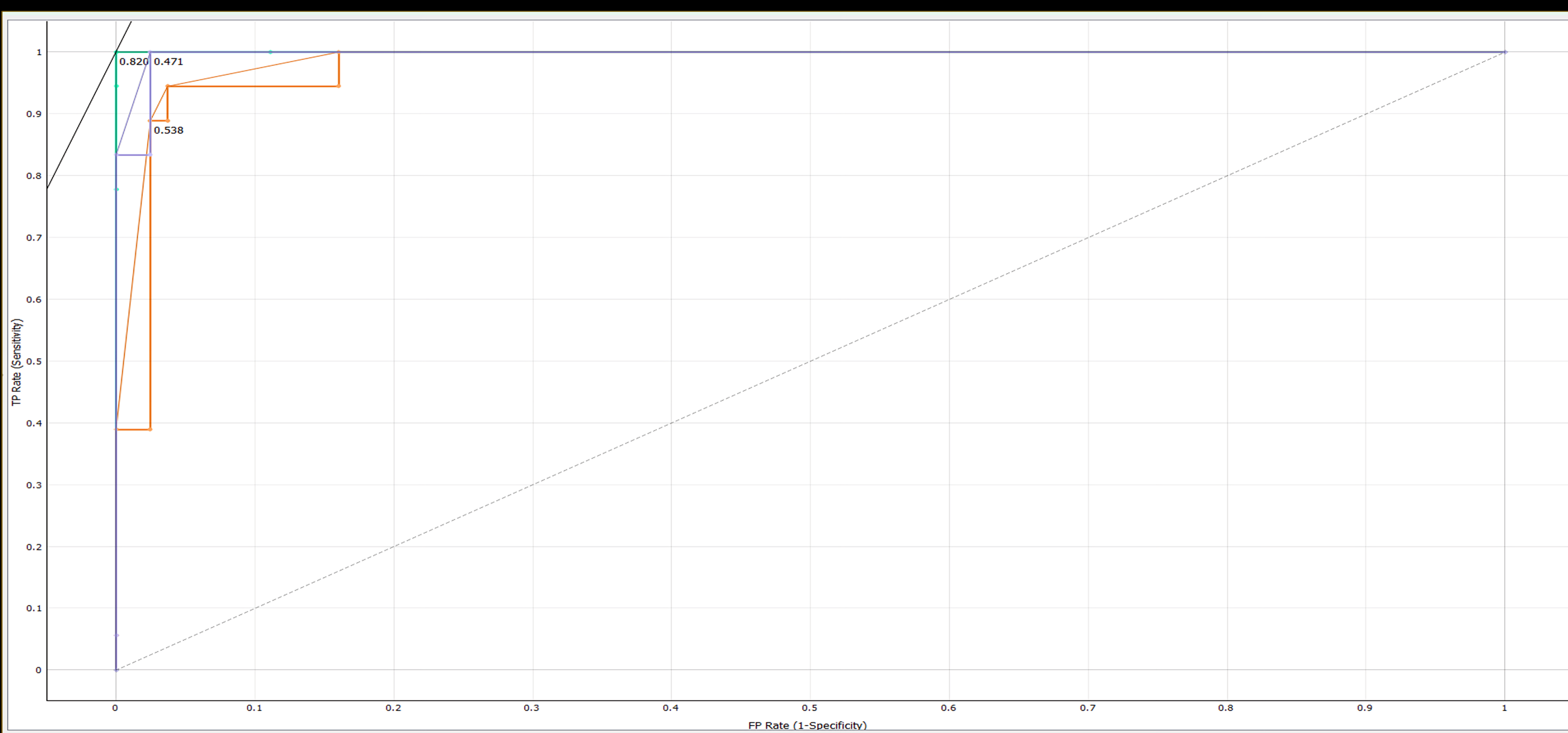


Fig 6 shows the ROC curve Shows a good predictive model for non-hub genes.

DISCUSSION

This research successfully employs machine learning algorithms to predict interactome hub genes associated with both periodontitis and cardiovascular disease. The identified hub genes reveal shared molecular mechanisms, suggesting potential common pathways. These genes hold promise as biomarkers for early detection and as therapeutic targets, offering personalized interventions for individuals affected by the intersection of chronic inflammatory diseases and cardiovascular issues. The study has significant clinical implications and sets the stage for future research in the dynamic field of computational biology and cardiovascular medicine.

CONCLUSION

Machine learning algorithms are effective in predicting interactome hub genes associated with both periodontitis and CVD. These hub genes could provide valuable insights into the shared molecular mechanisms underlying these two conditions. Moreover, they may serve as potential biomarkers and therapeutic targets for individuals affected by the intersection of chronic inflammatory diseases and cardiovascular issues.

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