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AI-Driven Predictive Analytics for Intelligent Healthcare Monitoring and Early Disease Detection

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Abstract

Incorporation of AI and ML into healthcare monitoring systems has driven the enhancement of the most significant progress in patient care, such as early detection, personalized care, and cost efficiency. This paper presents a new AI solution of a predictive analytics framework specifically designed for healthcare systems with an emphasis on the respiratory imbalance severity. Our experimental setup includes a combination of different machine learning algorithms, including Support Vector Machines (SVM), AdaBoost, and state-of-the-art advanced ensembles like Stacked Ensembles, as well as deep learning algorithms, including TabNet. Applying strict feature selection methods, data preprocessing with feature scaling, SMOTE, and other balancing methods guarantees the efficiency of the developed framework in terms of predictive performance and model interpretability. Concerning the prioritization of features, key findings show the importance of the respiratory rate and the type of first diagnosis when developing clinical models. The Stacked Ensemble classifiers, based on SVM, KNN and AdaBoost, provided nearly perfect accuracy of 99.92%, which was far superior to individual classifiers. Exploratory data analysis or EDA, and reducing dimensions with the help of PCA, gave additional specificity in data representation for building performance and scalable, efficient predictive models. Performance metrics integral to the confusion matrices and AUC scores provide additional validation that the framework is valuable in minimizing sources of misclassification error and providing actionable insights for operational decision-making. A use case of this research is the innovative capabilities of AI-enabled systems to revolutionize healthcare observation by identifying severe states at an early stage for certain conditions using revolutionary clinical procedures. It also shows the limitations of the study, including ethics issues, data normalization, and interdisciplinarity, to advance recommendations for future research to incorporate more sophisticated approaches to deep learning. Thus, the work demonstrated in this study brings together technological advancement and clinical ideas to make healthcare more intelligent in the future.

Keywords: *Predictive Analytics, Healthcare Monitoring Systems, Respiratory Imbalance, Stacked Ensemble Model, Personalized Medicine, Clinical Decision Support*

Introduction

Data-driven decision-making and improved patient care are taking place in the hands of the artificial intelligence (AI) and machine learning (ML) revolution [1, 2]. From simple diagnostic

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tools, healthcare monitoring systems have become more sophisticated platforms, capable of interpreting very large amounts of data in real-time [3-5]. Healthcare providers can now predict, diagnose, and treat medical conditions with greater accuracy and efficiency through these advancements [6, 7].

Decision-making support techniques that deal with probabilities, such as statistical algorithms and ML, are integrated into predictive analytics [8, 9]. In particular, when applied to healthcare monitoring systems [10], Such analytics make it possible to detect serious states at an earlier stage, manage resources more effectively, and choose individual treatment approaches [11]. These capabilities are especially important in critical care areas such as intensive care units, where the speed of action impacts patients' lives [12].

Nonetheless, there are still problems in building viable and scalable predictive analytics architectures for use in healthcare contexts. Challenges, including data heterogeneity [13, 14], feature selection complications [15], and model interpretability [16, 17] remain prohibitive factors to uptake and proper application in practice. Solving these problems is possible only by developing new heuristics that combine ideas from computational mathematics, general expertise, and real-life healthcare decisions [18, 19].

In this research study, we propose an enhanced AI-based predictive analytics model built for healthcare monitoring systems [20]. As such by considering various feature selection algorithms, feature ranking techniques, model selection algorithms, classification algorithms, and clustering algorithms we respond to the most important questions in patient monitoring and show how predictive models could revolutionize the healthcare systems. The framework used to achieve this integrates off-the-shelf healthcare population data to forecast significant patient metrics and deliver valuable information for caregivers. Our key contributions to this research study are:

- We proposed a new approach amid a set of multiple ML algorithms for estimating the severity of respiratory imbalance in healthcare frameworks [21].
- We introduced a new ensemble method that proved high efficiency and, therefore, reliability regarding the healthcare predictions, 99.92% for accuracy [22].
- We focused on the feature selection, emphasizing respiratory rate and the first diagnosis type as the critical features that determine the accuracy of the predictions [23].
- We showed the importance of developing effective and efficient solutions in AI to support patient surveillance and operational decision-making in a large setting [24].
- We suggested that future work should consider manageable concepts of combining superior deep learning algorithms with additional subject matters for better healthcare solutions [25].

This research aims to fill the gap between theoretical developments in the field of AI and real-life improvement of healthcare services by providing a reliable and easily expandable architecture for generating real-world predictive models. This brings out the revolutionary nature of AI in identifying and solving some of the major problems in healthcare, thus leading to improvement of patient care, organizational effectiveness, and organizational readiness against innovative change. It is this author’s hope that the study facilitates subsequent breakthroughs and lays the foundation for the deployment of an AI-enhanced healthcare monitoring environment.

1. Literature Review

Due to recent advancements in AI, predictive analytics has revolutionized the health industry, allowing for early patient care [26]. The use of data reduces risks, supports decision making, increases value for patients, and increases the quality of health care systems. This literature review studies the advanced healthcare monitoring approach based on AI, articles from different sources, main achievements, and the existing problems and possible missing links to provide insights on further development of the systems for predictive care [27-29].

2.1 Predictive Analytics and Disease Prevention

Many prior research works focus on how AI, in conjunction with ML, can identify diseases and assist in early, accurate diagnosis and individualized treatment. Rana et al.[30] emphasis on the achievement of using AI in predictive analysis for early diagnosis, and individualised treatment [26]. It also examines the application of AI-based decision-support technologies in improving workflow and patient care, while considering various ethical implications. In the article Ibrahim et al. [31] shows how ML can be used to prevent diseases and detect them at an early stage. The paper also describes how ML supports precision medicine, helps to personalize treatments, and deals with the data flood in forms such as genomics for risk assessment. The study by Rehan [32] describes the advantages of big data analytics (BDA) and ML for elaborating predictive healthcare analytics and performance. And likewise, Ramesh et al. [33] focused on Naïve Bayes, SVM, and Random Forest for heart disease prediction, where different feature selection techniques were examined to examine the prediction performance. Even all papers declare an aspect of 'predictive capability', Rana et al [30] enhances system incorporation and operation improvement, Ibrahim et al. [31] concentrates on diseases such as genomics and Ramesh et al. [33] narrows down the algorithm methods to heart diseases [7, 34].

2.2 Application of ML in Specific Medical Fields

The paper by Rashidi et al. [35] is based on supervised learning and Auto-ML, at length with its focus towards practical applications in laboratory medicine. In the article of Li et al. [36] propose a feature selection algorithm FCMIM, described to improve the performance of heart disease prediction models by identifying the most relevant features from patient data, therefore increasing the efficiency of the model. Additionally, the study by Rubinger et al. [37] sees health trauma surgery as a way of creating a framework where ML can predict mortality risks in trauma patients to help significant decision making and resource provision during crises. These investigations, while practical orientation, are presented under different categories of specialty [38]. Regarding general applications, [35, 39], whereas [36] and [37] dedicated to concrete cases connected to cardiology and trauma surgery, illustrate AI opportunities for everyday and extraordinary healthcare [40].

2.3 Integration of AI/ML into Healthcare Systems

The study by authors Garg et al. [41] offers a plain-language synapse of how AI/ML influences the healthcare systems which range from the disease prediction to a new effective drug or individualized treatment, and vice versa, presents the healthcare system's substantial drawbacks experienced while adopting AI, main of them being the necessity of interdisciplinary work. The paper articulated by Sharma et al. [42] provides an outlook of ML with IoT in a health care system where decision makers revolve around real time disease identification, customized care with the help of a few number of devices, and high prediction models, especially where the infrastructure is low. In the study by Alowais et al. [43] discuss real AI uses across various clinical specialties and say that integration of AI into clinical practices is essential, along with the problems like cost of implementation, physicians' engagement, and data privacy. Last, by authors Gadde et al. [44] looks into many-sided use of ML in the healthcare sphere, which may concern diagnostics, medical image analysis, or other things, is aimed to prove the positive impact AI may bring to the healthcare system and to patients [45, 46].

2.4 Ethical, Educational, and Deployment Perspectives

The paper studied by Hossain et al. [47, 48] explores how AI can effectively decrease the cost of the healthcare system while increasing the quality of the results received, as well as the respective ethical concerns to data protection and AI's involvement in the decision-making process. Also, Zhang et al. [49] focus on the transition from the model development stage to data quality, bias, and deployment issues in healthcare. Lastly, by authors James et al. [50] The proposition for the provision of education on AI/ML in medical schools is proposed as important to prepare future physicians to evaluate the application of such systems to inform their practice and improve patient care [29].

Some of the recognized limitations include the lack of practical experiments conducted, failure to provide real results that would make the findings more substantiated [7, 51]. As good sources for the generation of theories and 'big picture 'assessment, the constraints of the heavy use of secondary sources and descriptive analytics lessen the prospects for identifying measurable results. Lack of robustness, inadequate real-world data, and lack of data standardization pose challenges to generalization of the produced models. Additionally, the experimentation of certain types of ML models creates questions focusing on the interpretability of the models; meanwhile, the absorption of ethical factors such as data privacy and algorithmic bias remains a grey zone. Lastly, either the incorporation of AI into the clinical environment or the absence of experienced data analysts are challenges to implementation [52].

2. Methodology

This section describes the overall framework of this research study. The system framework for using predictive analytics for healthcare monitoring systems is presented in Figure 1 below. This paper evolves a methodology comprising several steps involved in data acquisition, data preprocessing, model development, model training, and model evaluation. Each of them helps to provide the right prediction and make a detailed analysis of the target variable, which is going to be "Causes Respiratory Imbalance".

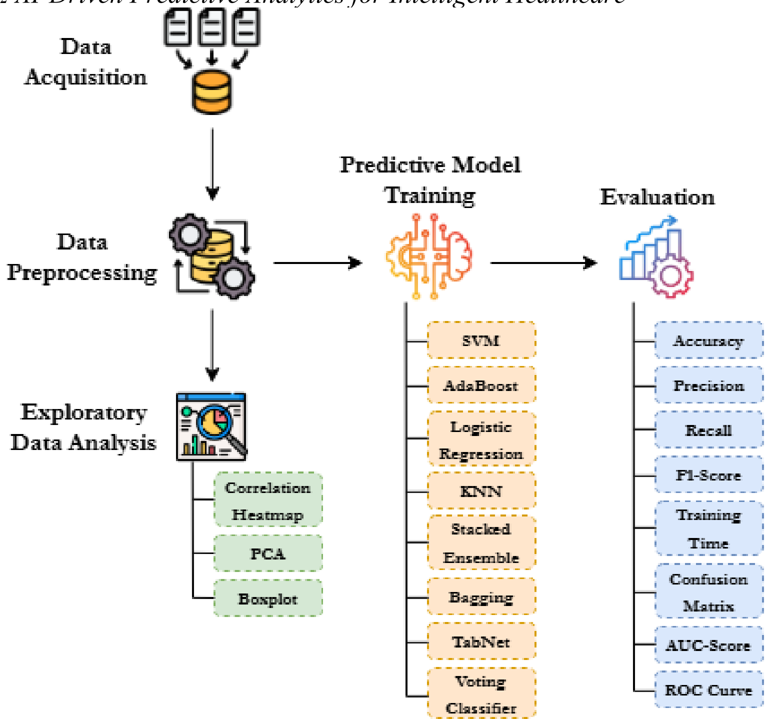


Figure 1: Workflow of our research study

3.1 Dataset Description

The Health Monitoring System Dataset [53, 54], available on Kaggle, is intended for a predictive study of healthcare applications. It has 4,286 rows of data and 20 attributes with columns referring to health information from the people concerned. It is designed to cater to the study of the mediating role of symptoms and physiological parameters to health condition severity which is useful in investigation or assessment. It contains features like vital physical signs, including heart rate, pulse, temperature, oxygen saturation, respiratory rate, and medical conditions which is a strong basis for activities such as respiratory imbalance classification in healthcare analytics. It comprises items such as temperature, blood pressure, pulse, chronic diseases, and other health parameters obtained from people. Also, the data set documents blood pH levels and respiratory disturber as “Severe”, “Normal”, “Mild” or “Chronic”. This dataset can be applied to data analytics, which makes it possible for researchers to sort different indicators and create models to facilitate the early symptoms of the disease monitor the patient’s health, and tailor the healthcare approach.

3.1.1. Data Availability

The datasets analysed during the current study are available in Kaggle, [https://www.kaggle.com/datasets/nraobommela/health-monitoring-system [53]. Also in the present study, the healthcare management data, which is freely accessible and known as “Health Monitoring System” dataset, can be exploited in a plethora of ways for numerous related research and development themes.s

3.2 Data Preprocessing

In the current study, the data collected is first cleaned in a way that can improve the feature and target data quality used in the construction of an ML model. Column names were also cleaned using the rename () with a lambda function that strips whitespace from the beginning and end of the column name string. Some of the columns had duplicities, for instance, Cold, Dehydration; these duplicities were deleted using the drop() technique, and for possible missing duplicates, the errors were set to ignore. This was done to ensure that in the creation of the column names, none were similar and all had sensible names in the dataset. For Cold, Cough, Dehydration, Medicine Overdose, and Acidious data types, the LabelEncoder() from the sklearn.preprocessing package was used to convert them to numerical entities. Specifically, the LabelEncoder() shall encode each category (or label) in the specific column into a different integer. This process can be represented as:

$$X_{encoded} = LabelEncoder(X) = \{y_1, y_2, \ldots, y_n\}$$

Each category of the features was given an integer from 0 to allow the features to work with a ML package. Also, the target variable Causes Respiratory Imbalance was coded to ordinal numerical values using the replace() function. The mapping preserved the natural order of the values: Normal was equated to 0, Mild to 1, Severe to 2, and Chronic to 3. After performing the categorical encoding, the overall data set was segregated into features (X) and the dependent variable (Y). The independent variable X comprised all columns apart from Causes Respiratory Imbalance; the dependent variable Y consisted of the ordinal counterparts of the maps. This was done to standardize the ranges of the various features used this was done using the StandardScaler() from sklearn.preprocessing. The scaling formula can be depicted as:

$$x_j^{scaled} = \frac{x_j - \mu_j}{\sigma_j}$$

where x_j is the original feature value, μ_j is the mean and σ_j is the standard deviation. Due to the imbalance in data distribution especially on the target variable, SMOTE was used using SMOTE function from imblearn.over_sampling. SMOTE generated synthetic samples for minority classes using the formula:

$$x_{new} = x_i + \lambda \,. (x_j - x_i)$$

where x_i and x_j are existing samples from the minority class, and λ is an arbitrary number which lies in between 0 and 1. This step balanced a number of records in each class, and as confirmed in the next section, data class distributions were checked by the value_counts().

Finally, the dataset was divided into training and testing sets with the help of the train_test_split() re-defined in sklearn.model_selection. A stratified split made certain that the classes in the target variable were well-represented within training and testing data sets. The ratio of splitting the data was 70% for training and 30% for testing, and the random_state was 42 for replication. The shape of the initial and resampled data frames and the train and test data frames were examined using the shape attribute to ensure the data was clean and balanced for training.

3.3 Exploratory Data Analysis (EDA)

Exploratory Data Analysis (EDA) is the first step in the data analysis process since it entails discovering the characteristics of the data set and getting insights into the data itself. To achieve a deeper understanding of the distribution of the variables and their interactions and data structure, an exploratory data analysis was conducted in this study. The data exploration process involves carrying out exploratory data analysis and generating output in terms of illustrations on aspects of the dataset for use in modeling plans and decision-making. The EDA involved several key analyses:

3.3.1 Feature Correlation Heatmap

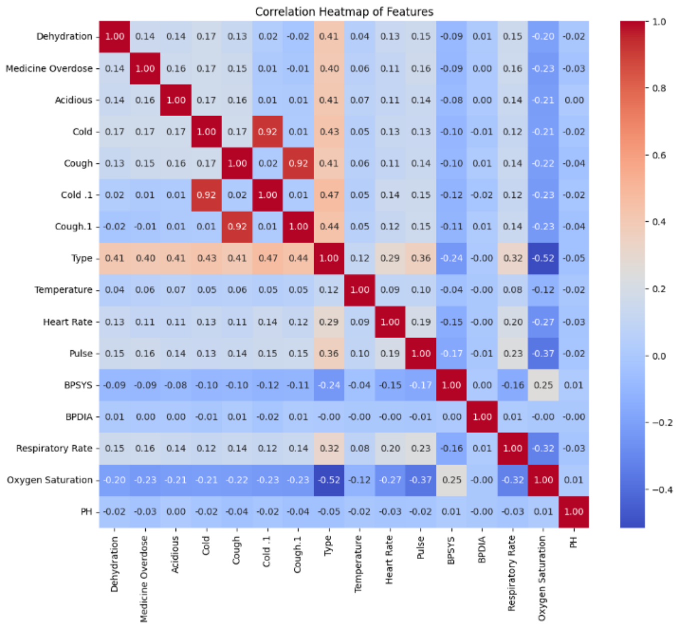


Figure 2: Correlation Heatmap of Different Features

Correlation heatmap allows us to define, how different values are tied to each other, or in other words, to see the proximity matrix of chosen fields, as shown in Figure 2. Looking at correlations within the heatmap, we see that a high correlation of 0.92 connects ‘Cold’ and ‘Cough’ meaning that as the presence of a cold increases, so does a cough. Likewise, “Acidious” has a fairly high positive correlation with “Cold” (0.43), yet it is not as strong as the correlation between the two previous sets of features. At the same time, there is a weak positive relationship between “Dehydration” and “Medicine Overdose” (0.14). There is a moderate positive correlation (0.41–0.47) to features that represent the patient’s symptoms, for example, “Dehydration”, “Medicine Overdose”, “Cough”, or other condition types, suggesting that the “Type” could indeed be related to such factors. Also, a heatmap reflects the degree of negative relationship between “Oxygen Saturation” and “Respiratory Rate”: -0.32. In addition, considering medical expertise, lower oxygen saturation is associated with a higher respiratory rate. This kind of correlation analysis is useful for outlining dependency between the health indicators, choosing features, and handling multicollinearity in health metrics-based predictive models.

3.3.2 Principal Component Analysis (PCA)

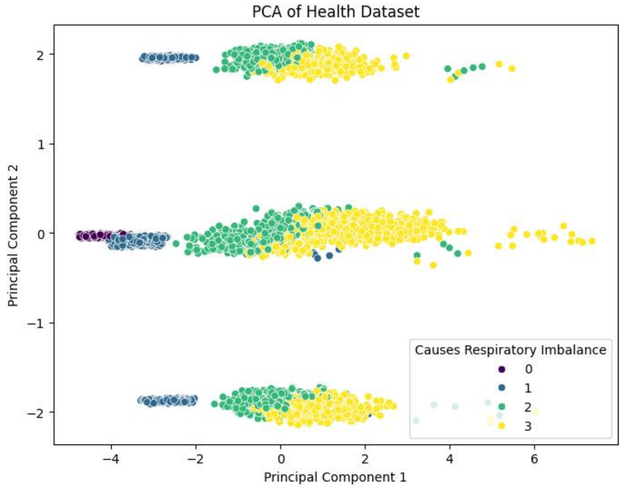


Figure 3: PCA Analysis for the Health Monitoring Dataset

The technique of PCA in Figure 3 is used in this study in order to determine the hidden structure of the dataset and to achieve dimensionality reduction. The analysis extended to the second principal component explained most of the variability of the data and thus, was retained. More specifically, the first component, PC1, was found to explain the most variance, while the second component, PC2, captured orthogonal variance and together they provided an effective, yet minimal means of data representation.

The two dimensions of data that emerged from the analysis, with the principal components compared to the dependent variable, “Causes Respiratory Imbalance”. The values also clearly demonstrate how the attributions of the dataset were reduced to a new form where observations are characterized by their distances in relation to the first and the second principal components.

The scatter plot of these components clearly delineates different clusters for the target classes which include Normal (0), Mild (1), Severe (2), and Chronic (3). Indeed, these clusters show how PCA is capable of successfully partitioning the data according to inherent features evidencing its ability to construct a summarization of the dataset while maintaining the variability peculiar to the classes involved. Since PCA retains the most information in a lower dimension space, it helps with the subsequent analysis of visualization and classification along with predictive modeling.

3.3.3 Distribution and Boxplot for Features Analysis

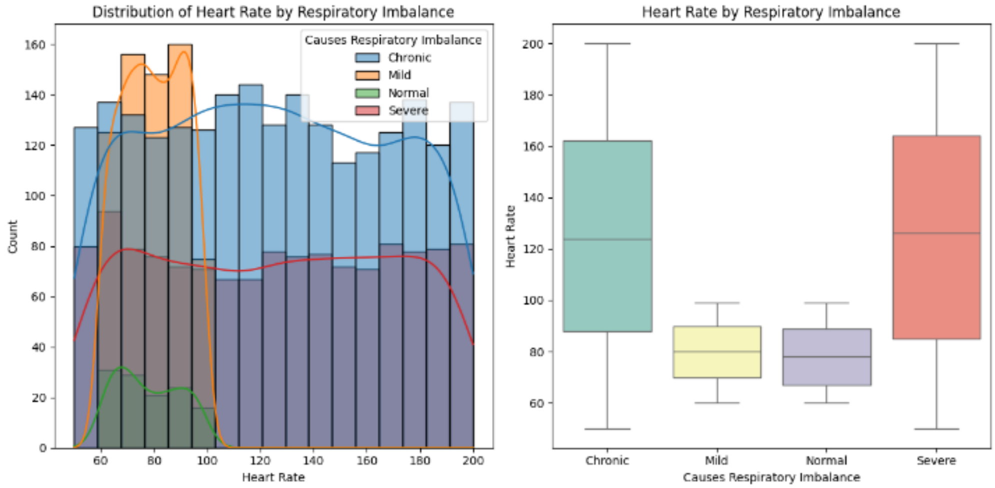


Figure 4: Distribution and Boxplot of Heart Rate by Respiratory Imbalance

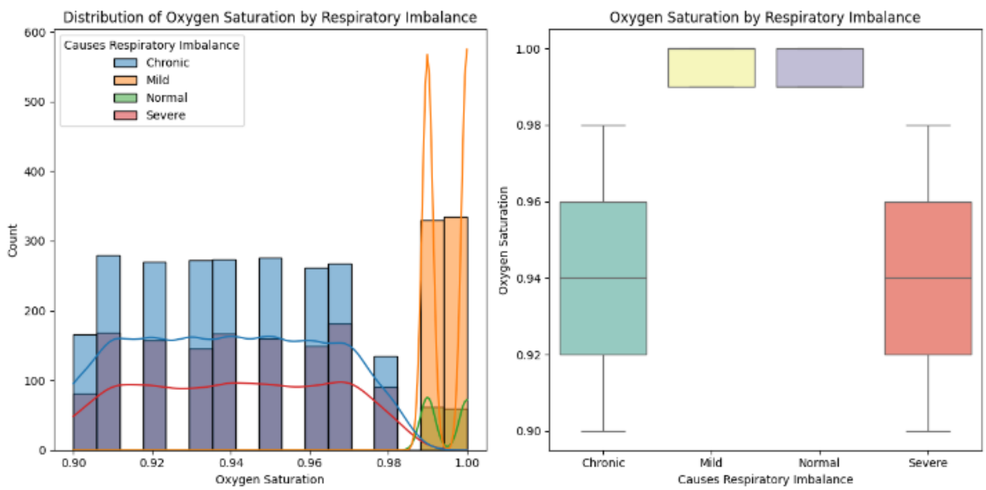


Figure 5: Distribution and Boxplot of Oxygen Saturation by Respiratoey Imbalance

The visualizations shown in Figure 4 and Figure 5 are aimed at analyzing the distribution and variability of two dependent variables: Heart Rate and Oxygen Saturation with regard to four independent variables, namely Chronic, Mild, Normal and Severe respiratory imbalances.

The heart rate analysis as presented in the top row shows the histograms of the results augmented by the density plot for each imbalance category. It leads to the finding of a new and marked variation in the amount of heart rate dispersion among the groups. Most notably, Severe cases show a numerically higher median of relative heart rate with a higher coefficient of variation, according to the boxplot on the right. Mild and Normal groups demonstrated lesser and more stable heart rate values which are different from the variables in the high group.

The oxygen saturation analysis (bottom row) employs the same method of logical flow. While analyzing the distribution of the results expressed in terms of oxygen saturation, higher concentrations are evident for the Mild and Normal groups with density located in the range of

0.98 – 1.00 for most of them, while the Severe and Chronic groups have more spread distribution with median values lower than those from the former group. The boxplots reinforce all these observations and particularly emphasize the dichotomy between normal and pathological respiratory function.

These findings underscore the usefulness of keeping track of physiological trends such as heart rates and oxygen levels for early identification and categorization of respiratory disharmony that can assist therapists in individualized treatments.

3.4 AI-based Predictive Models

In this study, we have used multiple ML approaches for predicting the disease types related to respiratory imbalance. All the models come with different benefits depending on the model used to manage various parts of the dataset.

3.4.1 Support Vector Machine (SVM) Classifier: The SVM classifier is a powerful and uninhibited algorithm of functional classification that prescribes the direction of the hyperplane that separates the classes with maximum distance in the high-dimensional space of features [55]. For binary classification, the decision function is [56]:

$$f(x) = sign(w^T x + b)$$

where w stands for weight vector, x is the feature vector and b is the bias. In this paper, SVM can help to distinguish health conditions as well as applicable when data distribution is complex.

3.4.2 AdaBoost (Adaptive Boosting) Classifier: AdaBoost is a boosting method that uses multiple weak classifiers, generally decision stumps to form a strong classifier [57]. The model increases the influence of misclassified samples and updates weights on each iteration of the process. The weighted classifier is defined as [58]:

$$H(x) = sign(\sum_{t=1}^{T} \alpha_t h_t(x))$$

where $h_t(x)$ is the weak classifier at iterations t We also have α_t as the weight for that classifier. Due to the problems with data imbalance in this particular area of healthcare, AdaBoost may be quite effective in the context of enhancing predictive ability and achievement.

3.4.3 Logistic Regression (LR) Classifier: A logistic regression is a type of method in analyzing categorical target having continuous values by applying the logistic sigmoid function [59]. For binary classification:

$$P(y = 1|x) = \frac{1}{1 + e^{-(w^T x + b)}}$$

Here $w^T x + b$ represents weights of the inputs of the feature space. Logistic regression is easy to perform yet effective in presenting the probability outcomes, which are essential in healthcare risks assessment.

3.4.4 K-Nearest Neighbors (KNN) Classifier: KNN is an algorithm that can be classified as non-parametric and the sample is classified according to the majority of its k-nearest neighbors [60]. The distance metric (e.g., Euclidean distance) between data points is calculated as [61]:

$$d(x_i, x_j) = \sqrt{\sum_{l=1}^{n} (x_i, l - x_j, l)^2}$$

KNN proves most effective when analyzing the similarity in small and specific regions of the data area.

3.4.5 Stacked Ensemble (SVM-AdaBoost-KNN) Classifier: Stacking involves combining the result of other base models (SVM, AdaBoost and KNN) to create a new model that learns from the final votes using a meta model (LR) [62]. The final prediction is determined by:

$$y_{final} = f_{LR}(f_{SVM}(X), f_{AdaBoost}(X), f_{KNN}(X))$$

Staking makes the generalization by allowing the best or strongest features from each model while also hiding their weak aspects.

3.4.6 Bagging (Bootstrap Aggregating) Classifier: Bagging decreases the variance since multiple models are trained to bootstrap samples of a dataset with the average of the different models' predictions [63]. For classification, the final prediction is:

$$H(x) = majority\_vote(h_1(x), h_2(x), \dots, h_T(x))$$

In other words, bagging is a process that creates feature subsets to decrease variance and protect from overfitting.

3.4.7 TabNet Classifier: TabNet is a state-of-the-art deep learning architecture on tabular data processing [64]. To identify which features are likely to be most helpful in the decision-making process it applies a sequential attention mechanism. TabNet's output is modeled as:

$$y = softmax(\sum_{i=1}^{N} W_i \odot attn_i(X)$$

where W_i means learned weights, $attn_i(X)$ means the attention scores of features. In particular, TabNet has been designed for use with complex and large datasets that are typical for healthcare analytics.

3.4.8 Voting Classifier: The voting classifier is used to make the final prediction from the multiple models by voting techniques using either hard or soft voting [65]. For soft voting, the final probability is:

$$P(y|x) = \frac{1}{M} \sum_{m=1}^{M} P_m(y|x)$$

where M is the number of models, and $P_m(y|x)$ the probability of y from the m model of x. The voting classifier increases overall certainty and reliability since diverse classifiers work synergistically.

3. Result and Discussions

4.4.1 Comparative Performance Metrics of Different Models:

The performance of the Stacked Ensemble model is formulated with the base learners SVM, AdaBoost, and KNN interlinked by a Logistic Regression integrative learner for purpose of fitting improved models. SVM works well in large feature space while AdaBoost deals with issues of bias and variance, KNN on the other hand focuses on local data distributions and the meta-learner integrates the outputs of these learners into a whole. In terms of the potential error margin, this architecture ensured 99.92% of accuracy with perfect precision, recall, and F1-scores, confirming the stability of the prediction model. Its flexible structure increases applicability across several datasets and domains useful in healthcare diagnosis and industrial flaw identification. Because of how the class imbalances and features were managed within the model, the solution provides good scalability, high robustness and excellent performance for real-world application. The AdaBoost classifier stood next with 97.20% accuracy, F1-score of 96%, perfect balancing of time and complexity and the training time taken was 1.154 seconds. Other models include selected Standalone models where svm with 93.78% and TabNet with 93.54% and significant large training time of 25.462s as compared to svm with 0.36s. Logistic Regression, a much simpler model, scored a meagre 92.37% and KNN scored 70.22% and took the longest time, 30.591 seconds to train. The Voting Classifier was more accurate at 92.38% due to averaging base learners yet again it was outperformed by the Stacked Ensemble. Thus, the Bagging Classifier's performance remained very low at only 62.27%, proving that default settings are insufficient. In general, the experiments clearly support the use of stacking to allow model differences to improve the forecasting accuracy. All the different characteristics of the compared models are given in the tabular form in Table 1 according to accuracy, precision, recall, F1-measure, and the time needed for training the model to highlight its advantages and disadvantages. And the graphical evaluations are portrayed in Figure 6.

Table 1: Comparative Performance of ML Models: Accuracy, Precision, Recall, F1-Score, and Training Time

Model	Accuracy (%)	Precision	Recal l	F1-score	Training Time(sec)
SVM	93.78	0.94	0.94	0.94	0.36
AdaBoost	97.20	0.95	0.97	0.96	1.154
Logistic Regression	92.37	0.90	0.92	0.91	0.797
KNN	70.22	0.69	0.70	0.65	30.591
Bagging	62.27	0.66	0.66	0.65	0.354
TabNet	93.54	0.91	0.94	0.92	25.462
Voting	92.38	0.91	0.92	0.91	2.203
Stacked Ensemble (SVM, AdaBoost, KNN) (Proposed)	**99.92**	**99.9**	**99.9**	**99.9**	15.018

4.4.2 Confusion Matrix Analysis:

From Figure 7, an initial look at the confusion matrices paints a picture of quite different performance characteristics of the four predictive models for a healthcare system. Both Voting Classifier and Bagging over-represent the "Chronic" category and it seems that this problem is aggravated with the increase of trees in the Bagging ensemble. This leads to a high amount of FP, in particular 'Normal' submitted to 'Chronic' (36 for Voting Classifier and 37 for Bagging), 'Mild' placed into 'Chronic' (199 for Voting Classifier and 200 for Bagging), and 'Severe' submitted to 'Chronic' (43 for Voting Classifier and 0 for Bagging). FPs of this type can result in a patient being labelled with a serious disease that they actually do not have, leading to unnecessary stress, aggressive investigations and expensive treatment. On the other hand, TabNet and Logistic Regression are relatively

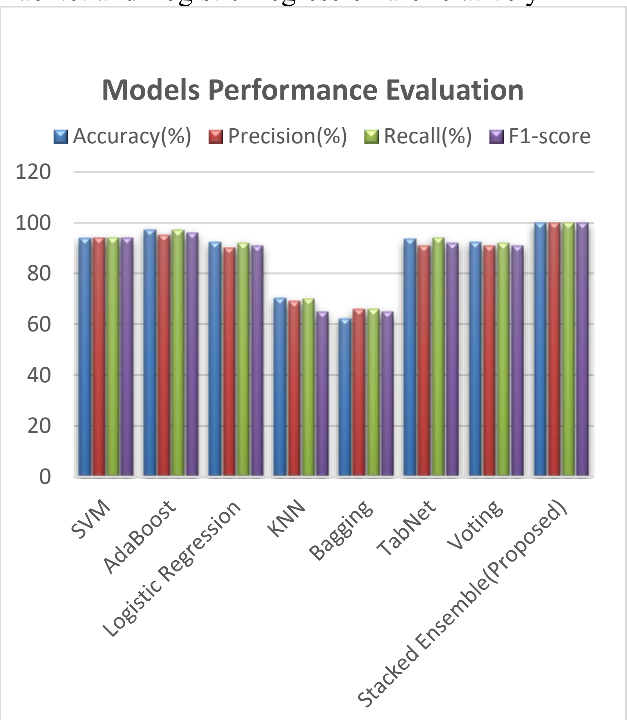


Figure 6: Comparison of performance metrics across different ML models

egalitarian, yet, TabNet outperforms in terms of accuracy for classifying cases as "Severe". However, Logistic Regression has a warning signal because it wrongly classifies approximately 370 "Severe" samples as "Mild." A high number of FNs would mean that such a situation would not be treated in time since it is falsely identified as not severe enough. These observations underscore the importance of addressing specific merits and limitations of each model in a healthcare setting where the costs of possible FPs and FNs remain high. It seems that TabNet provides the most comprehensive level of overall performance, while merely adjustment is needed for Voting Classifier and Bagging since they prioritize the "Chronic" label.

A closer look at the confusion matrices of Figure 8 models indicates additional details of their performance for a health care system. It can also be observed that like the previous case with Voting Classifier and Bagging, KNN and AdaBoost over predict when predicting the outcomes under the "Chronic" label. This results in a high number of FPs in as many classifying "Normal" as "Chronic" (36), "Mild" as "Chronic" (199) and "Severe" as "Chronic" (280 for KNN, 0 for AdaBoost). With these FPs, patients could be subjected to intimidating, and sometimes risky, procedures when they do not need to be. In fact unlike the other models, SVM and the Stacked Ensemble Model presents an entirely different picture when it comes to number of transactions. While they are also able to produce some FPs which are false negatives that comprises of "Normal" and "Mild" as "Chronic", theirs are few. Nevertheless, SVM has a large number of FNs where "Severe" is classified as "Mild" (345) and "Chronic" as "Severe" (34). These FNs are quite dangerous as an individual could be diagnosed with serious illness and could be denied quality treatment.

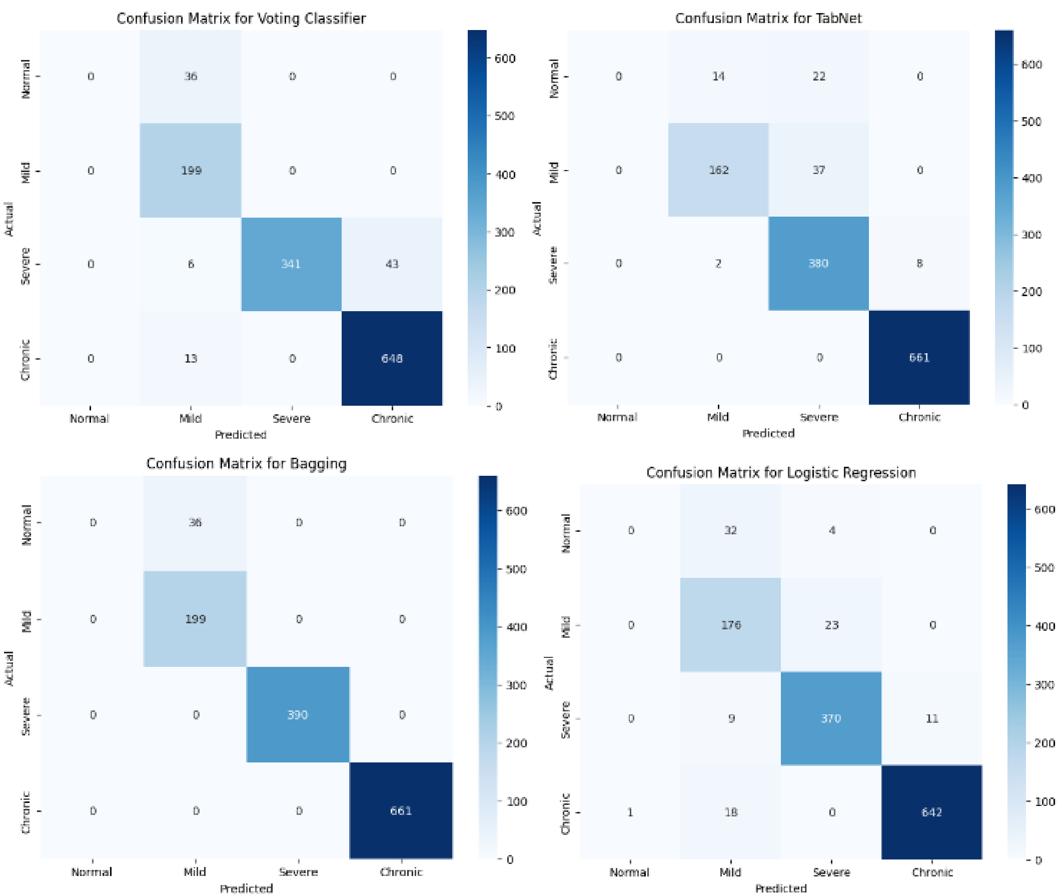
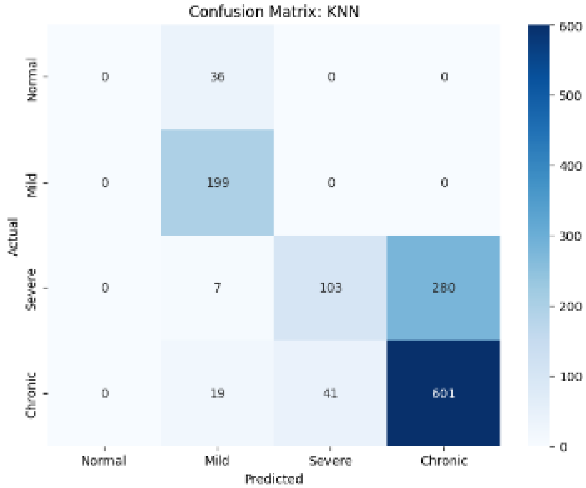


Figure 7: Confusion matrices for Predictive Healthcare Model: Voting, TabNet, Bagging, and Logistic Regression


Confusion Matrix: KNN
Actual
Normal
Mild
Severe
Chronic
Predicted
0
36
0
0
0
199
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7
103
280
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19
41
601
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100
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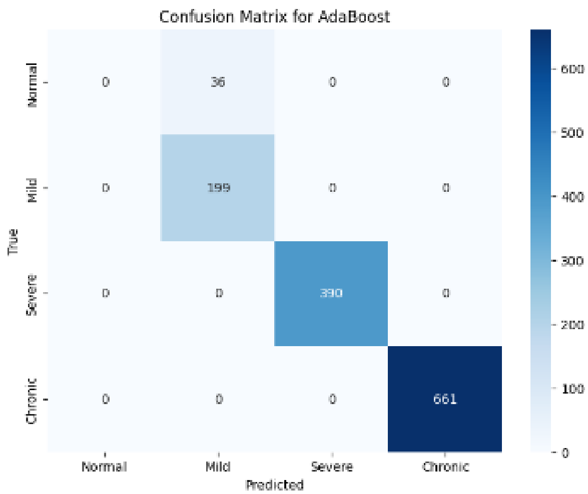
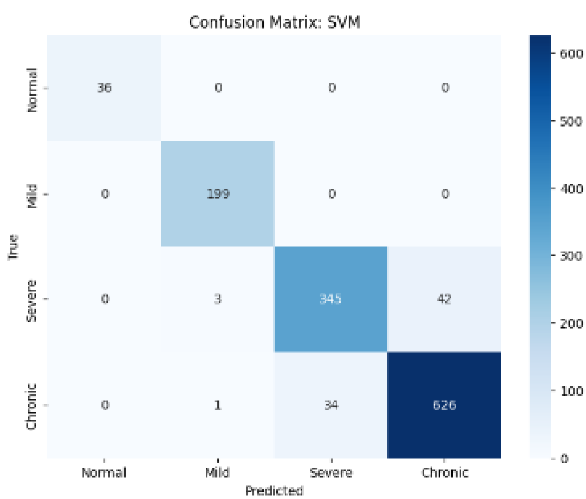

Confusion Matrix for AdaBoost
True
Normal
Mild
Severe
Chronic
Predicted
0
36
0
0
0
199
0
0
0
0
390
0
0
0
0
661
0
100
200
300
400
500
600


Confusion Matrix: SVM
True
Normal
Mild
Severe
Chronic
Predicted
36
0
0
0
0
199
0
0
0
3
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200
300
400
500
600

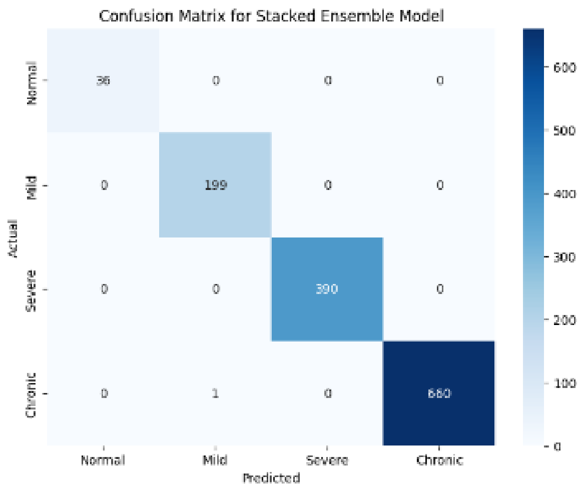


Figure 8: Confusion matrices for Predictive Healthcare models: KNN, AdaBoost, SVM and Stacked Ensemble (KNN-SVM-AdaBoost)

These results indicate that the Stacked Ensemble Model actually seems to have slightly more balanced results compared to the other three models, getting (1 FN) for Mild cases. These results indicate that the determination of the appropriate usage of these models should take into account the unique features of each model when used in the health care environment. The ideal choice in between the two will therefore be determined by the cost of FPs and FNs from the clinical perspective. Although both are anathema to the ideal diagnostic tests, focusing on reducing FNs may be more important in situations where an incorrect negative result would signify a critical disease when compared to a false positive.

4.4.3 Feature Importance Analysis:

Based on the Stacked Ensemble Model which, as we suggested, performs the best, we attribute the highest importance to respiratory rate when determining a patient's condition, and the second highest to the 'Type' as a pre-defined diagnosis separation parameter. Also because Type serves as an indicator of the main diagnosis (Normal, Dehydration, etc.), the high value of its importance suggests that this pre-selected classification aids the model in making those decisions. This implies that correct first diagnosis is essential for the model to work for the clients as planned. This underlines the need to stress adequate early identification and respiratory tracking in this healthcare system.

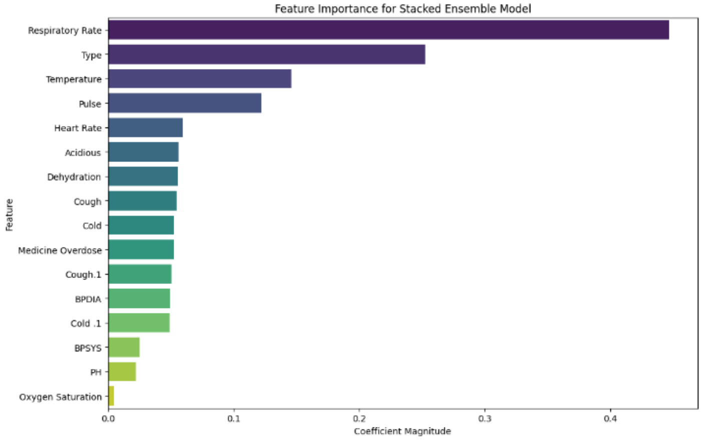


Figure 9: Feature Importance for the Stacked Ensemble Model (SVM-AdaBoost-KNN) in Predictive Healthcare

Basic parameters like temperature, pulse, and heart rate are also important for this, as are such conditions as “Acidious”, “Dehydration”, “Cough”, and “Cold”, which help to make a more accurate prognosis. Interestingly, the model assigns lower severity to identifiers “Medicine Overdose”, blood pressure, oxygen saturation, and pH, which might be attributed to the fact that their information is likely to be included in other dominant features or just does not have much bearing on the particular predictive task at hand. This highlights the need for domain knowledge when interpreting feature importance and designing AI models for certain applications, in this case, healthcare, and towards the development of better predictive models, such as our Stacked Ensemble Model. Figure 9 highlights the feature importance of the Stacked Ensemble Model.

4.4.4 ROC Curve and AUC Score:

The ROC curves and AUC scores give a broad comparison of where the four predictive models stand in healthcare. From Figure 10 Both Voting and Bagging show a high performance in identifying “Severe” and “Chronic” cases by returning AUC rates close to 1. Nevertheless, their AUCs for “Normal” are 0.97 and 0.91, and for “Mild” are 0.89 and 0.89, respectively, meaning that the former is prone to over-estimation of more severe conditions. However, it can be observed that TabNet showed average performance on all classes quite evenly, with an AUC higher than 0.6 for all and especially a high AUC of 0.70 in the Chronic class. Logistic Regression also has a good average AUC, about 0.9, for “Severe” and “Chronic”; however, similar to Voting and Bagging, Logistic Regression can slightly classify between “Normal” and “Mild.” This analysis emphasizes the choice of the correct model according to the requirements of the healthcare system with regard to the outcomes of different types of errors in classification.

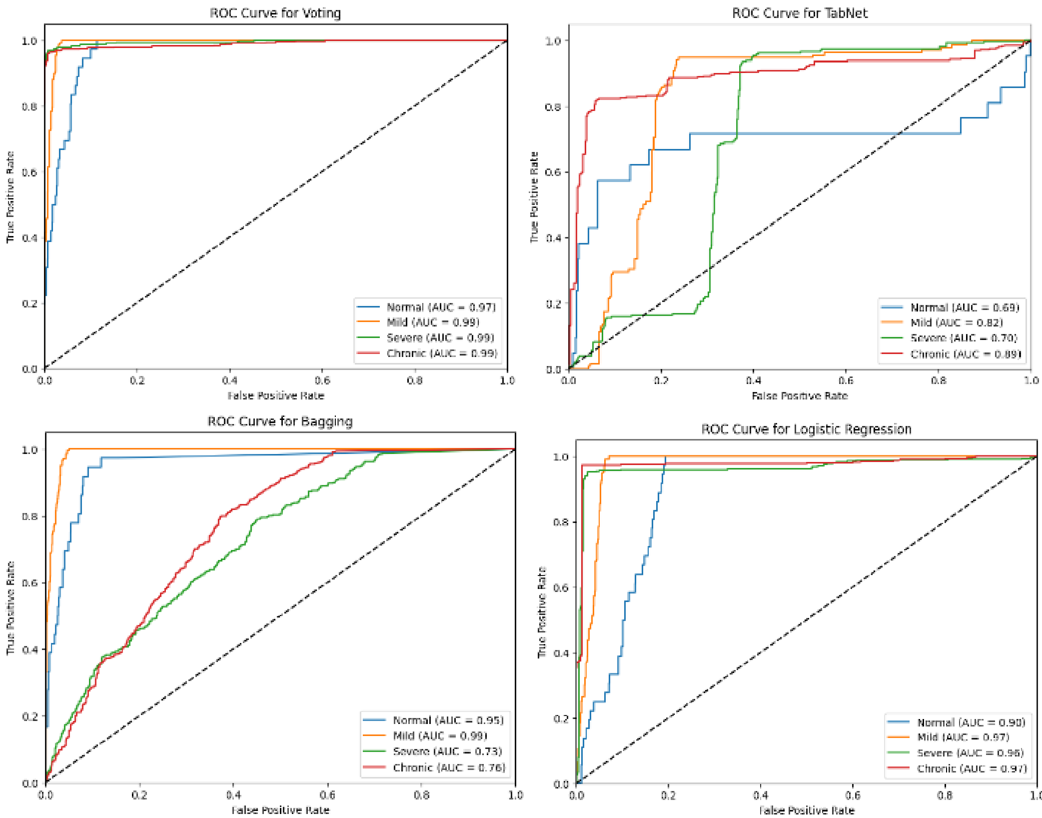
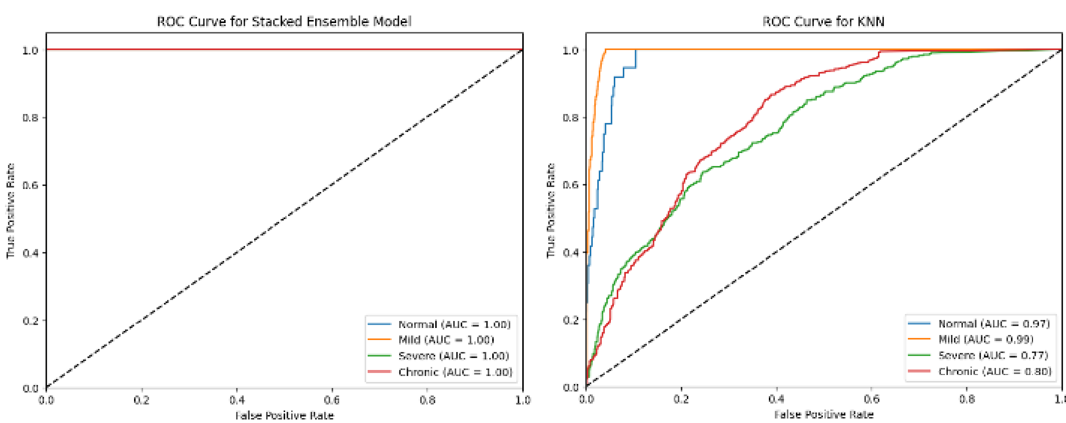


Figure 10: ROC Curve Comparison with AUC scores for (Voting, TabNet, Bagging, Logistic Regression) Models in Healthcare Prediction Model



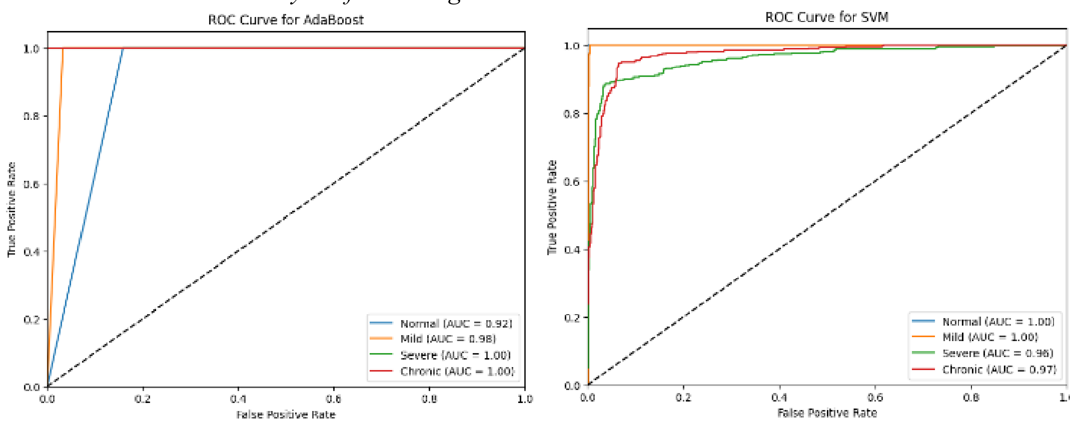


Figure 11: ROC Curve Comparison with AUC scores for Stacket Ensemble(KNN-AdaBoost-SVM), KNN, AdaBoost, SVM Models in Healthcare Prediction

From Figure 11**Error! Reference source not found.** the ROC curves and AUC scores of four different models to perform comparison of K-NN, SVM, Bayes and Cart in a healthcare scenario. The Stacked Ensemble Model performs remarkably well in terms of accuracy, with a AUC Score of 1.00 for all the classes and hence, ideal discrimination between “Normal”, “Mild”, “Severe” and “Chronic” categories has beens achieved. The explicitly evaluated measures prove exactly the high over-all capability of KNN, where it specifies the maximum potential for the “Normal” and “Mild” classes with an AUC of 0.97 and 0.99 respectively, but the less extent for “Severe” (AUC of 0.77) and “Chronic” (AUC of 0.80). AdaBoost is good at “Chronic” (AUC = 1) and “Severe” (AUC = 0.98), but the measurement for “Normal” (AUC = 0.92) and “Mild”(AUC = 0.91) indicates that AdaBoost may be slightly overfitting and might better predict severe conditions. From the ROC curves, SVM achives almost 100% for “Normal”, and close to 100% for “Mild” and “Chronic”, while it is 96% for “Severe”. This evaluation also compares the characteristics of the models’ performances and underlines the target of choosing the model that best meets the clinical requirements and the impact of other types of misclassification.

Figure 12 reveals that the Stacked Ensemble Model achieves perfect discrimination across all classes, outperforming KNN, AdaBoost, and SVM, each of which exhibit varying strengths and weaknesses in classifying different health conditions.

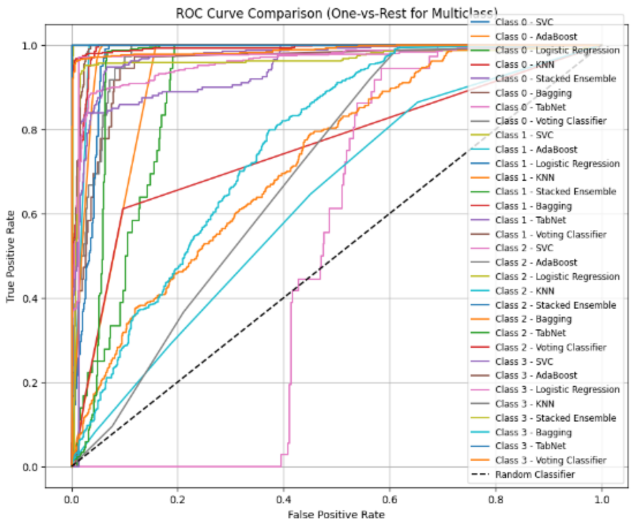


Figure 12: ROC Curve Comparison for Multiclass Classification for all Models for Predictive Healthcare System

II. Conclusion and Future Direction

This study shows how AI ad ML have revolutionized the healthcare monitoring systems especially predicting severity of respiratory imbalance. When the models were stacked and combined, the accuracy was even higher, reaching 99.92% in the Stacked Ensemble (SVM+AdaBoost+KNN), which formed a very high increase as compared to the individual calculated traditional models. This shows how high-complicated the data preprocessing pipeline was, that involves SMOTE for achieving better distribution and balance of data and overall the principal component analysis for dimensionality reduction in order to obtain highly reliable and certain results. Primary feature selection revealed respiratory rate and first-diagnosis type as the most important determiners of scope of care and mortality respectively, underlining the role of feature selection in clinical practice.

These results further validate the application of ensemble learning techniques in the domain of healthcare analytics, and it is with these considerations that this research also acknowledges potential limitations such as ethical dilemmas, data normalization discrepancies alongside the implementation of AI models into clinical practices. Removing these barriers, therefore, remains crucial to improved uptake and practical application. The further research should be devoted to deep learning and the usage of real-time data from the IoT devices' to identify the opportunities of improving the prediction models' accuracy and usability in practice.

In making technology work as the glue between medical discoveries and practice, this work provides a strong foundation for a future intelligent healthcare system, which can better supply specific needs, enhance the experiences of patients and patients' families, and better utilize available medical resources.

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