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Support Vector Machine-Based Model for the Classification of Effective Antibiotic Combination for Pediatrics: A Comparative Analysis of Pre-COVID-19 and COVID-19 Era

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ABSTRACT

The COVID-19 virus is suspected to have introduced a different layer of resistance to antibiotics for pediatric patients. Traditional methods for selecting antibiotics often yield suboptimal results due to their inability to adapt to evolving patterns of microbial culture and sensitivity. Therefore, to provide a more precise and individualized approach to selecting antibiotics and ascertaining their effectiveness before and after the onset of the pandemic, it is necessary to leverage the power of Artificial Intelligence. In this study, the Support Vector Machine (SVM), a machine learning algorithm, is proposed. The model trained on extensive datasets of microbial responses and different antibiotic combinations was designed and implemented. Findings revealed that the model outperforms conventional techniques with an accuracy of 83% and 89% respectively for the pre-COVID-19 and COVID-19 era in predicting effective antibiotic combinations. More importantly, the results showed that 75.6% of drugs in our dataset were effective before COVID-19 while 72.9 % were effective after the pandemic, indicating that more antibiotic drugs were effective before COVID-19 than afterward. Results also indicated an increase in resistance to antibiotics and antibiotics combination after the onset of COVID-19, substantiating the suspicion that COVID-19 has a significant negative impact on the effectiveness of antibiotic therapy in pediatric patients.

Keywords Pediatrics, COVID-19, Machine Learning, Drug Combination, Antibiotic Resistance, Diagnoses, Support Vector Machine, Clinical Decision Support System, Artificial Intelligence

INTRODUCTION

The growing issue of antibiotic resistance presents a challenge in effectively treating infections in pediatric patients. Treatment options are likely going to be increasingly limited because drug-resistant bacteria have emerged as a result of antibiotic misuse or due to interference by other drugs or microbial activities. Also, medical professionals encounter challenges in accurately prescribing the most effective antibiotic combinations to treat pediatric infections due to limited available information. This issue is significant, as incorrect or delayed diagnoses can lead to high mortality rates (Ekong et al., 2021). Treatment of Pediatric patients before and after COVID-19 requires effective antibiotic combinations which could be achieved by precise classification. However, the global COVID-19 pandemic, which began in 2019, posed previously unheard-of difficulties for healthcare systems around the globe. The patterns of bacterial resistance and the efficacy of antibiotic combinations for pediatric patients may have been further impacted by the increased demand for antibiotics to treat COVID-19-related complications and it becomes necessary to check if the COVID-19 pandemic had any effect on the resistance to antibiotics in pediatric patients. In recent years, machine learning (ML) algorithms, such as SVM, have shown promise in various medical applications, including antibiotic effectiveness classifications (James et al., 2023). The employment of the ML approach for classification is innovative and its choice is noteworthy for its ability to deliver precise outcomes from intricate datasets (Ekong et al., 2023).

Recent advances in Artificial Intelligence (AI) have shown promising results for the use of ML algorithms in a variety of clinical domains. The employment of the ML approach for classification is innovative and its choice is noteworthy for its ability to deliver precise outcomes from intricate datasets (Ekong et al., 2023). Amongst the various ML algorithms, Support Vector Machine (SVM) has gained popularity for its suitability in various medical applications, including antibiotic effectiveness classifications. SVM is a compelling tool for analyzing complex clinical data since it has been applied successfully in clinical decision-making making including but not limited to risk prediction and treatment selection. The choice of SVM is based on its ability to effectively handle high-dimensional data, perform well with limited training samples, and accommodate non-linear classification through the use of kernel functions.

The goal of this study is to use SVM to classify the efficacy of antibiotic drugs in the pre-COVID-19 and after the onset of COVID-19 and compare their relative effectiveness. This will be done using microbial culture and sensitivity data from 2018-2019 for the pre-COVID-19 era and 2020-2022 for the COVID-19 era. The study will also investigate the potential shifts in antibiotic resistance patterns between the pre-COVID-19 and the COVID-19 eras and their implications for antibiotic treatment decisions in pediatric care. The study will assess the effectiveness of the SVM algorithm in classifying the effectiveness of antibiotic combinations for pediatric patients based on microbial culture and sensitivity patterns in the pre-COVID-19 era, evaluate the performance of the SVM model on COVID-19 era, and compare it with the results obtained from the pre-COVID-19 era. Lastly, the study will provide evidence-based insights into the efficacy of the SVM algorithm in guiding antibiotic treatment decisions for pediatric patients and their potential contribution toward combating antibiotic resistance in pediatric healthcare.

The results of this study could have a big impact on efforts to promote antibiotic stewardship and pediatric healthcare. Through the utilization of machine learning algorithms, physicians can enhance their decision-making abilities, thereby optimizing antibiotic treatments for pediatric patients and mitigating the obstacles associated with antibiotic resistance. Furthermore, by comprehending how the COVID-19 pandemic has affected patterns of microbial resistance, evidence-based approaches to combating new threats to infectious diseases and preserving the effectiveness of antibiotics for future generations can be developed.

To succeed in this task, the study will be carried out as retrospective observational research using only microbial culture and sensitivity data from the medical records and laboratory reports of pediatric patients. There will be no in-person patient interaction throughout the study. More importantly, the datasets are void of personally identifiable information; thus, ensuring that ethical standards are rigorously upheld at every stage of the investigation. The datasets will undergo pre-processing to guarantee data consistency and quality before the application of machine learning algorithms for classification purposes.

RELATED LITERATURE

Several researches have been carried out on drug resistance using AI. One such study is a work by Gajic et al. (2022), who carried out antimicrobial susceptibility testing and comprehensively reviewed methods and antibiotics.

Abdullah et al. (2022) assessed the utility of AI in pediatric emergencies. Results indicated that AI played a crucial role in aiding pediatricians by enabling early diagnosis, predicting disease severity, assisting in drug dosage determination, and optimizing resource allocation in emergency departments. He concluded that AI techniques are reliable techniques for pediatricians in managing emergency cases. However, the limitations included the need for more extensive population data,

Also, Mustafa et al. (2021) researched efficient COVID-19 diagnostic tests using the artificial neural networks (ANN) approach, substantiated by modeling and simulation, this study aimed to develop a cost-effective solution to enhance testing capacity. The methodology involved the utilization of ANN to collect pertinent COVID-19 and testing data. ML and probabilistic algorithms were then applied to derive statistically validated testing solutions. The results demonstrated that sample pooling, especially when disease prevalence is low, served as an effective and even a "Gold standard" method for testing. These findings underscore the potential of large-scale sample pooling to significantly bolster testing capacity while preserving specificity. By offering scientifically validated algorithms, this approach not only saves valuable time and resources but also contributes to pandemic containment in densely populated areas, including vulnerable communities such as nursing homes, and hospitals.

Andrews et al. (2022) researched on Respiratory antibacterial prescription. They analyzed changes in antibacterial prescribing for respiratory tract infections (RTIs). The measurement of RTI antibacterial prescribing was conducted using prescription items per 1000 population for primary care from January 2014 onwards and in Defined Daily Doses (DDDs) per 1000 population per day for the overall RTI prescribing the results revealed a notable reduction of 12.4% per season in antibacterial prescriptions for RTIs when compared to pre-COVID levels ($P < 0.001$).

Hui et al. (2020) conducted a study on the effect of Coronavirus disease in 2019 on children, this study aimed to provide insights into the conditions of COVID-19 in children. The methodology involved a retrospective summary of pediatric cases. The analysis included characteristics, treatment approaches, and outcomes. Factors associated with clinical outcomes were evaluated using Cox proportional hazards regression analysis. The results indicated that 75 children had been discharged, with only one case of severe pneumonia and one critical case. Notably, children under 2 years old appeared to be more susceptible to COVID-19. In conclusion, the study noted that COVID-19 in pediatric cases tended to be less severe compared to adults. However, it emphasized the need for further evaluation of the efficacy of antiviral therapy in children with COVID-19 with the aid of artificial intelligence.

Eyad et al. (2020) proposed a system on a comprehensive examination of existing machine learning approaches for addressing Anti-microbial Resistance (AMR). It begins by presenting an overview of AMR as a worldwide public health concern and its impact on Low-to-Middle-Income Countries (LMICs). Particular emphasis was placed on methods that utilized readily available demographic, clinical, and microbiological data from laboratory cultures and sensitivity tests related to multi-drug-resistant infections. It proposes a framework for accelerating the use of data-driven solutions with the aid of AI to address AMR, with a focus on practical implementation in Low-to-Middle-Income Countries (LMICs).

Moran et al. (2020) researched personalized guidelines to help develop an electronic decision support system that could reduce the use of inappropriate or ineffective empirical antibiotics. Data were used to train a machine-learning algorithm called XGBoost to predict resistance to specific antibiotics (co-amoxiclav and piperacillin/tazobactam). However, the machine-learning system performed slightly better and had the potential to reduce the use of unnecessary broad-spectrum antibiotics by up to 40% for patients receiving co-amoxiclav, piperacillin/tazobactam, or carbapenems.

Lewin-Epstein et al. (2021) proposed a system for predicting antibiotic resistance in patients, by employing multiple ML algorithms, including lasso logistic regression, neural networks, gradient-boosted trees, and an ensemble approach that combined all three algorithms, to predict antibiotic resistance. Variable significance was assessed through permutation tests and Shapely Additive Explanations analysis. The results indicated that the ensemble model, which combined the individual models, outperformed them and provided accurate predictions when tested against independent data. In scenarios where no prior knowledge about the infecting bacterial species was assumed, the ensemble achieved area under the receiver-operating characteristic (auROC) scores ranging from 0.73 to 0.79 for different antibiotics.

Sohail et al. (2023) proposed a Techniques for Antimicrobial Resistance Prediction of Pseudomonas Aeruginosa The study employs the Random Forest (RF) and BioWeka machine learning techniques for classification accuracy assessment. Logistic regression (LR) is utilized for statistical analysis. The findings reveal that 44.66% of isolates displayed resistance to twelve antimicrobial agents, while 55.33% exhibited sensitivity. Remarkably high classification accuracy rates were achieved: BioWeka surpassed 98%, and RF exceeded 96% for these antimicrobial families.

Research by Ekong et al. (2023) on the Bayesian Beliefs Network (BBN) and classification of bladder state underscores the power of Artificial intelligence in classification and in addressing the challenges of erroneous and delayed diagnoses due to its unique ability to model causation and correlation.

Ekong et al. (2023) proposed a simple, non-invasive model to classify diabetes mellitus based on readily recognizable and related risk factors using machine learning. The model was developed using six (6) input variables. Missing value and outlier removal, min-max normalization, feature extraction and feature selection using principal component analysis were methods of data preprocessing applied to the raw dataset. 5-fold cross-validation was used to train and validate the model. Performance evaluation measures included accuracy, sensitivity, specificity, and area under the receiver operating characteristic curve (AU-ROC). The model development and analysis were carried out using Python 3.9. The classification accuracy, precision, F1-score, and recall for the healthy class were 98%, 97%, 98%, and 98%, respectively while for the diabetic class, 99% precision, 97% recall, 98% F1-score, and 98% accuracy were obtained.

Moreso Ekong (2020) researched the effectiveness of Machine Learning (ML) algorithms: Support Vector Machine, Random Forest, and K-Nearest Neighbour (KNN) techniques for the early diagnosis of heart diseases. The ML algorithms were trained and tested for the diagnosis of cardiovascular diseases (CVD). The training performances of these models were evaluated with a k-fold cross-validation algorithm using 10 folds. The test results also show KNN with an accuracy of 0.8, SVM with an accuracy of 0.7889, and RF with an accuracy of 0.7667. KNN emerged as the best model both in training and test performances and is recommended for the early diagnosis of CVD. This underscored the effectiveness of machines in disease clinical decision support systems.

Moses et al. (2021) proposed an approach to drug resistance classification in a mixed HIV dataset, this study employs a transfer learning methodology to classify patients; responses to failed treatments specifically due to adverse drug reactions. A soft computing model was pre-trained to cluster CD4+ counts and viral loads from treatment change episodes (TCEs) originating from two distinct sources: the Stanford HIV drug-resistant database and locally obtained patient records from selected health centers in Akwa Ibom State, Nigeria. Both datasets underwent experimentation involving a traditional 2-layer neural network (NN) and a 5-layer deep neural network (DNN) with unique dropout neuron distributions. It achieved a classification accuracy of 99.40%.

Snehal et al. (2023), proposed a system to determine the antibiotic resistance level in Klebsiella. Due to the growing antimicrobial drug resistance driven by the selective pressure on antibiotics. AI was employed to expedite the detection of AMR, especially in cases where antibiotic susceptibility testing results were delayed. This study utilized machine learning (ML), a mathematical AI tool, to develop a model for predicting resistance to β-lactam drugs in Klebsiella pneumoniae. Six ML classification models were employed, with KNN and random forest proving to be the most effective among them.

Georgios et al. (2020) proposed the use of Machine Learning Off-the-Shelf Techniques to Guide Empiric Antimicrobial treatment, the study aimed to expedite the early identification and treatment of multi-drug-resistant infections among critically ill patients. Utilizing an antimicrobial susceptibility dataset of 11,496 instances from 499 patients, Microsoft Azure AutoML was employed to assess antibiotic susceptibility predictions based solely on patients' basic demographic characteristics and prior antibiotic susceptibility testing, without concurrent clinical data. Both the original and balanced datasets were analyzed, with the stack ensemble technique yielding the most favorable results, achieving an area under the curve-weighted metric of 0.822 for the original dataset and 0.850 for the balanced dataset.

Yuepeng Sun et al. (2021) conducted research on Predicting antibiotic resistance genes using shotgun metagenomics, in this study, the microbiome within activated sludge (AS) of wastewater treatment plants (WWTPs) and its influence on the resistance were investigated. The research aimed to determine the feasibility of using a machine learning approach, specifically random forests (RFs), to establish associations between ARGs and bacterial taxa in metagenomic datasets from WWTP AS. The correlations between predicted and observed ARG abundance ranged from moderate to strong when validated on testing datasets, suggesting that certain general, especially those in the (opportunistic) pathogens and indicators group, may have served as hosts for selected ARGs.

Ting Yu et al (2023) researched and came up with an algorithm to Identify Antibiotic Resistance in ESKAPE Pathogens using Machine Learning. This approach enables the identification of antibiotic resistance in 12 ESKAPE pathogens in less than 20 minutes, achieving an impressive overall accuracy rate of 89.74%. This machine-learning-based approach shows promise as a clinical tool for rapid biomedical diagnosis, facilitating the identification of antibiotic-resistant pathogens in patients.

Sanjat Kanjilal et al (2022) proposed an algorithm for estimating the impact of antibiotic exposure on antibiotic resistance in Urinary Tract Infection, to bridge this gap, they applied causal inference with targeted maximum likelihood estimation (TMLE) using machine learning on electronic health record data. Employing TMLE with logistic regression, random forests, multilayer perceptrons, and XGBoost to mitigate confounding, they calculated the average treatment effect (ATE) of nitrofurantoin (NIT) or fluoroquinolones (FQs) exposure versus other antibiotics on the risk of AMR to NIT, FQs, or amoxicillin-clavulanate at 12 months post-exposure. The final cohort included 4,573 patients with no baseline AMR or antibiotic exposure in the previous 12 months, treated with NIT, FQs, or oral beta-lactams. XGBoost models outperformed others, and the results revealed that NIT-treated outpatients had a higher risk of AMR at 12 months compared to those treated with FQs.

RESEARCH METHODOLOGY

It is critical to recognize that the analysis of the available data for pediatric patients is the exclusive data focus of this study. The study will concentrate on the larger trends and patterns in microbial resistance and antibiotic effectiveness for the pediatric population during the designated time frames rather than examining the direct effects of COVID-19 on specific patients. Access to medical records and laboratory reports, as well as the availability of appropriate data, determined the study's primary geographical scope. The detailed exposition of the classification model is delineated within the framework illustrated in Figure 1.

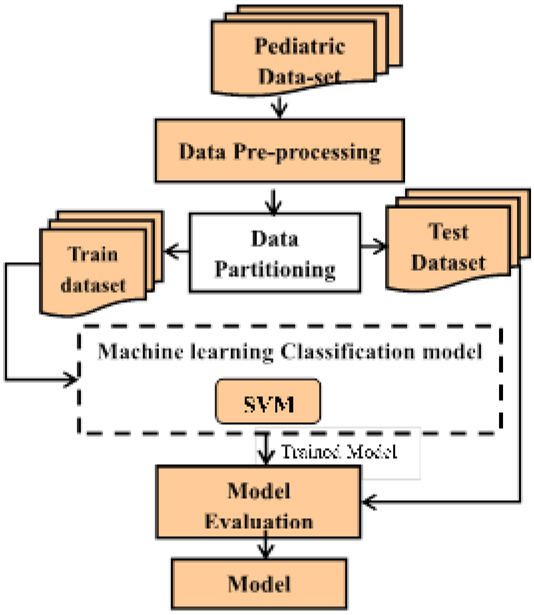


Figure 1: Diagram of Proposed System Architecture

(i.) **Data Sources:** Pediatric data was obtained from Immanuel General Hospital in Eket and the University of Uyo Teaching Hospital to compile a database of medications administered to pediatric patients and assess their efficacy. The data included microbial culture results and antibiotic prescription history, spanning both the pre-COVID-19 and COVID-19 periods. The inclusion of patients' names and personal details was deemed unnecessary and therefore not incorporated into the database. A cross-section of the sample dataset is shown in Figure 2.

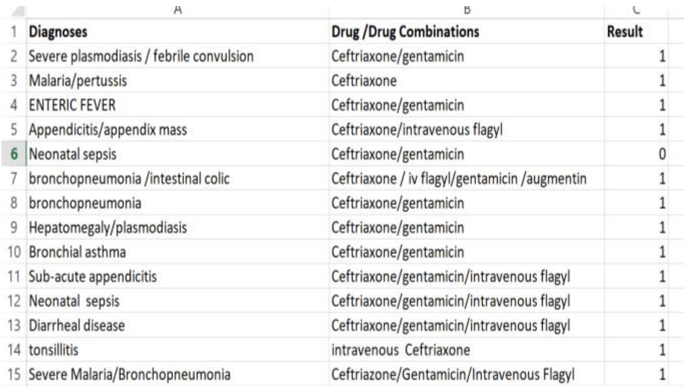
(ii.) **Data Pre-processing:** The data has been subjected to cleaning and preprocessing, which involves addressing missing values, standardizing formats, and verifying data integrity.

(iii.) **Data Splitting:** The dataset was divided into training, validation, and testing sets. A typical split might be 70% for training, 15% for validation, and 15% for testing.

(iv.) **Model Training:** The SVM model underwent training using the designated training dataset, during which hyper-parameters were optimized and the model was adjusted as necessary to achieve optimal performance.

(v.) **Model Evaluation:** The model underwent evaluation using the validation dataset, with a focus on metrics such as accuracy, precision, recall, and F1-score.

(vi.) **Model Testing:** The support vector machine (SVM) model underwent validation on the testing dataset to assess its performance and real-world suitability. This process yielded valuable insights into the model's practical application.



	A	B	C
1	**Diagnoses**	**Drug /Drug Combinations**	**Result**
2	Severe plasmodiasis / febrile convulsion	Ceftriaxone/gentamicin	1
3	Malaria/pertussis	Ceftriaxone	1
4	ENTERIC FEVER	Ceftriaxone/gentamicin	1
5	Appendicitis/appendix mass	Ceftriaxone/intravenous flagyl	1
6	Neonatal sepsis	Ceftriaxone/gentamicin	0
7	bronchopneumonia /intestinal colic	Ceftriaxone / iv flagyl/gentamicin /augmentin	1
8	bronchopneumonia	Ceftriaxone/gentamicin	1
9	Hepatomegaly/plasmodiasis	Ceftriaxone/gentamicin	1
10	Bronchial asthma	Ceftriaxone/gentamicin	1
11	Sub-acute appendicitis	Ceftriaxone/gentamicin/intravenous flagyl	1
12	Neonatal sepsis	Ceftriaxone/gentamicin/intravenous flagyl	1
13	Diarrheal disease	Ceftriaxone/gentamicin/intravenous flagyl	1
14	tonsillitis	intravenous Ceftriaxone	1
15	Severe Malaria/Bronchopneumonia	Ceftriazone/Gentamicin/Intravenous Flagyl	1

Figure 2: Cross section of the dataset

Support Vector Machine (SVM)

Support vector machine (SVM) is a powerful supervised machine learning algorithm used for classification and regression tasks (James *et al.*, 2024a; James *et al.*, 2024b). SVM is also a powerful machine learning algorithm that is applied to classify effective antibiotic combinations for pediatrics. It is a powerful algorithm for classifying effective antibiotic combinations for pediatrics, offering high accuracy, robustness to noise, and flexibility. However, careful attention must be paid to kernel selection, hyperparameter tuning, and scalability. SVM is effective in handling high-dimensional data, such as genomic or proteomic data by capturing non-linear relationships between antibiotic combinations and their effectiveness. As such, missing data, which is common in clinical datasets are handled. For a Support Vector Machine (SVM) model to classify effective antibiotic combinations for pediatrics, the following models hold:

To minimize the objective function (FM): This balanced the trade-off between model complexity w^T*w and misclassification error ε_i.

$$F_M = 1/2 * w^T * w + C * \sum_{i=1}^{n} \varepsilon_i \qquad (i)$$

Subject to constraints:

$$F_{CM} = w^T * \varphi(X_i) + b) \geq 1 - \varepsilon_i \qquad (ii)$$

This ensures correct classification with a margin of at least $-\varepsilon i \geq 0$: and allows for some misclassifications (slack variables). To predict the label (effective or ineffective) for a new antibiotic combination X;

$$f(X) = sign(w^T * \varphi(X) + b) \qquad (iii)$$

Therefore, mapping the input data to a higher-dimensional space using the Kernel Function (RBF) to enable non-linear classification;

$$K(X_i, X_j) = \exp\left(-\gamma * \left\|X_i - X_j\right\|^2\right) \qquad (iv)$$

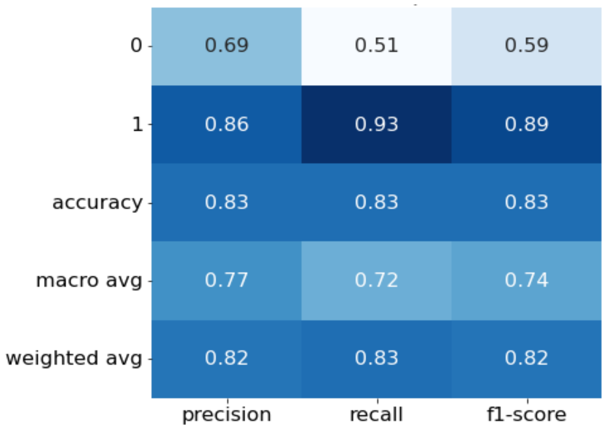


Figure 3a: Pre-COVID-19 Data Classification Report

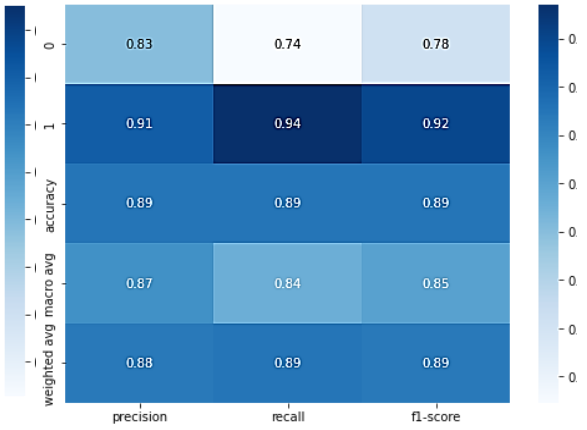


Figure 3b: Classification Report of SVM Model

Where;
X = feature matrix (antibiotic combination characteristics)
Y = label vector (effective or ineffective)
C = regularization parameter kernel coefficient
K = kernel function (e.g., radial basis function (RBF))
w = weight vector
- b = bias term
- ε_i = slack variable
- $\varphi(X_i)$ = feature mapping (kernel trick)

RESULTS AND DISCUSSION

Figure 3a shows a report that was generated using data from the pre-COVID-19 era covered in this research. It shows a precision of 86% and 69% for effective drug and less effective drug combinations respectively for the pre-COVID-19 era while Figure 3b shows a precision of 91% and 83% for effective drug and less effective drug combinations respectively. Also, Figure 3a shows a recall rate was 93% and 51% for the effective and non-effective drug combinations respectively for the pre-COVID-19 while Figure 3b shows 94% and 74 % using the same parameter. The recall values show the model's ability to capture instances of each class.

More so, Figure 3a shows that the F1-score of 0.89 and 0.59 were obtained for effective and non-effective combinations respectively, indicating that there is a harmonic mean of precision and recall. It provides a balanced measure of the model's performance for each class with an overall accuracy of the model as 0.83 i.e. 83%, Figure 3b shows that the F1-score of 0.93 and 0.83 were obtained for effective and non-effective combinations respectively for the COVID-19 onset era. It provides a balanced measure of the model's performance for each class with an overall accuracy of the model is 0.89 i.e. 89%

In summary, while the model shows balanced performance in terms of F1-score for both classes, it demonstrates higher precision and recall for the "Effective" class compared to the "non-effective" class. This evaluation provides insights into the strengths and weaknesses of the model's predictions, which can guide further model refinement and optimization.

636 numbers of instances were correctly predicted as positive (Effective) by the model, while 112 instances were correctly predicted as negative (Ineffective) by the model. Also, 106 instances were incorrectly predicted as positive (Effective) when they were negative (Ineffective). Lastly, we had 51 instances that were misclassified which means they were incorrectly predicted as non-effective when they are effective.

Figure 4a is the Confusion Matrix of SVM Model Post-COVID-19 dataset, while Figure 4b Confusion Matrix of SVM Model for Before COVID-19.

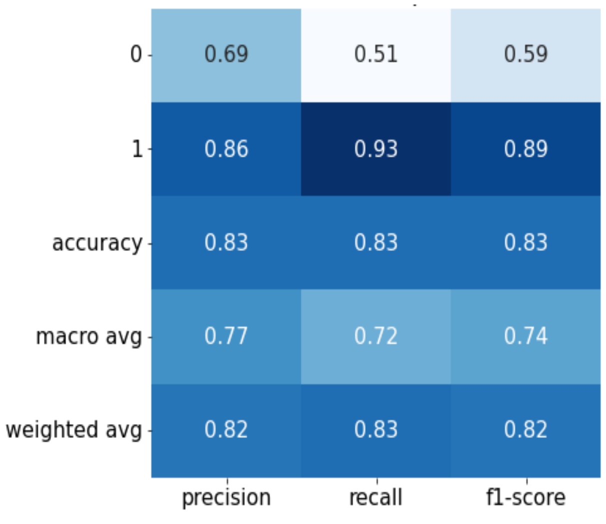


Figure 4a: Confusion Matrix of SVM Model Post-COVID-19 dataset

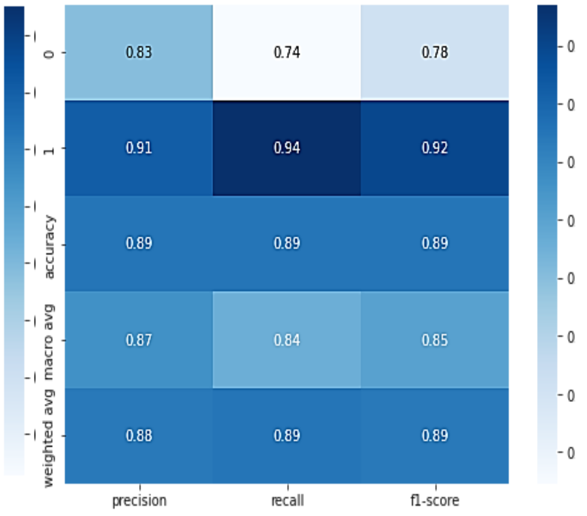


Figure 4b: Confusion Matrix of SVM Model for Before COVID-19

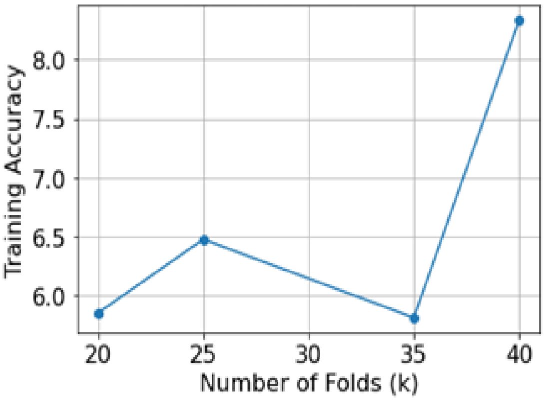


Figure 5a: SVM - Training Accuracy vs K –folds

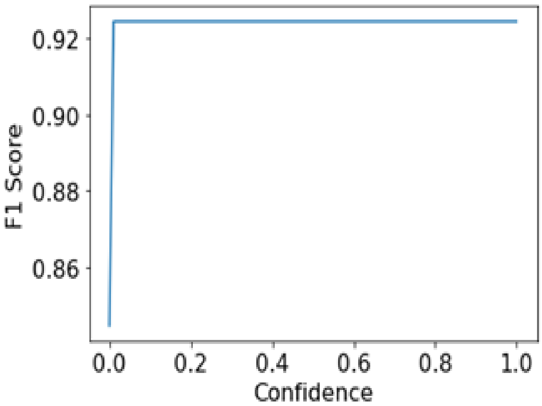


Figure 5b: F1 Confidence Curve

Here, 856 number of instances were correctly predicted as positive (Effective) by the model, while 246 instances were correctly predicted as negative (Ineffective) by the model. 88 number of instances were incorrectly predicted as positive (Effective) when they were negative (Ineffective). Lastly, we had 52 instances incorrectly predicted as Ineffective when they were effective.

Figure 5a shows SVM - Training Accuracy vs K –folds. The performance of the SVM model trained using the training dataset is evaluated using a 40-40-fold cross-validation algorithm. The accuracy curve of the ML models across 40-folds of the 40-fold cross-validation is presented in Figure 5a. The figure shows that the accuracy fluctuates between k-20 and k=35 and increases drastically thereafter stressing the need for higher folds in achieving a better accuracy. We built the final accuracy we used at 40 folds.

Figure 5b shows the F1 Confidence Curve shows the model's performance as the required level of prediction confidence changes. It combines the notions of F1 score with certainty about confidence. In this instance, prediction accuracy rises as the model gets more confident in its predictions.

Figure 6a shows the Precision-Recall Curve of the model while Figure 6b shows the Precision-Confidence Curve. This curve illustrates how well the model predicts the various antibiotic combination outcomes (recall) and ensures that the predictions are accurate (precision). Precision rises with recall until it reaches its average number of right predictions, at which point it falls.

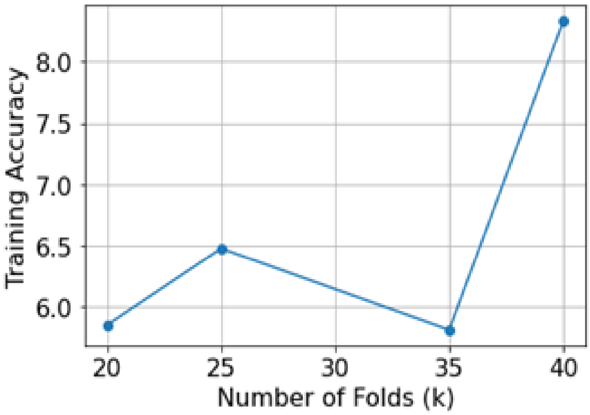


Figure 6a: Precision-Recall Curve

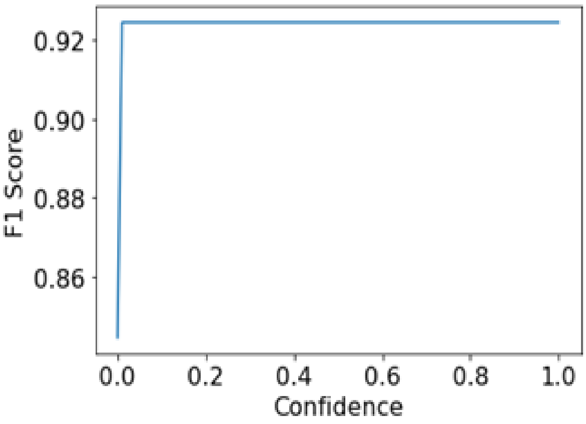


Figure 6b: Precision-Confidence Curve

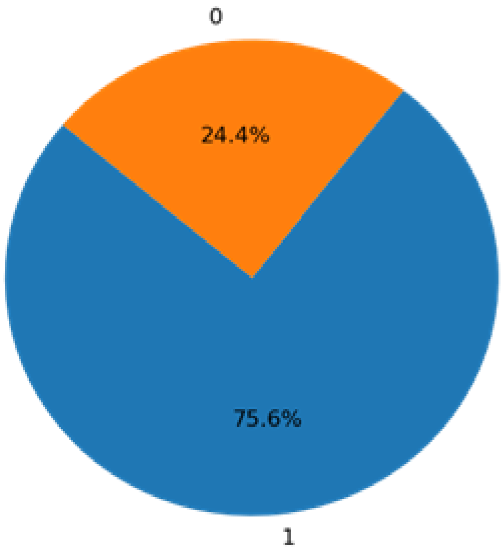


Figure 7a: Percentage ratio of classification of result (before COVID-19)

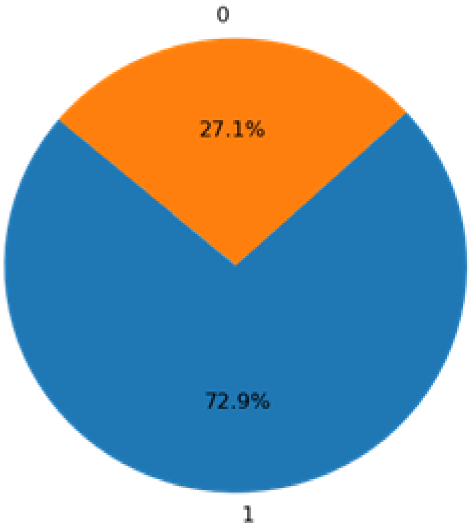


Figure 7b: Percentage ratio of classification of result (after the onset of COVID-19)

Whereas Figure 7a shows the extent of effectiveness in the percentage of the effective and non-effective drug combinations for pediatrics before COVID-19 indicating 75.6% and 24.4% for effective and non-effective combinations respectively, Figure 7b indicates 72.9% and 27.1% for effective and non-effective combinations in the period after the onset of COVID-19. The results indicate that there has been an increase in resistance to antibiotics and antibiotic combinations after the onset of COVID-19 in pediatric patients.

CONCLUSION

The findings of this research highlight the effectiveness of machine learning algorithms in classifying antibiotic combinations for pediatric patients based on microbial culture and sensitivity patterns. Through the implementation of the proposed system, we successfully answered the question of whether there has been an increase in resistance to antibiotics among pediatric patients after the onset of COVID-19 in the affirmative. The system demonstrated promising results in predicting effective antibiotic combinations with a percentage accuracy of 83% for the pre-COVID era and 89% for the COVID-19 era, thereby assisting healthcare providers in making informed treatment decisions. By leveraging machine learning technology, we have successfully assessed the effectiveness of antibiotic treatment, which will ultimately result in improved patient outcomes and targeted interventions. In addition, the research also provides insight into the evolving landscape of antibiotic resistance in light of the COVID-19 pandemic. The analysis of data before and after the COVID-19 pandemic provides valuable insights into the evolving patterns of antibiotic resistance. This underscores the importance of flexible strategies to address emerging challenges. The study underscores the importance of implementing preventive measures to mitigate antibiotic resistance and improve pediatric healthcare outcomes. The significance of this research lies in its potential to advance pediatric healthcare, combat antibiotic resistance, leverage machine learning in medicine, and provide crucial insights into the impact of the COVID-19 pandemic on antibiotic effectiveness. By addressing these important areas, the study can drive evidence-based practices, contribute to academic knowledge, and have a positive impact on global health outcomes, ultimately working towards a more sustainable and effective approach to pediatric antibiotic treatment. To sum up, this study offers a ground-breaking remedy for the growing problem of antibiotic resistance in pediatric patients. The machine learning-based approach, which offers excellent accuracy and versatility, represents a paradigm shift in antibiotic selection. This research adds a useful tool to improve antimicrobial stewardship, which will ultimately improve patient outcomes in pediatric healthcare as we navigate the challenges imposed on humanity by COVID-19.

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