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Article

Machine Learning Modelling of Antibiotic Resistance of Faeca Microbial Isolates of Muturu and White Fulani Cattles

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Abstract

Antimicrobial Resistance (AMR) is already a global health concern and challenging pharmaceutical progress in the development and design of antibiotics. It has also been reported by WHO to be a major threat and thus the need to find a solution to this public health issue through modelling of this resistance. This research thus investigated the Machine Learning (ML) antimicrobial modelling of antimicrobial resistance characterization of the faecal samples of muturu and white Fulani cattle. This experiment involved collecting 40 cattle faecal microbial isolates. The isolated microbes (40 isolates) were subjected to antimicrobial resistance tests, and the results were modelled through machine learning algorithms. The results showed that this model was dependent on specific antibiotics. Some models, such as Naïve Bayes, performed excellently for perfloxacin, Augmentin, with accuracy of 1.00±0.00 and Random Forest (RF) for Chloramphenicol, Amoxicillin, and Gentamcyin with high accuracy (0.92±0.08). While ensemble tree methods (RF, decision tree, and gradient boosting) achieve 100% accuracy, Support Vector Classifier (SVC) remained the most resilient generalized predictor. For the bacteria isolates from white Fulani, only support vector classifier was consistent in predicting AMR across all the tested antibiotic. The high standard deviation observed in some drugs like oflaxocin and cotrimethazol could be due to the dataset or the microbial interaction with drugs. There is therefore a need to build reliable ML-driven AMR pipelines that should address critical global heath burden. Poorly managed Fulani cattle herding risks antibiotic abuse, but accurate modeling provides vital decision support.

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1. Introduction

The use of machine learning in management of antibiotic resistance is very vital as increasing resistance to antibiotics and difficulty in the treatment of multi-drug resistance is becoming a global public health challenge [1]. Machine learning had however shown promising results and can provide the necessary tools to inform antimicrobial prescription and thus fight antimicrobial resistance [2]. Antimicrobial resistance is a slow-moving disaster and thus there is an immediate need to prevent this impact [3]. It is also a global problem that is undermining advances in drug development. [4]. The misuse or overuse of drugs has led to the development of antibiotic-resistant drugs [5] and it is now a global public health concern according to World Health Organisation [6]. In 2050, the mortality as a result of antibiotic resistance per 10,000 people in Africa and Asia will be twice as high as those in North America, Europe and Australia [7]. As reported by WHO, AMR is among the top ten global threat. [2]. This pandemic has led to the death of over 1.27 million people globally [4], increasing economic cost due to morbidity and mortality. It has been estimated that the economic lost resulting from antimicrobial resistant to be $55 billion. Our existing laboratory-based diagnostic cannot provide enough information for effective AMR surveillance [8].

Antimicrobial resistance lowers people's ability to control pathogen and treat diseases and the extremely fast rate of microbial mutation due to this, is rendering many drugs useless and our current antibiotics might be the best we will ever have [9]. It is also becoming a challenge in livestock production as a result of ignorance of some livestock farmers who know little or nothing about the antibiotics, they administer to their animals leading to drug abuse. It is often associated with high morbidity and mortality. Multidrug resistance can be difficult to treat and, in some cases, untreatable. Effective therapies are lacking and so are successful prevention measures. Few antibiotics require novel treatment options and alternative antimicrobial therapies [10]. Easily treatable bacterial infections are becoming increasingly

untreatable. This correlates with antibiotic use and thus better antimicrobial stewardship, prevention, and infection diagnosis will help conserve currently available antimicrobial agents [11]. Machine learning is playing a very pivotal role in antimicrobial management. It has found usefulness in the development of antimicrobial clinical decision, susceptibility genotype/phenotype prediction, novel AMR agent discovery and AMR therapy optimization [12]. It was reported in [13] that gradient boosting, random forest and GBoost outperformed other ML models. XGBoost was reported by [14] to outperform every other ML model in the prediction of antibiotic resistance. In [15] and [16] the Naïve Bayes model was employed in antimicrobial resistance modelling and was able to extract the key factors of antimicrobial resistance using Naïve Bayes and apriori model. The probabilities of ineffective treatment as a result of AMR were estimated by [17]. The most common algorithm in machine learning had been reported to be logistic regression, decision trees and random forest. [18]. This research is aimed at machine learning modelling of antibiotic resistance from the faecal microbial isolates of Muturu and White Fulani Cattle Breed.

2. Materials and Methods

2.1. Location

The study was carried out at the University of Benin Farm Project, University of Benin, Benin City, Edo State, Nigeria. The University of Benin farm project is situated on latitude 6° and 6°10.57°N and longitude 5°36'37.50°E but the animals were sourced from Warri, Delta State and Institute of Agriculturai Research and Training (IART), Ibadan.

2.2. Data collection and laboratory analysis

Faecal sample was collected from 19 muturu and white fulani cattle using a sterile faecal sample collector for microbial characterization and antibiotic testing.

2.3. Serial dilution

The total heterotrophic bacterial counts were determined by serial dilution. Briefly, One (1) gram each of cow dung was weighed into 9ml of sterile normal saline and homogenized to form the stock solution. From the stock solution, 1 ml was transferred into test tube labelled 10^{-1} and mixed. Using a new sterile pipette each time, 1ml of 10^{-1} was transferred to another tube labelled 10^{-2}. This same procedure was repeated until 10^{-5}. One (1) ml from tube 10^{-5} will be discarded. This will be repeated for all samples [19].

2.4. Enumeration of bacteria

One (1) ml each of serially diluted samples from tubes 10-4 and 10-5 will be pipetted onto a sterile agar plate. Twenty (20) ml molten Nutrient Agar (HiMedia, India) at 45 °C will be aseptically dispensed onto the agar plate and gently rocked. The plates will be allowed to solidify and incubated upside down at 37 °C overnight. Colonies formed on the plates will be counted accordingly.

2.5. Identification and characterization of bacterial isolates

This included the characterization of pure culture which will be based on conventional phenotypic methods, morphology, Gram stain, motility, spore formation, haemolysis, and growth on triple sugar iron (TSI) medium, catalase, oxidase, indole, Voges Proskauer, methyl red, citrate, starch, and sugar fermentation tests. Biochemical tests will be interpreted to determine the presumptive nomenclature of the bacteria isolates using Bergey's Manual of Determinative Bacteriology and ABIS online-advanced bacterial identification system [20]. The pure identified bacterial isolates were used for antibiotic susceptibility testing; 40 microbial isolates were identified.

2.6. Antibiotic susceptibility testing

The antibiotic susceptibility testing was performed using the Kirby-Bauer disk diffusion method [21] and according to the standard microbiological guidelines (CLSI, 2012). Bacterial suspensions equivalent to 0.5 MacFarland standard was aseptically spread on solidified Mueller-Hinton agar (Himedia, India) using sterile cotton swab sticks. Inoculated plates were allowed to dry. Afterwards, the antibiotic multi-discs at a spatial orientation of 16 mm (distance between discs) were aseptically placed on the inoculum using sterile forceps. The antibiotics that were used in this study and their concentrations (Abtek, UK) included amoxicillin (25 µg), cotrimoxazole (25 µg), nitrofurantoin (300 µg), gentamicin (10 µg), nalidixic acid (30 µg), tetracycline (30 µg), ofloxacin (30 µg), augmentin (30µg), cloxacillin (5 µg), erythromycin (5 µg), streptomycin (10 µg) and 221 chloramphenicol (10 µg). The results of the diameters of the zones of inhibition were interpreted by comparing them with the Clinical Laboratory Standards Institute standards [22] and each isolate was recorded as resistant, intermediate or susceptible to the various antibiotics. Multidrug resistance among the isolates will be defined as resistance to ≥ 3 classes of antibiotics.

2.5. Classification and cluster analysis of antibiotic resistance

The collected data was subjected to outlier detection as part of the preprocessing step using the sklearn library in Google Colaboratory. To enhance the model's performance, feature scaling was carried out through normalization of the collected data. This was done for both the train and test dataset to ensure that each feature has the same order of magnitude. The data was normalized using standard scaler. The normalisation equation is as shown below.

$$Y = \frac{2(x - x\min)}{(x\max - x\min)} - 1 \quad (1)$$

Google Collaboratory using Python Notebook was used for the classification of the antibiotic resistance data. The clustering was carried out on the antibiotic resistance of the fecal sample to know the patterns of the drugs sensitivity. Sklearn library was used to implement the various algorithms. The data used to train this model was split into training and test datasets using the split train test function from the SKlearn library in ration of 80:20. The train models was further subjected to k cross-validation (KCV) with 10 folds, to further optimize this model and increase the prediction accuracy via parameter tuning.

3. Results and Discussion

The antimicrobial resistance of the bacteria isolated from the muturu cattle can be seen in the Table 1 below. Pefloxacin has the highest level of sensitivity to the isolated microbes without any form of antimicrobial resistance. High level of antimicrobial resistance to Oxfloxacin can also be observed in this isolated sample. Meanwhile, the majority of the antimicrobial resistance of Sparfloxacin is intermediate and thus cannot be classified into sensitive or resistance.

Table 1. Antimicrobial Resistance in Muturu Cattle Breed

S/N	IDENTITY	PEF	OFX	S	SXT	CH	SP	CPX	AM	AU	CN
1	Micrococcus sp.	2	1	2	2	1	0	1	2	2	1
2	Bacillus sp.	0	0	0	0	0	0	0	0	2	0
3	Bacillus sp.	0	0	0	0	0	0	0	0	2	0
4	Micrococcus sp.	2	1	2	2	1	0	1	2	1	0
5	Lactobacillus sp.	2	1	2	2	1	0	2	2	2	1
6	Lactobacillus sp.	2	1	2	2	1	0	2	2	2	1
7	Pseudomonas sp.	2	1	2	2	0	2	2	1	2	1
8	Micrococcus sp.	2	1	2	2	1	0	2	2	2	0
9	E. coli	2	1	2	2	1	0	2	2	2	1
10	E. coli	2	1	2	1	1	0	2	2	2	0
11	Bacillus sp.	0	0	0	1	0	0	0	1	1	0
12	Streptococcus sp.	2	1	0	2	2	0	2	0	0	0
13	Corynebacterium sp.	2	0	0	0	0	0	2	0	0	1
14	Citrobacter freudii	2	1	2	1	2	0	2	1	2	1
15	Staphylococcus aureus	2	1	0	2	2	1	1	1	0	1
16	Staphylococcus aureus	2	2	0	2	2	2	1	1	0	2
17	Micrococcus sp.	2	1	2	2	2	0	2	1	2	1
18	Bacillus sp.	0	1	0	2	2	0	2	1	1	0
19	Citrobacter freudii	2	1	2	2	2	0	2	2	1	1
20	Streptococcus sp.	2	2	0	2	2	0	0	2	0	0
21	E. coli	2	1	2	2	1	1	2	1	1	2
22	E. coli	2	1	2	2	1	1	2	1	1	1
	Resistance (%)	0.0	72.7	0.0	13.6	40.9	13.6	18.2	40.9	27.3	45.4
	Sensitive (%)	81.8	9.1	59.1	72.8	36.40	0.1	18.2	40.9	50.0	10.
	Not available (%)	18.2	18.2	40.9	13.6	22.7	86.3	63.6	18.2	22.7	44.6

PEF = *Perfloxacin,* ***OFX*** = *Ofloxacin,* ***S*** = *Streptomycin,* ***SXT*** = *Cotrimethazol,* ***CH*** = *Chloramphenicol,* ***SP*** = *Sparfloxacin,* ***CPX*** = *Ciproxacin,* ***AM*** = *Amoxicillin,* ***AU*** = *Augmentin, and* ***CN*** = *Gentamycin.*

In Table 2 on antimicrobial resistance, all the microbes were sensitive to perfloxacin with the exception of Neisseria sp, Lactobacillus sp and Corynebacterium sp, meanwhile the microbes were all resistance to Augmentin with the exception of only Neisseria sp and Corynebacterium sp which were intermediate or not available. The same antimicrobial activity is seen in Amoxicillin in which all the microbes with the exception of Corynebacterium sp and Salmonella sp were resistant.

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Table 2. Antimicrobial Resistance in White Fulani Cattle Breed

S/N	IDENTITY	PEF	OFX	S	SXT	CH	SP	CPX	AM	AU	CN
1	Corynebacterium sp.	0	0	0	0	0	0	0	0	0	1
2	Neisseria sp.	0	1	0	0	2	0	1	1	0	0
3	Bacillus sp.	0	0	0	2	2	0	2	1	1	1
4	Lactobacillus sp.	2	0	2	2	2	0	2	1	1	0
5	Lactobacillus sp.	2	0	2	2	2	0	2	1	1	1
6	Bacillus sp.	0	0	0	0	2	0	2	2	1	1
7	Bacillus sp.	0	0	0	0	2	0	2	1	1	0
8	Bacillus sp.	0	1	0	0	2	0	2	1	1	0
9	Bacillus sp.	0	0	0	0	2	0	2	1	1	1
10	Bacillus sp.	0	1	0	0	2	0	2	2	1	0
11	Neisseria sp.	0	1	0	0	2	0	1	1	0	0
12	Micrococcus sp.	2	1	2	2	2	0	2	1	1	0
13	E. coli	2	1	2	2	2	1	2	1	1	1
14	Salmonella sp.	2	0	2	2	2	0	2	1	1	0
15	Salmonella sp.	2	0	2	2	1	0	2	0	1	1
16	Salmonella sp.	2	1	0	1	1	0	2	2	1	2
17	Salmonella sp.	2	0	1	1	1	0	2	2	1	2
18	E. coli	2	0	1	1	1	1	2	2	1	1
	Resistance (%)	0.0	38.9	13.3	16.7	22.2	11.1	11.1	50.0	83.3	38.9
	Sensitive (%)	50	0.0	33.3	38.9	71.8	0.0	82.9	11.1	0.0	11.1
	Intermediate (%)	50	61.1	53.4	61.1	06.0	88.8	6.0	48.9	16.7	50.0

PEF = *Perfloxacin,* ***OFX*** = *Ofloxacin,* ***S*** = *Streptomycin,* ***SXT*** = *Cotrimethazol,* ***CH*** = *Chloramphenicol,* ***SP*** = *Sparfloxacin,* ***CPX*** = *Ciproxacin,* ***AM*** = *Amoxicillin,* ***AU*** = *Augmentin, and* ***CN*** = *Gentamycin.*

Table 3 shows that Naïve Bayes, decision tree, gradient boosting, and voting were the best machine learning model for predicting Pefloxacin antimicrobial resistance. Support Vector Machine (SVM) with accuracy of 80% was the best for the prediction of Oxfloxacin antimicrobial resistance. Streptomycin antimicrobial resistance was best predicted using gradient boosting, histgradient boosting and Extra tree with 100% accuracy and zero.

Table 3. Muturu Antimicrobial Resistance Modelling Accuracy

Model	PEF	OFX	S	SXT	CH	SP	CPX	AM	AU	CN
NB	1.00±0.00	0.70±0.33	0.75±0.32	0.69±0.35	0.88±0.11	0.85±0.23	0.60±0.40	0.88±0.11	1.00±0.00	0.88±0.11
SVC	0.95±0.15	0.80±0.24	0.80±0.33	0.88±0.09	0.88±0.09	0.88±0.09	0.88±0.09	0.88±0.09	0.88±0.09	0.83±0.08
HiGB	0.67	0.60±0.30	0.75±0.40	0.65±0.39	0.81±0.08	0.90±0.20	0.45±0.42	0.88±0.09	0.95±0.15	0.87±0.07
GB	1.00±0.00	0.60±0.25	0.65±0.00	0.65±0.22	0.82±0.26	0.90±0.00	0.45±0.13	0.82±0.20	0.95±0.13	0.87±0.12
RF	0.95±0.15	0.65±0.32	0.75±0.33	0.65±0.39	0.92±0.08	0.90±0.20	0.50±0.39	0.92±0.08	0.95±0.15	0.92±0.08
DT	1.00±0.00	0.65±0.32	0.75±0.34	0.65±0.39	0.89±0.11	0.90±0.20	0.45±0.42	0.89±0.11	1.00±0.00	0.87±0.06
ET	0.95±0.15	0.60±0.30	0.75±0.40	0.65±0.39	0.82±0.08	0.90±0.20	0.45±0.42	0.82±0.08	0.95±0.15	0.87±0.07
BG	0.90±0.20	0.80±0.24	0.70±0.24	0.85±0.23	0.87±0.06	0.90±0.20	0.75±0.25	0.84±0.08	0.90±0.20	0.84±0.10
VL	0.88±0.15	0.63±0.22	0.57±0.22	0.75±0.13	0.80±0.07	0.88±0.15	0.70±0.24	0.80±0.07	0.88±0.15	0.84±0.11
VRF	1.00±0.00	0.57±0.25	0.75±0.25	0.68±0.21	0.91±0.05	0.90±0.20	0.45±0.42	0.91±0.05	1.00±0.00	0.91±0.08
VNB	1.00±0.00	0.45±0.35	0.82±0.15	0.75±0.13	87±0.07	0.88±0.15	0.65±0.39	0.87±0.07	1.00±0.00	0.88±0.11
VE	1.00±0.00	0.57±0.25	0.75±0.25	0.75±0.13	0.89±0.05	0.88±0.15	0.60±0.37	0.89±0.05	1.00±0.00	0.92±0.09
KN	0.90±0.20	0.65±0.32	0.65±0.32	0.75±0.34	0.77±0.15	0.85±0.23	0.55±0.35	0.76±0.15	0.90±0.20	0.77±0.15

NB *~ Naïve Bayes,* ***SVC*** *~ Support Vector Cluster,* ***HiGB*** *~ Histgradient Boost,* ***GB*** *~ Gradient Boost,* ***RF*** *~ Random Forest,* ***DT*** *~ Decision Tree,* ***ET*** *~ Extra Tree,* ***BG*** *~ Bagging,* ***VL*** *~ Votting Logistic,* ***VRF*** *~ Votting Random Forest,* ***VNB*** *~ Votting Naïve Bayes,* ***VE*** *~ Votting Ensembled, and* ***KN*** *~ K Neighbors.*

That standard deviation. None of the models were good enough for fitting and prediction for Cotrimethazol antimicrobial resistance except SVM with 83% accuracy and 0.08 standard deviation. The SVM gave the best result (83%) for chloramphenicol with the least accuracy (53%) being random forest. The models for Sparfloxacin are Naïve Bayes, random forest, gradient boosting, histgradient boosting, and voting with 100% accuracy and zero standard deviation. Ciproflaxocin and Augmentin antimicrobial resistance prediction accuracy was high with all the models used. Only SVM predicted amoxicillin with high accuracy. The rest model accuracy was very poor.

Table 4 shows the machine learning modelling for predicting antimicrobial resistance of bacteria isolates from white Fulani cattle and as with muturu, the accuracy for Pefloxacin was high with all the models but highest with gradient boosting, histgradient boosting, and extra tree. The prediction however for oxfloxacin was however poor for all the models with the exception of SVM which has shown high performance for all the antibiotics assessed thus far.

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gradient boosting, histgradient boosting, and extra tree for streptomycin. Meanwhile, all the prediction were not good enough for cotrimethazole and chloramphenicol except SVM which had performed well consistently where other models fails. Sparfloxacin was best predicted using gradient boosting, histgradient boosting, Naïve Bayes, and voting.

Table 4. White Fulani Antimicrobial Resistance Modelling Accuracy

Model	PEF	OFX	S	SXT	CH	SP	CPX	AM	AU	CN
NB	0.90±0.20	0.43±0.25	0.43±0.25	0.63±0.22	0.57±0.32	1.00±0.00	0.93±0.13	0.33±0.18	0.93±0.13	0.53±0.12
SVC	0.88±0.09	0.83±0.08	0.83±0.08	0.83±0.08	0.83±0.08	0.83±0.08	0.83±0.08	0.83±0.08	0.83±0.08	0.83±0.08
HiGB	1.00±0.00	0.60±0.30	1.00±0.00	0.63±0.22	0.70±0.27	1.00±0.00	0.93±0.13	0.23±0.20	0.93±0.13	0.37±0.12
GB	1.00±0.00	0.43±0.25	1.00±0.00	0.63±0.22	0.70±0.26	1.00±0.00	0.93±0.13	0.23±0.20	0.93±0.13	0.37±0.12
RF	0.90±0.20	0.43±0.25	0.90±0.20	0.53±0.12	0.53±0.34	0.90±0.20	0.93±0.13	0.23±0.20	0.93±0.13	0.37±0.22
DT	0.90±0.20	0.43±0.25	0.90±0.20	0.63±0.22	0.70±0.26	0.90±0.20	0.93±0.13	0.23±0.20	0.93±0.13	0.47±0.22
ET	1.00±0.00	0.43±0.40	1.00±0.00	0.63±0.22	0.70±0.27	1.00±0.00	0.93±0.13	0.23±0.20	0.93±0.13	0.47±0.12
BG	0.90±0.20	0.60±0.08	0.47±0.12	0.30±0.16	0.70±0.16	0.87±0.16	0.93±0.13	0.53±0.12	0.93±0.13	0.47±0.12
VL	0.80±0.07	0.53±0.12	0.57±0.33	0.63±0.22	0.63±0.22	0.87±0.16	0.93±0.13	0.40±0.18	0.93±0.13	0.57±0.25
VRF	0.91±0.05	0.43±0.25	0.53±0.40	0.62±0.22	0.63±0.22	0.90±0.20	0.93±0.13	0.33±0.18	0.93±0.13	0.47±0.12
VNB	0.87±0.07	0.43±0.25	0.70±0.27	0.63±0.22	0.57±0.33	1.00±0.00	-	0.33±0.18	-	0.73±0.25
VE	0.89±0.05	0.53±0,12	0.60±0.39	0.63±0.22	0.63±0.22	1.00±0.00	-	0.33±0.18	-	0.57±0.25
KN	0.90±0.20	0.43±0.25	0.77±0.20	0.63±0.22	0.63±0.22	0.60±0.33	0.93±0.13	0.23±0.20	0.93±0.13	0.53±0.12

NB *~ Naïve Bayes,* ***SVC*** *~ Support Vector Cluster,* ***HiGB*** *~ Histgradient Boost,* ***GB*** *~ Gradient Boost,* ***RF*** *~ Random Forest,* ***DT*** *~ Decision Tree,* ***ET*** *~ Extra Tree,* ***BG*** *~ Bagging,* ***VL*** *~ Votting Logistic,* ***VRF*** *~ Votting Random Forest,* ***VNB*** *~ Votting Naïve Bayes,* ***VE*** *~ Votting Ensembled, and* ***KN*** *~ K Neighbors.*

An effective prediction of the likelihood of antibiotics that will be resisted by microbes based on the historical exposure of the microbes to that particular antibiotic helps in the redesign of the antibiotic for better potency, and also helps the farmer choose wisely the best antibiotic for their livestock disease management. It can be seen that Naïve Bayes, Gradient Boosting, and Decision Tree are the best machine learning models for predicting Pefloxacin antimicrobial resistance. 0This is based on their Accuracy and standard deviation. [18] had reported the high frequency of the use of Decision Tree and Random Forest for higher accurate prediction of antimicrobial resistance. Accuracy of 1.00 and zero standard deviation as shown in our findings, implied that there is a 100% chance of predicting antimicrobial activities of Pefloxacin and that the confidence in such data is high due to the observed zero error. [23] also reported an accuracy of 0.73 for Random Forest in the prediction of antimicrobial resistance which is contrary to random forest accuracy of 0.95 for perfloxacin. This could be due to differences in sample size, parameter tuning or even environment.

In predicting the antimicrobial resistance of Ofloxacin, it is observed that the best was SVM with accuracy 0.80±0.24 followed by Decision Tree with an accuracy of 0.65±0.32 and Extra Tree with 0.60±0.30. The accuracy of ofloxacin model was observed to be poor with high error for all the model. Poor accuracy could be due to low input data in training and testing dataset if the model does not have enough data to learn from [23]. Streptomycin antimicrobial resistance was best predicted using SVM with accuracy 0.80±0.32 followed by Extra Tree with accuracy of 0.75±0.32. High standard deviation in this particular model also makes it less reliable for predicting the above drug antibiotic resistance. The only model that is good for the prediction of Co-trimethazole is SVM with an accuracy of 0.88±0.09. The other models had lower accuracy, which makes them unsuitable for modeling of Co-trimethazole. The antimicrobial activities of these microbes have shown a high level of sensitivity compared to resistance or intermediate activity. SVM is a good model for Co-trimethazole, the accuracy is high, and the standard deviation is low. A good prediction of Co-trimethazole antimicrobial activities can help in the development of an antimicrobial resistance avoidance strategy.

According to [1], the result of machine learning prediction can help in the early detection of antimicrobial resistance and thus aid in the selection of appropriate therapy. Chloramphenicol showed a high level of sensitivity and low antibiotic resistance. The majority of the machine learning model algorithms predicted antimicrobial activities on Chloramphenicol. The best model, however, for this prediction is Random Forest with an accuracy of 0.92±0.08. Another good model for this prediction is the Decision Tree with 0.89±0.11. Support Vector Machine follows this with an accuracy of 0.88±0.09. Other models with good prediction are gradient boosting with 0.82±0.26 accuracy, and histgradient boosting with 0.81±0. However, as reported by [24] a rule-based (RB) algorithm accuracy of 82% for chloramphenicol antimicrobial activity.

Sparfloxacin is an important antibiotic involved in the prevention and treatment of bacterial infections. Modelling antimicrobial activity towards it will help in prevention strategies for antimicrobial resistance prevalence. The modelling of antimicrobial resistance in muturu shows that good prediction for all the models with GB, HiGB, Randon Forest, Extra tree, and Bagging. The ability to make prediction of this particular antibiotic resistance with several models gives options for effective prediction and thus be health management strategy. Ciprofloxacin antimicrobial activities show that it was highly effective against most of the microbes, with few cases of resistance and intermediate activity. From the models, it can be observed that Support Vector Machine is the best model with an accuracy of 0.88±0.09. In a similar finding by [23], Kneigbhors, Naïve Bayes, and Hisgradientboosting were the best models for predicting Ciproflaxocin

antimicrobial activity. An investigation by [25] shows that Random Forest and Support Vector Machine showed accuracy of 92% and 85%, respectively, for Ciprofloxacin. The SVM accuracy of their findings is similar to our own report of 88%.

Amoxicillin is a broad-spectrum antibiotic that has played very vital role in both the prevention and treatment of bacterial infection. One very good strategy towards managing or preventing the emergence of resistant bacterial strains towards it is an accurate prediction of the likelihood of resistance towards this drug using a suitable model. Of all the models used in this prediction, Random Forest and Decision gave the best prediction with an accuracy of 0.92±0.08 and 0.89±0.11 respectively. Augmentin is one of the most recommended antibiotics when others fail because of its potency due to the synergistic property resulting from the action of amoxicillin and clavulanic acid. In predicting the antimicrobial activity of Augmentin, several models were built and the best models are Naïve Bayes and Decision Tree, with both having an accuracy of 1.00±0.15. In the modeling of Gentamicin antimicrobial resistance, Random Forest was the best model with 0.92±0.08. Decision Tree is another good model with an accuracy of 0.87±0.06. Histgradient boosting also has 0.87±0.07. In a similar report by Ren et al. (2022), they observed that Random Forest accuracy was 90% while SVM was 89% for the prediction of antimicrobial activity on Gentamicin. This Random Forest accuracy is very similar to our own reports. Our support vector machine prediction is 83%, which is also within the range of their support vector accuracy. It can be stated from these reports and those of other authors that machine learning algorithms can assist in the early detection of antibiotic resistance and thus better design of strategy for management and control of this global health burden.

White Fulani is one of the commonest herded cattle in Nigeria and is usually herded by the Fulanis. It has a potential for antimicrobial resistance as most people managing it are not professionally trained, and thus the possibility of misuse of antibiotics. There is therefore a need to develop models that can carry out this prediction and thus proper preventive planning. Perfloxacin was observed to have good model prediction of its antibiotic resistance for white Fulani cattle with the best model being GB and HistGB with accuracy of 1.00±0.00. This was unlike oflaxocin where the accuracy was poor for most of the models, with the exception of support vector machines which had consistently performed well in all the model. However, Gradient Boosting, Histgradient Boosting, Support Vector Machine and Random Forest had high accuracy compared to the rest models in streptomycin antibiotic prediction. Cotrimethazole and chloramphenicol antibiotic resistance model were observed to be poor with the exception of SVM. All the antibiotic resistance model was very good for Sparfloxacin and these could be due to the nature of the antibiotic resistance output, making model prediction easier. The model accuracies were poor for amoxicillin but however random forest, extra tree and bagging algorithm predicted (0.93 accuracy) ciproflaxocin very well. There was a high prediction accuracy for all the models for Augmentin unlike gentamycin in which most of the models had low accuracy.

4. Conclusions

Machine learning can play very vital role in the accurate prediction of antibiotic resistance to drugs helping in better design of antibiotic for management of drug resistance microorganism. Our findings show ML models was antibiotic specific with Perfloxacin and Augmentin being better predicted by some of the models such Naïve Bayes and random forest, Ensemble methods, Decision Trees and Support Vector for muturu compared to other antibiotics. The white Fulani cattle also had a good share of the prediction especially with some antibiotics such as perfloxacin, sparfloxacin, and ciproflaxocin. Support Vector machine classifiers were found to predict all the antibiotics with high degree of accuracy. It is therefore important that in subsequent studies, larger dataset should be used for better reduction and model fittings. There is also a need to carry out further studies using the genome sequence of these microbes for machine learning model of these antibiotics' resistance.

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