

Food Quality Detection by Identification of Bacterial Contaminants: A Comparative Analysis of Machine Learning Predictive Models

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Abstract: Meat is one of the essential food items consumed by humans. Meat is vibrant is protein and has other nutrients that provide good health for human beings. Under certain circumstances, adulteration can be done in the meat. This leads to the presence of harmful pathogens to be present in it. These bacteria, namely *Escherichia coli*, *Ecoli Staphylococcus* and *Staphylococcus Aureus*, can lead to severe health problems when consumed with meat. Hence the detection of these harmful pathogens in meat is mandatory. This paper aims to detect the presence of these bacteria by using machine learning models. In this paper, four different classification algorithms have been implemented for bacterial identification. The algorithms used are modified support vector machine, optimized k means clustering, advanced random forest, and artificial neural network. The result obtained using the proposed algorithms have been compared, and the results have been plotted. Advanced random forest method has produced the best results and the artificial neural network has produced comparatively lower results than the other algorithms taken into account.

Keywords: Food, Meat, Adulteration, Bacteria, SVM, ANN, Random Forest, K-means, pathogen, *Escherichia coli*, *Ecoli Staphylococcus* and *Staphylococcus Aureus*.

1. Introduction

Meat is one of the essential food items continuously consumed by humans in their daily lives. It is necessary to consider the quality of the meat before it is consumed. Adulteration could be done in meat and this might lead to the prevalence of harmful bacteria. When the meat is not properly preserved, it might lead to several diseases that might be foodborne. Earlier researchers have put forth several studies regarding the importance of food quality and its effects.

Machine learning algorithms have greatly helped in detecting spoiled and adulterated food over the recent years. Authors: Xinxin Wang, Yasmine Bouzembrak, AGJM Oude Lansink and H. J. Fels-Klerx have given a literature survey of the ML techniques that can be used to detect unwanted bacteria in the food items [1]. Food safety tends to threaten society at many circumstances. Health is the prime importance of all human beings [2].

Machine learning techniques can detect the pathogens present in the food as per the paper published by Xiangyu Deng and his co authors.

Managing food safety is important to maintain a healthy life style nation wide. The earlier researchers have used adaptive network-based fuzzy inference system (ANFIS) and multilayer perceptron (MLP) methods. They have considered livestock production and agricultural yields as input data sets [3]. The study was done based in Iran. About 70 percent of the data was used to train the ANFIS and MLP models. The remaining data were used for testing the models. All food items must be verified whether they are of good quality before consuming. It is essential to check the food products received from other countries if they meet the standards of our country's food quality. Amina Batool and Souvik Ganguli, along with their co authors, have devised a method for detecting the quality of food imported using the internet of things and machine learning models.

Photos were taken using cameras with high resolution. These were later segmented using K means clustering technique [4]. The extraction of features was done using the prime component analysis method followed by training.

Junming Han, Tong Li, Yun He, and Quan Gao have proposed a method for detecting food quality using fruits. Fruits of high quality are necessary for the proper functioning of the human lungs [5]. Therefore the freshness detection of the fruits is necessary. The authors

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propose a nondestructive freshness detection method using convolutional neural networks. Artificial intelligence has a wide range of applications in several upcoming technological fields. Authors have utilized this technology for the detection of food quality. A survey based analysis has been done using about 150 candidates selected from the health care related industries. Statistical analysis has been carried out using the SPSS software [6]. Rajnish Kler and Ghada Elkady and their co authors have done a work to prove the advantages of artificial intelligence and machine learning models over the other available techniques. According to their study, both AI and ML are promising technologies for food quality detection [7]. The economic losses can be overcome by both of these techniques, which in turn helps the industries produce positive results. Xin Zhang and Weiguo Tian have carried out a study on the grids of food safety. Food safety has attracted the attention of the people in the recent years. The management of the grid has effectively helped in the analysis of the foods more efficiently [8]. The attained error using the proposed method was only 2 percent.

2. Literature Survey

Street foods have become more popular these days, and people tend to eat them a lot. The knowledge of the street food vendors regarding the quality and safety of food is a question mark. Raymond Addo-Tham and his co-authors have performed a survey. About 350 participants who continually take street food were selected. A questionnaire was given to them, and they were asked to answer the survey [9]. The result obtained during this survey proved that about 98 percent of the vendors were familiar with the importance of food safety and its quality.

Abebe Bersisa, Dereje Tulu, and Chaluma Negara have studied to detect the presence of bacteria, namely, staphylococcus aureus, Escherichia coli, and salmonellae species in the butcher shops [10]. A survey was conducted with the help of a questionnaire. The results obtained proved that Escherichia coli were more dominant among the three. They were followed by Escherichia coli, which was staphylococcus aureus. Salmonellae species was the least found species. Human beings do the consumption of vegetables each day. In such a case, it is necessary to determine whether harmful pathogens contaminate these vegetables. The main motive of the study done by the authors in [11] is to create awareness among the producers, retailers, and the consumers regarding the presence of harmful bacteria like Cystoisospora belli, Toxoplasma gondii, and many more in the consumed vegetables. The removal of these bacteria can, however, be done by implementing certain measures like treatment of the water used during

irrigation, utilization of disinfectants and many more. Though vegetables are highly nutritious, checking their quality before consumption plays a vital role indeed.

Certain vegetables like carrots, tomatoes, onions, and many others are ready to eat even without being cooked. When they are taken raw, in the presence of Escherichia coli, they tend to create health problems. It might lead to stomach upset issues, colitis, uremic syndrome, and other problems. The vegetables might get contaminated by the bacteria at any point from pre-harvesting to post-harvesting [12]. The behavior of this bacteria in the ready-to-eat vegetable preparations has been analyzed by J. Luna-Guevara, M. M. P. Arenas-Hernandez, along with their co-authors. Authors have done a study to analyze the bacteria in beef in Ghana [13]. Beef is one of the essential sources of protein. The beef was selected from six different shops and subjected to a total aerobic count test and coliform count test. The results obtained during this study proved that harmful pathogens contaminated most meats. E-nose, Computer vision, and artificial tactile can be used to detect meat freshness. The freshness of the meat in the proposed method has been estimated through the amount of volatile nitrogen content present in it. Principle component analysis and support vector machine algorithm has been used to recognize the pattern and fusion of the mentioned techniques [14]. The results proved that the root means square values of the pork and chicken meat were 0.20 and 0.95, respectively. The correlation coefficient of pork and chicken meat was 0.92 and 0.95, respectively. This, in turn, enables the proposed method for meat freshness detection and for the determination of storage duration. A light scattering sensor is developed by Akova F, Dundar M, Davisson VJ, Hirtleman ED, Bhunia AK, Robinson JP, and Rajwa B. To detect unwanted bacteria, the training library must be loaded with all types of bacteria. The supervised classification learning algorithm has been used for this purpose. The bayesian approach has been used to detect unmatched bacteria [15]. The training data sets would be updated regularly to produce more accurate results.

3. Proposed Work

In the proposed method, about five machine learning algorithms have been used to detect adulteration in the meat consumed in Morocco. These algorithms are optimized K means clustering, Modified support vector machine, advanced random forest, and artificial neural network. The data processing flow used in the proposed method is shown in the following flow diagram in figure 1.

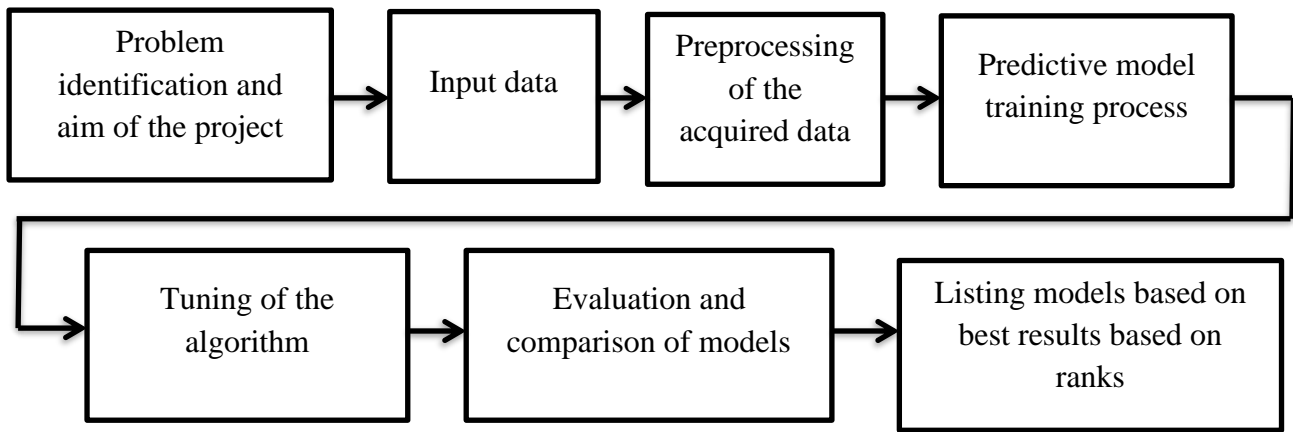


Fig1: Flow of the proposed system

The initial step is identifying the problem statement and the project's ambition. Here the objective is to identify the adulteration done in the meat. The next step is the acquisition of the input data. The ppm value of the gases emitted from the meat is collected and sent to one of the open-source terminals. Here we have chosen Tera Terms. This open-source terminal creates a CSV file of the given data, which can be directly uploaded to a shyni web app to predict bacteria. In the proposed work, animal meat is the input. The third step is the preprocessing step. Pre-processing involves acquiring a clean and tidy data set from the raw data. Following by training process of the predictive model, next is the algorithm tuning step. This involves the variation of the hyperparameters and comparing the results obtained to predict which hyperparameter has produced better performance. The evaluation and comparison of the models is made and the models are listed in a rank-wise manner based on the results obtained.

3.1 Training of model based on modified support vector machine

Support vector machine is a classifier algorithm. It can also be used to deal with regression challenges. The plotting of the values takes place in the space of n

dimension. The main motive of the support vector machine classification algorithm is to find the hyperplane in the n-dimensional space and the classification of the data points is done. The hyperplane's dimensional value depends upon the values of the features. The first step is the selection of data sets for the purpose of training. The input parameters for training the data sets are determined. The next step involves the analysis of the prime component. This step helps to overcome the problems associated with recognizing the pattern. Followed by this step, centralization and scalability are carried out. Then predictive models are trained, followed by repetitive cross-substantiation. The cost and degree are selected and the SVM model is created. The flow diagram of the modified support vector machine is shown in figure 2. The understanding of the support vector machine can be done using the seperatable datasets, unseperatable datasets, and the non-linear kernel transition.

Seperatable datasets: SVM can be used in only two classes among the data sets. The classifier will classify by identifying the best hyperplane. The plane that has the highest margin among the two classes is represented as the best hyperplane.

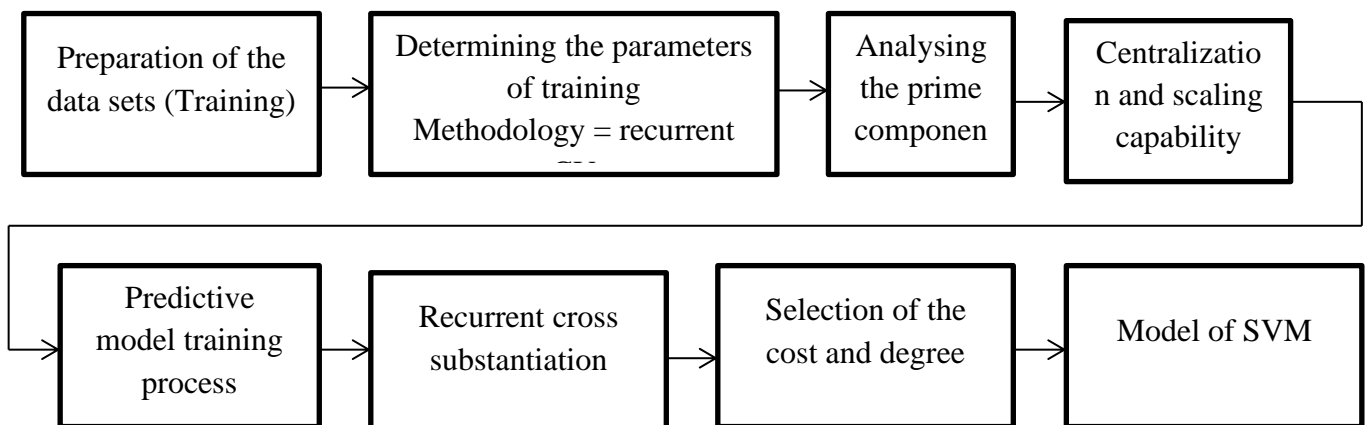


Fig 2: Flow diagram of modified support vector machine

Unseperatable datasets: Sometimes the data will not follow a hyperplane that can be separated. Under such

circumstances, a soft margin can be used by the classifier. The soft margin separated various classes but not every point of data. These two can be done by the addition of the limp variable and the penalty parameter. Let the limp variable be denoted by L_i and the penalty parameter be denoted by P .

The problem of normalization is Z and it is given by

$$Z = \min\left(\frac{1}{2}(w, w) + P \sum_i L_i\right) \quad (1)$$

$$x_i((w, y_i) + a \geq 1 - L_i$$

$$L_i \geq 0$$

The normalization value can be minimized by the SVM classifier. This minimized value is given by

$$Z = \min\left(\frac{1}{2}(w, w) + P \sum_i L_i^2\right) \quad (2)$$

An increased weight can be put on the limp variable when the value of P increases. When this happens, the accuracy of the classification improves.

Nonlinear kernel transition: When the hyper plane is a little tough to deal with, the non linear kernel transition can be used. Let S denote the space that is linear, and θ be the function that maps Y to the space S .

$$K(X, Y) = \langle \theta(X), \theta(Y) \rangle \quad (3)$$

For polynomials with a +ve integer value of d ,

$$K(X, Y) = (1 + \langle X, Y \rangle)^d \quad (4)$$

For a radial function with a +ve number ϵ ,

$$K(X, Y) = e^{-\langle (X - Y), (X - Y) \rangle / (2\epsilon^2)} \quad (5)$$

For a +ve P_1 and -ve P_2 numbers,

$$K(X, Y) = \tanh(P_1 \langle X, Y \rangle + P_2) \quad (6)$$

3.2 Training of model based on optimized k-means clustering method

The steps involved in the k-means clustering algorithm are the same as that of the SVM algorithm. The only difference is that, instead of using a support vector machine for the classification at the final stage, k clusters are formed. The colors in the images can be classified, and their hue values can be identified with the help of k-means clustering algorithms. This technique segments the images into smaller pieces called clusters and compares each piece with the other. When this is done with the input meat images, the areas affected by the bacteria tend to be different; hence, the adulteration can be proved if present. The flow diagram of the k-means clustering is shown in figure 3. The value of k and the mean values will be the same. The mean values can also be denoted as the centroid of the cluster that is randomly taken out from the data. Depending upon the value of K , a novel cluster can be brought in. The centroid point is called the cluster head. One particular cluster head will take all the data points nearer to it as its members. The data points that are adjacent to the next cluster head will tend to form a different cluster. Likewise, several clusters will be formed among the data sets.

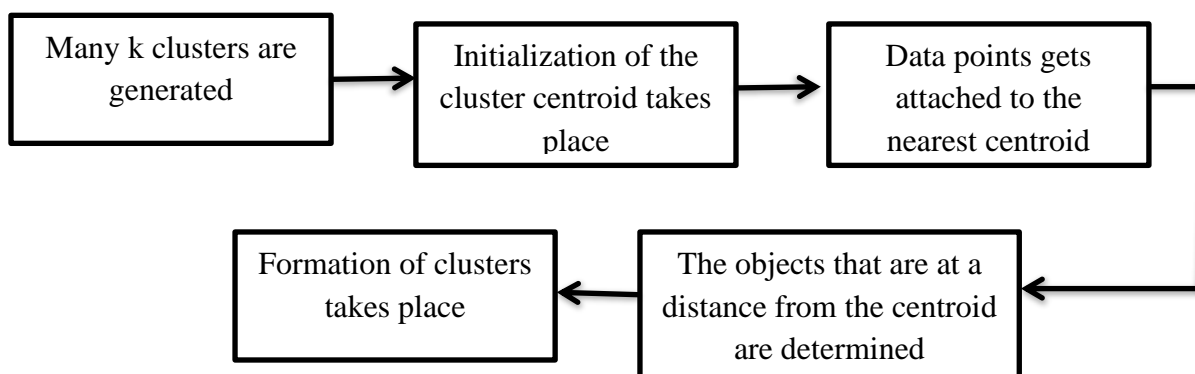


Fig3: Flow diagram of k means clustering

K-means clustering separates the needed data by eliminating the data in the background. The RGB image will be changed in size using the interpolation technique. Variation in image size tends to zoom the image for detailed analysis of the data. The pixel value gets increased at the clusters' means value, which emerges as the updated centroid. The dominant colour can be

identified, which in turn tells whether the meat is spoiled or not.

3.3 Training of model based on advanced random forest method

The random forest algorithm can be used to face the challenges of classification and regression.

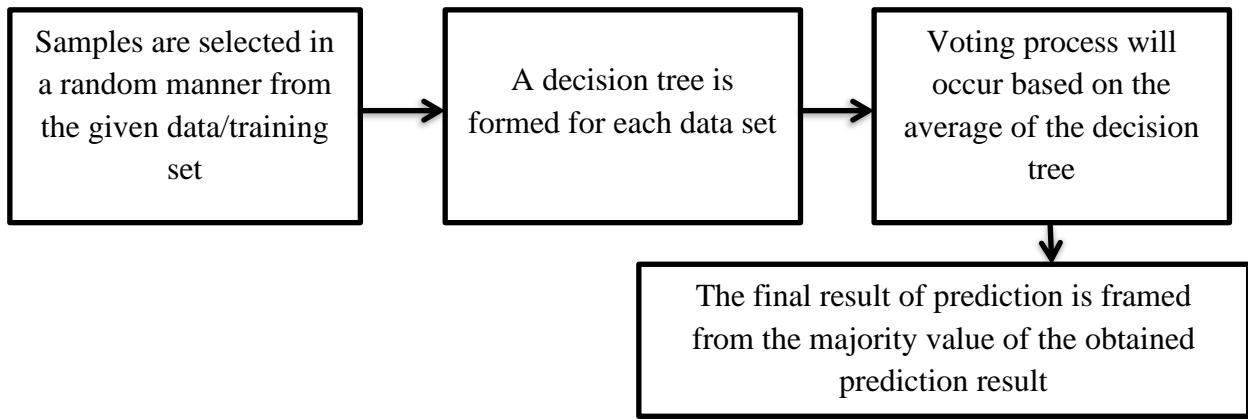


Fig4: Flow diagram of random forest method

A forest looks efficient when the number of trees is more. Similarly, when the number of trees is high in the random forest algorithm, the algorithm tends to produce précised results. The average values of the trees are considered to improve the accuracy. The underlying principle is the concept of ensemble learning. In ensemble learning, several classifiers are considered to bring out a solution for a complex problem. The flow diagram of the advanced random forest method is shown in figure 4.

3.4 Training of model based on artificial neural network

The artificial neural network is based on the combination of the individual component and their weights. The equation of the neural network can be represented as follows.

$$Y = I + U_1Z_1 + U_2Z_2 + \dots + U_nZ_n \quad (7)$$

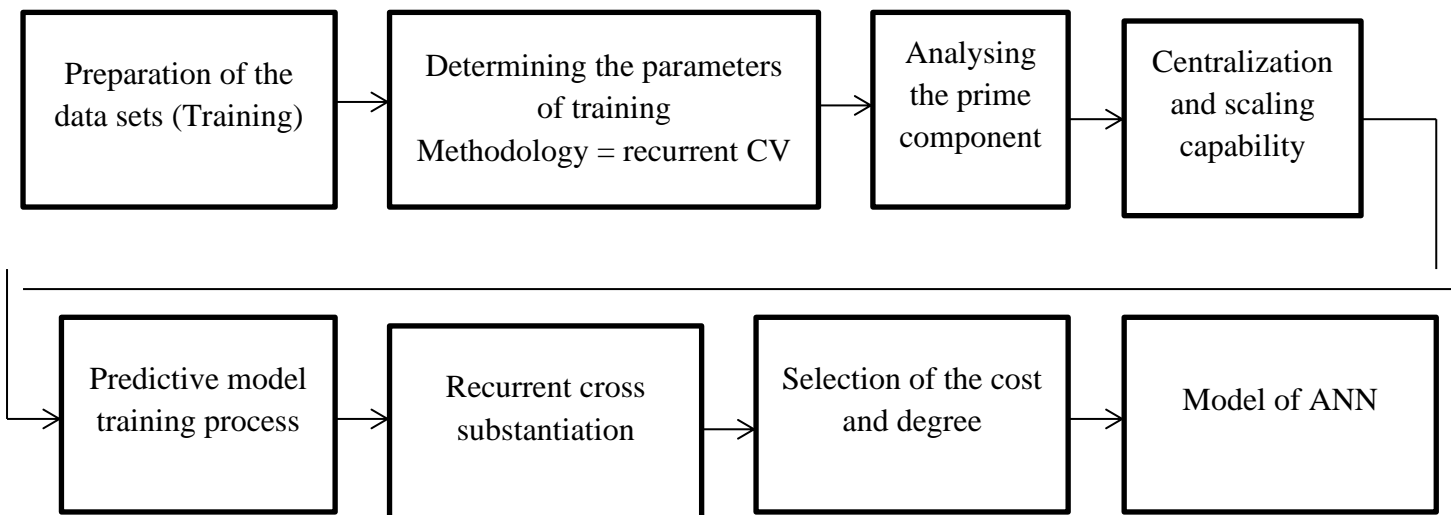


Fig5: Flow diagram of artificial neural network

The output of the artificial neural network is denoted by Y, U represents the weights, Z represents the individual components, and I denote the intercept. The prediction output can be determined by using the above equation. The calculation of error is done. Error represents the variation between the actual value and the predicted value. Eventually, the minimization of the error is done. The flow diagram of the artificial neural network is shown in figure 5.

4. Results and Discussion

The presence of three different types of bacteria, namely Escherichia coli, ecoli staphylococcus, and staphylococcus Aureus has been determined with the help of four different machine-learning algorithms. The results have been tabulated and also shown by means of graphical representation in the following sections.

Table 1: Matrix of confusion (Modified SVM)

		Class of prediction			
		Esche richia Coli	Ecoli Staphylococcus	None	Staphylococcus Aureus
Authentic class	Escherichia Coli	125	1	0	0
	Ecoli Staph	1	139	0	1
	None	18	4	144	18
	Staphylococcus Aureus	0	1	0	125

The matrix of confusion of the modified support vector machine algorithm is shown the table 1. Table 2 shows the overall statistical results of the modified SVM model. The precision value obtained is about 91.83 percentage. The null rate information is about 0.24 and the kappa value is found to be 0.8922. The values of P for Precision > null information rate and through Mcnemar's test are determined to be <2.3e-15 and 8.507e-07 respectively.

Table 2: Overall statistical result of modified SVM model.

Parameter	Value
Precision	0.9183
Confidence level (95 percent)	(0.982, 0.9383)
Null rate of information (NRI)	0.24
Value of P [Precision > NRI]	<2.3e-15

Kappa	0.8922
P-Value through Mcnemar's Test	8.507e-07

The summary of the result obtained through the modified SVM model is tabulated in table 3. The parameters, namely sensitivity, specificity, positive prediction values, negative prediction values, occurrence, rate of prediction and the precision balancing, are taken into account.

Table 3: Summary of the result obtained through modified SVM model.

Parameter	Escherichia Coli	Ecoli Staphylococcus	None	Staphylococcus Aureus
Sensitivity	0.8712	0.9582	0.981	0.8674
Specific type	0.9958	0.9935	0.9004	0.9988
Prediction value (+ve)	0.9921	0.9865	0.7677	0.9921
Prediction value (-ve)	0.9556	0.9856	0.9937	0.9554
Occurrence	0.24	0.24	0.24	0.24
Rate of identification	0.2135	0.2394	0.2468	0.2135
Identification of occurrence	0.2180	0.2413	0.32296	0.2180
Balancing of precision	0.9293	0.9781	0.9568	0.2980

The graphical representation of the result obtained through the modified SVM model is shown in figure 6. The sensitivity values of Escherichia coli, ecoli staphylococcus, and staphylococcus aureus are 0.8712,

0.9582, and 0.8674, respectively. The precision balancing of Escherichia coli, ecoli staphylococcus, and staphylococcus aureus are 0.9293, 0.9781, and 0.2980 respectively.

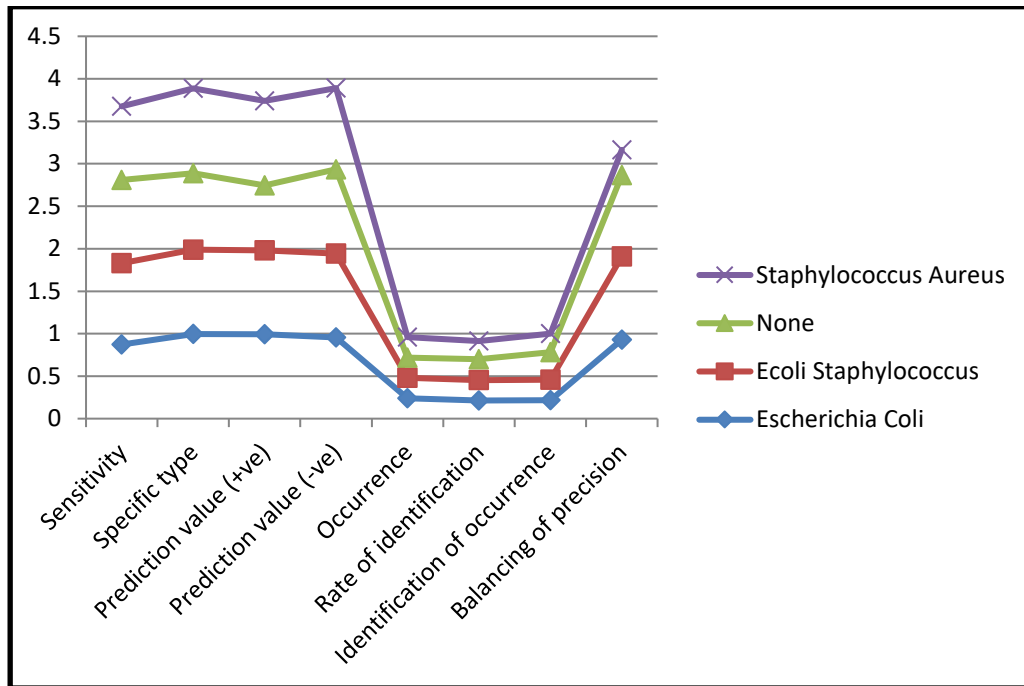


Fig 6: Graphical representation of result obtained through modified SVM model

The matrix of confusion of the optimized k means clustering algorithm is shown the table 4. Table 5 shows

the overall statistical results of the optimized k-means clustering model. The precision value obtained is about 94.56 percentages.

Table 4: Matrix of confusion(Optimized K means clustering)

		Class of prediction			
		Escherichia Coli	Ecoli Staphylococcus	None	Staphylococcus Aureus
Authentic class	Escherichia Coli	131	0	3	1
	Ecoli Staph	1	141	1	1
	None	8	2	136	3
	Staphylococcus Aureus	1	0	4	141

The null rate information is about 0.24 and the kappa value is found to be 0.9325. The value of P for Precision > null information rate is determined to be $2.3e-15$. The value of P and through McNemar's test is not applicable in case of K means clustering algorithm.

Table 5: Overall statistical result of optimized K means clustering model.

Parameter	Value
Precision	0.9456
Confidence level (95 percent)	(0.9456, 0.977)
Null rate of information (NRI)	0.24

Value of P [Precision > NRI)	$2.3e-15$
Kappa	0.9325
P-Value through McNemar's Test	Not applicable

The Summary of the result obtained through the K means clustering model is shown in table 6. The positive predictive value of Escherichia coli, ecoli staphylococcus

and staphylococcus aureus are 0.964, 0.9945 and 0.9653 respectively. Similarly, the negative predictive value of Escherichia coli, ecoli staphylococcus, and staphylococcus aureus are 0.9651, 0.9906 and 0.9905 respectively.

Table 6: Summary of the result obtained through optimized K means clustering model.

Parameter	Escherichia Coli	Ecoli Staphylococcus	None	Staphylococcus Aureus
Sensitivity	.9021	0	.9415	0.9712
Specific type	.9883	0	.9645	0.9448
Prediction value (+ve)	.964	0	.8895	0.9653
Prediction value (-ve)	.9651	0	.9841	0.9905
Occurrence	.24	0	.24	0.24

Rate of identification	.2264	0	.2314	0.2415
Identification of occurrence	.2334	0	.2651	0.2516
Balancing of precision	.9546	0	.954	0.9821

Figure 7 shows the graphical representation of result obtained through optimized K means clustering model.

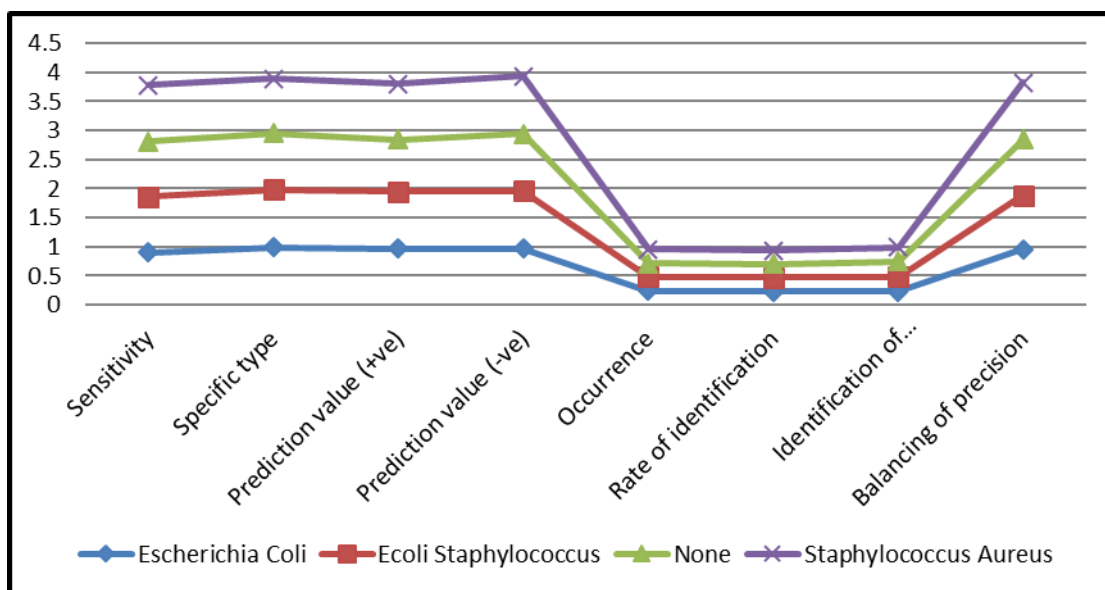


Fig 7: Graphical representation of result obtained through optimized K means clustering model

The matrix of confusion of the advanced random forest algorithm is shown the table 7. Table 8 shows the overall statistical results of the advanced random forest model.

The precision value obtained is about 96.58 percentage. The null rate information is about 0.24 and the kappa value is found to be 0.9656.

Table 7: Matrix of confusion (Advanced Random forest model)

		Class of prediction			
		Escherichia Coli	Ecoli Staphylococcus	None	Staphylococcus Aureus
Authentic	Escherichia Coli	142	1	0	1
	Ecoli Staph	1	139	1	0

class	None	0	4	145	3
	Staphylococcus Aureus	1	2	0	138

Table 8: Overall statistical result of advanced Random forest model.

Parameter	Value
Precision	0.9658
Confidence level (95 percent)	(0.9624, 0.9897)
Null rate of information (NRI)	0.24
Value of P [Precision > NRI)	<2.3e-15
Kappa	0.9656
P-Value through Mcnemar's Test	6.24e-01

The value of P for Precision > null information rate is determined to be <2.3e-15. The value of P and through Mcnemar's test is identified to be 6.24e-01. Table 9 summarizes the results obtained through the advanced obtained through Advanced random forest model.

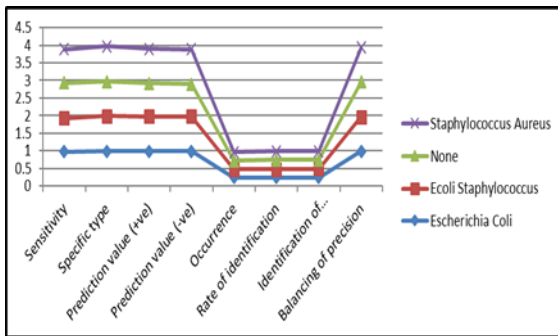


Fig 8: Graphical representation of result

The matrix of confusion of the modified Artificial neural network algorithm is shown the table 10. Table 11 shows the overall statistical results of the Artificial neural network model. The precision value obtained is about 64.12 percentage. The null rate information is about 0.24 and the kappa value is found to be 0.4852. The values of P for Precision > null information rate and through Mcnemar's test are determined to be <2.1e-15 for both the cases.

Table 10: Matrix of confusion (ANN model)

		Class of prediction			
		Escherichia Coli	Ecoli Staphylococcus	None	Staphylococcus Aureus
Authentic class	Escherichia Coli	127	97	3	5
	Ecoli Staph	1	27	0	10

random forest model. The rate of identification of Escherichia coli, ecoli staphylococcus and staphylococcus aureus are 0.2418, 0.2342 and 0.2415, respectively. Similarly, the occurrence identification of Escherichia coli, ecoli staphylococcus, and staphylococcus aureus are 0.2418, 0.2415 and 0.2419 respectively.

Table 9: Summary of the result obtained through advanced random forest model.

Figure 8 depicts the graphical representation of result obtained through Advanced random forest model.

Parameter	Escherichia Coli	Ecoli Staphylococcus	None	Staphylococcus Aureus
Sensitivity	.9712	0.9554		0.9629
Specific type	.9935	0.9931	.9876	0.9921
Prediction value (+ve)	.9838	0.9932	.9437	0.9755
Prediction value (-ve)	.9916	0.9865	.181	0.9867
Occurrence	.24	0.24	.24	0.24
Rate of identification	.2418	0.2342	.2643	0.2415
Identification of occurrence	.2418	0.2415	.2653	0.2419
Balancing of precision	.9851	0.9857	.9902	0.9751

	None	10	8	107	36
	Staphylococcus Aureus	31	8	33	93

Table 12: Summary of the result obtained through ANN model.

Table 11: Overall statistical result of ANN model.

Parameter	Value
Precision	0.6412
Confidence level (95 percent)	(0.5721, 0.6517)
Null rate of information (NRI)	0.24
Value of P [Precision > NRI)	<21e-15
Kappa	0.4852
P-Value through Mcnemar's Test	<2.1e-15

Table 12 summarizes the result obtained through the artificial neural network model. The rate of identification of Escherichia coli, e coli staphylococcus and staphylococcus aureus are 0.2185, 0.04512, and 0.1592 respectively. In the same manner, the occurrence identification of Escherichia coli, Ecoli staphylococcus and staphylococcus aureus are 0.4028, 0.07142 and 0.2394 respectively.

Parameter	Escherichia Coli	Ecoli Staphylococcus	None	Staphylococcus Aureus
Sensitivity	0.874	0.19877	0.73	0.6351
Specific type	0.73	0.96882	0.8175	0.8935
Prediction value (+ve)	0.5384	0.68458	0.6627	0.6641
Prediction value (-ve)	0.9457	0.78522	0.9128	0.8815
Occurrence	0.24	0.24	0.24	0.24
Rate of identification	0.2185	0.04512	0.1873	0.1592
Identification of occurrence	0.4028	0.07142	0.284	0.2394
Balancing of precision	0.8162	0.5841	0.8124	0.7663

Figure 9 depicts the graphical representation of result obtained through Artificial neural network.

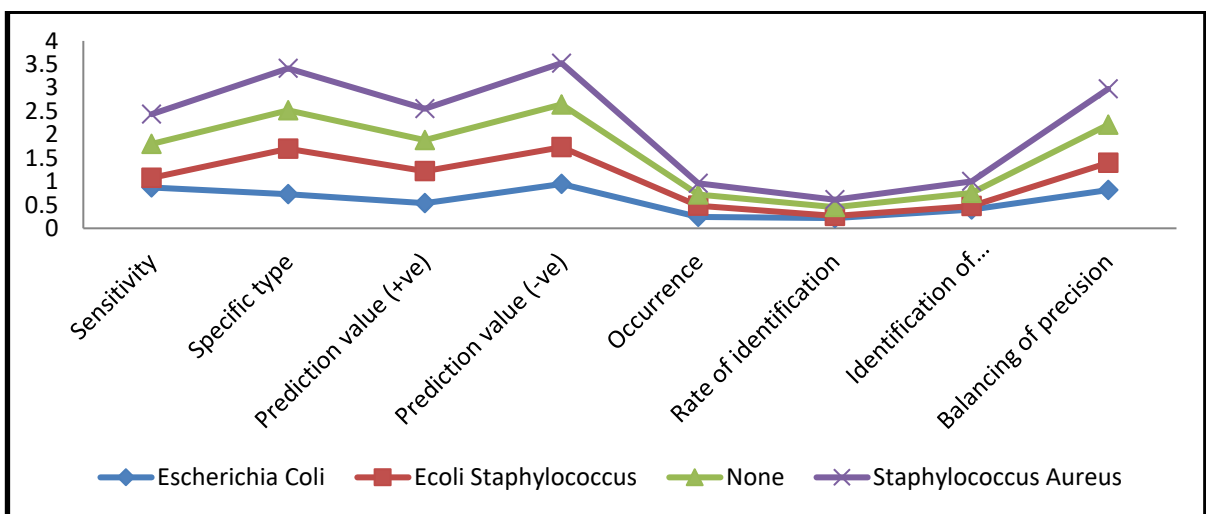


Fig9: Graphical representation of result obtained through Artificial Neural Network

It can be seen that the resultant parameters obtained through the artificial neural network are lesser than the

other three models. A comparative analysis of the CV and CM accuracy obtained through the distinct algorithms is tabulated in table 13.

Table 13: Comparison of different models

Model	CV accuracy	CM accuracy
Advanced Random forest	0.9754	0.9729
Optimized K means clustering	0.9568	0.9418
Modified Support vector machine	0.9035	0.9174
Artificial neural network	0.7152	0.6163

The CV and CM accuracy of the advanced random forest model are 0.9754 and 0.9729, respectively. Similarly, the CV and CM accuracy of Optimized k means clustering are 0.9568 and 0.9418, respectively. The CV accuracy of the modified support vector machine and artificial neural network are 0.9035 and 0.7152. Likewise, the CM accuracy of the modified support vector machine and artificial neural network are 0.9174 and 0.6163, respectively.

5. Conclusion

The presence of bacterial species in the meat has been detected using four different algorithms: modified support vector machine, optimized k means clustering, advanced random forest, and artificial neural network. The results obtained using the different algorithms have been tabulated. The efficiency of the algorithms has been ranked based on the values of CV and CM accuracies. The advanced random forest method has produced the highest accuracy, and the artificial neural network has reduced the lowest accuracy among the four different algorithms considered.

References.

[1] Wang, Xinxin & Bouzembrak, Yamine & Lansink, AGJM & Fels-Klerx, H.. (2021). Application of machine learning to the monitoring and prediction of food safety: A review. *Comprehensive Reviews in Food Science and Food Safety*. 21. 10.1111/1541-4337.12868.

[2] Rajakumar, G., T. Ananth Kumar, T. A. Samuel, and E. Muthu Kumaran. "Iot based milk monitoring system for detection of milk adulteration." *International Journal of Pure and Applied Mathematics* 118, no. 9 (2018): 21-32.

[3] Nosratabadi, Saeed, Sina Ardabili, Zoltan Lakner, Csaba Mako, and Amir Mosavi. 2021. "Prediction

of Food Production Using Machine Learning Algorithms of Multilayer Perceptron and ANFIS" *Agriculture* 11, no. 5: 408.

[4] Hashem Ali Almashaqbeh,3Muhammad Shafiq,4A. L. Vallikannu,5K. Sakthidasan Sankaran,5Samrat Ray,6and F. Sammy7, "An IoT and Machine Learning-Based Model to Monitor Perishable Food towards Improving Food Safety and Quality", Volume 2022 | Article ID 6302331

[5] Junming Han, Tong Li, Yun He, Quan Gao, "Using Machine Learning Approaches for Food Quality Detection", *Mathematical Problems in Engineering*, vol. 2022, Article ID 6852022, 9 pages, 2022..

[6] Pugazhendiran, P., K. Suresh Kumar, T. Ananth Kumar, and S. Sundaresan. "An Advanced Revealing and Classification System for Plant Illnesses Using Unsupervised Bayesian-based SVM Classifier and Modified HOG-ROI Algorithm." In *Contemporary Issues in Communication, Cloud and Big Data Analytics*, pp. 259-269. Springer, Singapore, 2022.

[7] Rajnish Kler, Ghada Elkady, Kantilal Rane, Abha Singh, Md Shamim Hossain, Dheeraj Malhotra, Samrat Ray, Komal Kumar Bhatia, "Machine Learning and Artificial Intelligence in the Food Industry: A Sustainable Approach", *Journal of Food Quality*, vol. 2022, Article ID 8521236, 9 pages, 2022.

[8] Xin Zhang, Weiguo Tian, "Grid Supervision Path of Platform Food Safety Collaborative Governance Based on Big Data", *International Transactions on Electrical Energy Systems*, vol. 2022, Article ID 2605934, 14 pages, 2022..

[9] Raymond Addo-Tham, Emmanuel Appiah-Brempong, Hasehni Vampere, Emmanuel Acquah-Gyan, Adjei Gyimah Akwasi, "Knowledge on Food Safety and Food-Handling Practices of Street Food Vendors in Ejisu-Juaben Municipality of Ghana", *Advances in Public Health*, vol. 2020, Article ID 4579573, 7 pages, 2020.

[10] Abebe Bersisa, Dereje Tulu, Chaluma Negera, "Investigation of Bacteriological Quality of Meat from Abattoir and Butcher Shops in Bishoftu, Central Ethiopia", *International Journal of Microbiology*, vol. 2019, Article ID 6416803, 8 pages, 2019.

[11] Richard Osafo, Gadafi Iddrisu Balali, Papa Kofi Amissah-Reynolds, Francis Gyapong, Rockson Addy, Alberta Agyapong Nyarko, Prince Wiafe, "Microbial and Parasitic Contamination of

Vegetables in Developing Countries and Their Food Safety Guidelines", *Journal of Food Quality*, vol. 2022, Article ID 4141914, 24 pages, 2022.

- [12] J. J. Luna-Guevara, M. M. P. Arenas-Hernandez, C. Martínez de la Peña, Juan L. Silva, M. L. Luna-Guevara, "The Role of Pathogenic E. coli in Fresh Vegetables: Behavior, Contamination Factors, and Preventive Measures", *International Journal of Microbiology*, vol. 2019, Article ID 2894328, 10 pages, 2019.
- [13] Michael Olu-Taiwo, Prince Obeng, Akua Obeng Forson, "Bacteriological Analysis of Raw Beef Retailed in Selected Open Markets in Accra, Ghana", *Journal of Food Quality*, vol. 2021, Article ID 6666683, 7 pages, 2021.
- [14] Xiaohui Weng, Xiangyu Luan, Cheng Kong, Zhiyong Chang, Yinwu Li, Shujun Zhang, Salah Al-Majeed, Yingkui Xiao, "A Comprehensive Method for Assessing Meat Freshness Using Fusing Electronic Nose, Computer Vision, and Artificial Tactile Technologies", *Journal of Sensors*, vol. 2020, Article ID 8838535, 14 pages, 2020.
- [15] Akova F, Dundar M, Davisson VJ, Hirleman ED, Bhunia AK, Robinson JP, Rajwa B. A Machine-Learning Approach to Detecting Unknown Bacterial Serovars. *Stat Anal Data Min.* 2010 Oct;3(5):289-301. doi: 10.1002/sam.10085. PMID: 22162745; PMCID: PMC3230886.