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Development of a Model for the Prediction of Lumpy Skin Diseases using Machine Learning Techniques

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Abstract: *Lumpy skin diseases virus (LSDV) is a dangerous and contagious diseases that are mostly common in Sub-Saharan African, South Eastern Europe, South Asia and as well as Middle East, China. LSDV is transmitted through blood sucking insects which are double stranded DNA virus and belong to the family of Capri poxvirus genus family. The recent study proved and clarified that lumpy skin diseases viruses (LSDV) affected mostly cattle and buffalo in Africa, Asia and Europe with population of 29 966, 8 837 and 2 471 outbreaks respectively, between the years 2005 – 2021. Different machine learning approaches have been adopted for the prediction of lumpy skin diseases. An enhanced model was developed to improve the predictive performance of existing model and also, compared the performance of stacked ensemble of single classifiers with respect to optimized artificial neural network. The implementation was done with python 3.7 on Core i5, 16G RAM Intel hardware. The single classifiers are decision tree (DT), k-nearest neighbor, random forest (RF) and support vector machine (SVM). A feature wiz feature selection technique was adopted on lumpy skin diseases dataset coupled with the parameters tuning of the model before classification. Both stacked ensemble and optimized artificial neural network model outperformed the existing model. Stacked ensemble model gives accuracy, precision, f1-score and recall of 97.69%, 98.44%, 98.93% and 98.68% respectively. The results also showed that optimized artificial neural networks of 200 epochs outperformed stacked ensemble classifiers with accuracy of 98.89% and 98.66% of training and validation respectively. The developed model in a real world would assist in reducing the occurrence of lumpy skin diseases.*

Keywords: *Decision tree, k-nearest neighbor, Lumpy skin diseases, Random forest, Support vector machine*

1. INTRODUCTION

Machine learning algorithms have been widely applied in different disciplines to analyze data intelligently [1–3]. Examples of such applications include development of neonatal monitoring model, development of diabetes, diabetic retinopathy and flood prediction models [4–7]. Apart from deep learning as a broader family of machine learning, other machine learning algorithms are sub divided into different categories namely supervised, semi supervised, unsupervised and reinforcement learning [1, 8]. Supervised machine learning algorithms map input to an output based on the excerpt of input-output pairs to learn a given function [1]. Supervised machine learning algorithms are classified into majorly regression and classification algorithms which can be applied on spam filtering, fraud detection, image classification and assessment of risks [9, 10]. Examples of these supervised machine learning algorithms are random forest, decision tree, logistic and linear regressions, support vector machine, polynomial regression and Bayesian linear regression [11]. Unsupervised machine learning algorithms are machine learning algorithms which contained known and unknown inputs and output respectively that are mostly applied on transactional data [12, 13]. Examples of unsupervised machine learning algorithms are k-means clustering and k-median clustering [1, 2]. Semi supervised machine learning algorithms are obtained from the hybridization of both or either the supervised and unsupervised machine learning algorithms as it function on both labelled and unlabelled data [1]. These machine learning algorithms are employed in the development of better predictive model as it falls between learning with or without supervision [14]. Reinforcement learning is a science of decision making and sub division of the machine learning algorithms that apply artificial intelligence system to learn through trial and error using feedback from its actions [15]. Different predictive models have been developed with the application of these described machine learning algorithms, for instance [4, 16, 17, 55, 56]. The recent studies encourage ensemble techniques of two or more algorithms and have been employed in different disciplines for better predictive

performance. There is a growing need in the health care applications to store and organize sizeable clinical data, analyze the data, assist the health care professionals in decision making, and develop data mining methodologies to mine hidden patterns and discover new knowledge from clinical data [18]. Data mining plays important roles in decision making [8].

Lumpy skin diseases is a highly contagious viral diseases caused by the lumpy skin diseases virus which belongs to the family and genus of poxviridae and capripoxvirus respectively [19, 20]. Lumpy skin diseases are transmitted by sucking insects and are mostly common in Africa but recently spread to the countries like Europe and parts of Asian [1]. Lumpy skin diseases has caused a lot of economic losses as a result of the death of animal, low production of milk, hides damage and high infertility rate [21]. Lumpy skin diseases is categorized as the most noticeable infectious diseases in the most affected or epidemic countries according to World Organization for Animal Health [21]. Lumpy skin diseases virus has affected 29 966, 8 837 and 2 471 cattle's in Africa, Asia and Europe respectively between the years 2005 – 2021 [20]. LSDs are majorly transmitted in buffalo and cattle. Report has not showing its transmission in animals such as goats and sheep [22, 23]. Cattles and Buffalo can contact lumpy skin diseases through different sources; some of the sources in which lumpy skin diseases are transmitted are scabs and crusts, skin nodules and can be removed from different materials up to or more than 35 days [19]. Infected animals with lumpy skin diseases (LSD) would show the symptoms of reduced milk production, fever, emaciation and depression, enlarged lymph and conjunctivitis. Records of recent epidemic case of lumpy skin diseases transmission in Western Asia has shown that, measures like detection of index case of the lumpy skin diseases identification coupled with widespread of vaccination campaign process would help in reducing the number of its occurrence [20]. Further prevention measures can be carried out in unaffected countries to avoid the transmission of the diseases; such actions include restriction of imported domestic cattle and buffaloes, surveillance monitoring of cattle of not more than 20 kilometers from the affected zones, removal of the affected animals from the healthy animals, adequate and regular vaccination of the animals and proper of dead animals [1, 24]. Lumpy skin diseases are highly contagious and double stranded DNA viral diseases of cattle and buffalo which are transmitted through blood sucking insects, such as some kind of flies and mosquitoes species [22] and excerpts of its occurrence is given in Figure 1. Lumpy skin diseases virus (LSDV) has also benefitted over years with the help of the machine learning algorithms and some of these researches are elucidated as follows. Authors in [19] developed a novel model with artificial neural network for effective prediction of lumpy skin diseases using geospatial and meteorological features. The developed model was able to effectively classify lumpy skin diseases with testing and training accuracies of 97% and 94% respectively. Also, authors in [25] applied random forest, support vector machine (SVM), multilayer perception (MLP) algorithm, and k-nearest neighbour algorithms to classify the occurrence of lumpy skin diseases infection (LSD). Random Forest (RF) algorithm has the highest accuracy of 97.7% compare to other algorithms. This research work is aimed at applying feature wiz feature selection coupled with adoption of machine learning classifiers on lumpy skin diseases dataset of different identified features.

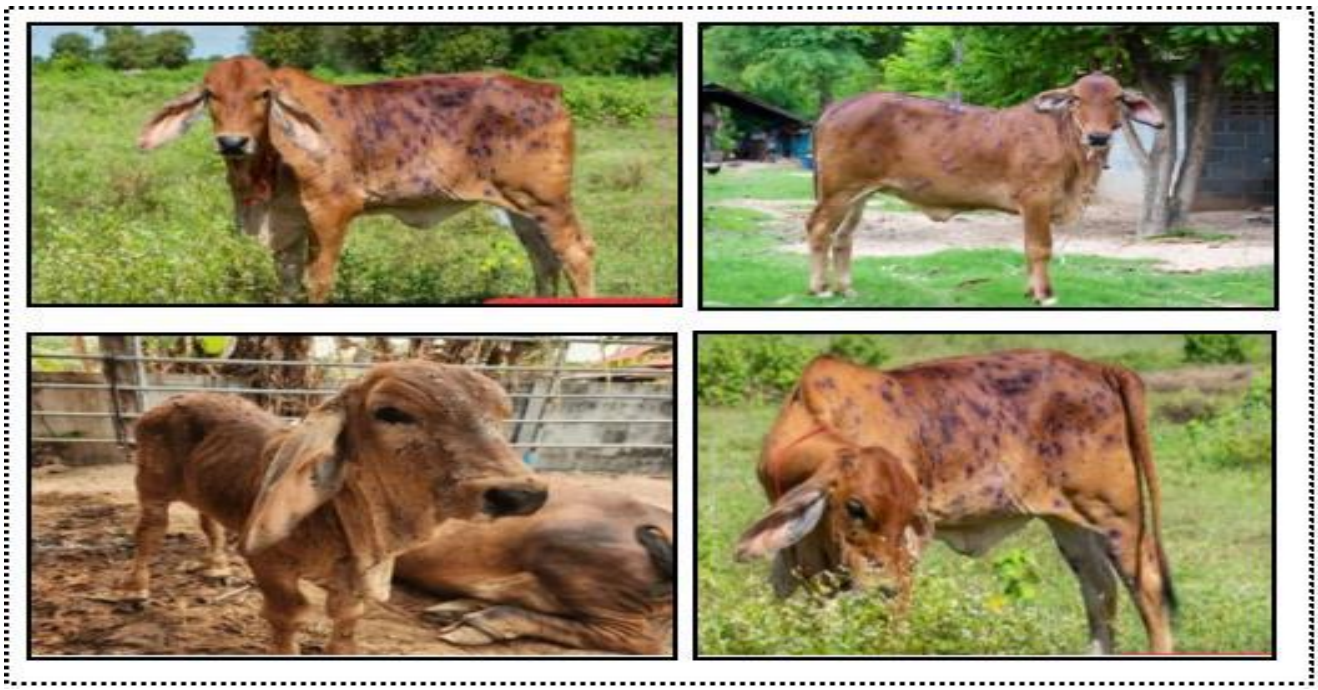

Figure 1: Excerpts of lumpy skin diseases virus [19]

Different works have been carried out on the prediction of lumpy skin diseases (LSD) using different machine learning algorithms. This section summarizes some of these research works. [19] applied different machine learning algorithms for the prediction of lumpy skin diseases; such algorithms include logistic regression (LR), support vector machine (SVM), decision tree (DT), random forest and artificial neural network on the LSD dataset with meteorological and geospatial

features. The dataset contained features which were pre-processed through one – hot encoding approach and divided using percentage split approach. Assessment of the developed model indicated that, artificial neural network out performed all other algorithms with accuracy, precision, f1 score and area under curve of 97%, 88%, 94% and 97% respectively. Authors in [26] compared the results of machine learning models on the prediction of lumpy skin diseases. Ten (10) different classifiers were applied on the lumpy skin diseases dataset to determine the algorithms that will give best predictive performance. The results showed that random forest classifier coupled with light gradient boosted machine classifier outperformed other models with 98% F1 score. Authors in [27] performed the comparative analysis of random forest with respect to K-nearest neighbor (KNN) algorithms on the prediction of lumpy skin diseases. Medical diagnosis using traditional approach consumes more time and cost demanding; therefore a novel model was developed to classify the occurrence of lumpy skin diseases primary. The evaluation of the developed model indicated that K-nearest neighbor (KNN) outperformed than RF with accuracy and F1 score of 95.23% and 95.98% respectively. A novel model was developed with Random Forest (RF) and hyper parameter tuning by [28]. The model was evaluated and the result showed that Random forest with SMOTE and GA increases the recall from 90% to 99% and area under curve (AUC) from 94% to 98%. Two (2) different models were developed by [29] for the prediction of lumpy skin diseases (LSD); those models include artificial neural network trained with particle swarm optimization algorithm (ANN trained with PSO) and artificial neural network trained with cuckoo search (ANN trained with Cuckoo search). Artificial neural network trained with particle swarm algorithm outperformed other model. Deep learning approach was compared with traditional machine learning algorithms introduced for the prediction of lumpy skin diseases by [30]. The traditional algorithms that were employed are support vector machine, logistic regression (LR), Naive Bayes (NB), support vector machine (SVM) and artificial neural network (ANN) outperformed the listed traditional machine learning algorithm with 92.5% accuracy. Skin diseases were classified by [54] using the integration of Long Short Term Memory (LSTM) with MobileNetV2. The model developed has accuracy, precision, f-measure and recall of 86.57%, 93.34%, 92.68% and 86.34% respectively. Authors in [31] applied different machine learning algorithms; those algorithms are decision tree (DT), support vector machine, boosted trees, k-means clustering, convolutional neural networks, genetic algorithms for effective prediction of lumpy skin diseases image dataset. Convolution neural networks outperformed other machine learning algorithms with accuracy of 98.9%. A novel model was also developed using convolutional neural network for the effective prediction of lumpy skin diseases by [32] . The input system was classified with an accuracy of 95%. Mobile based intelligent system was developed by [33] for the effective prediction of lumpy skin diseases . The technology introduced would assist people who are not in a community or city where there is an adequate supply of medical facilities. The experimental results proved that the developed model can classify lumpy skin diseases between normal and abnormal with an accuracy of 80%. Models such as Auto Regressive Integrated Moving Average (ARIMA), fuzzy time series (FTS) and Neural Network Auto – Regressive (NNAR) were applied for forecasting lumpy skin diseases by [53]. The results shown that fuzzy time series performed better other models in five datasets out of seven sets of dataset employed. Authors in [52] highlighted paucity of Artificial Intelligence (AI) based models for improving the healthcare situation in Sub-Saharan Africa (SSA). The paper employed PRISMA to give analysis of works that applied deep learning and machine learning models for the improvement of health care in the Sub-Saharan Africa. Apart from the introductory part of this work, other sections are sub divided into section two which describes materials and methods employed in terms of data pre-processing and application of selected machine learning algorithms; section three analysed and compared the results obtained from selected single classifiers in relation with results obtained from ensemble of single classifiers and the results obtained from optimized artificial neural networks. The last section (conclusion part) describes the observed deductions from the research and recommendation appropriately.

2. METHODS AND MATERIALS

This section explains the architectural design, implementation and evaluation of the developed model using selected classifiers for the prediction of LSD datasets. Figure 1 depicts the developed model for lumpy skin diseases (LSD) prediction. The architectural design consists of the sources of dataset, preprocessing (feature wiz feature selection), machine learning classification techniques and evaluation of the designed model. A comparative analysis between stacked ensembles of decision tree (DT), k-nearest neighbor, random forest (RF) and support vector machine (SVM) algorithms were compared with optimized artificial neural network (ANN). Figure 2 depicts the architectural flow chart of the developed model.

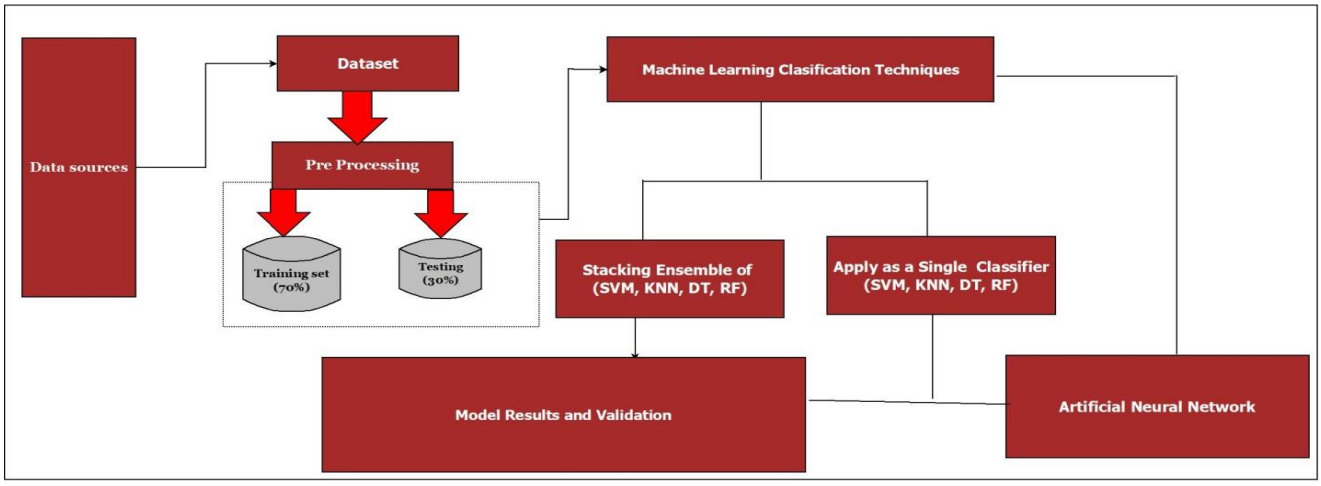

Figure 2: Flow chart of the developed model

2.1 Data Sources and Pre processing

Percentage split method of 70% and 30% of the training and testing dataset respectively were employed and depicted in Table 1. The dataset was obtained from [34] with twenty (20) attributes and 24803 instances. The attributes are grouped into two major groups namely meteorological and geospatial features. The dataset has 19 independent variables and one (1) dependent variable. The dependent variable can either be class "1" with lumpy skin disease and class "0" without lumpy skin diseases. The dataset was already in csv format. Dataset dimensionality can be reduced by either feature selection or feature extraction techniques[35]. The techniques for feature selection in machine learning can be broadly classified wrapper, embedded and filter feature selection techniques. Feature wiz feature selection was employed for lumpy skin diseases parameter selection. Feature wiz feature (SULOV Method) selection approach was employed to select best features to predict the presence of lumpy skin diseases. Seven (7) highly correlated features were removed in the lumpy skin dataset as indicated in the Figure 3.

Table 1: Percentage split of training and testing dataset

Dataset	Training set	Testing set
24803	**17362**	**7441**

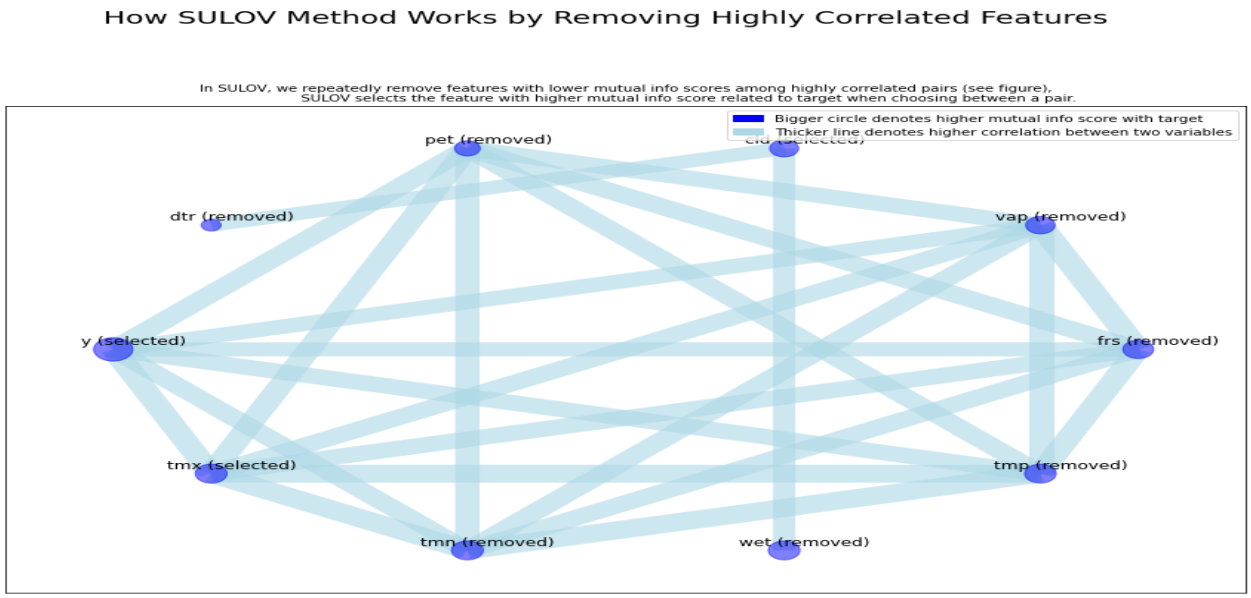

Figure 3: Removal of highly correlated features

2 .2 Machine Learning Classification Algorithms

Different algorithms have been adopted for the lumpy skin diseases prediction. A novel model was developed with stacked ensemble of k-nearest neighbor, support vector machine (SVM), random forest (RF) and decision tree (DT) algorithms as a base model and LR as a meta classifier. A comparative analysis was further made between stacked ensemble of single classifiers and ANN. The parameters setting of all the single classifiers were left unchanged while artificial neural networks were modified as depicted in Table 2. K-nearest neighbour algorithm (k-NN) tests the degree of similarity by comparing each of the training documents to the test documents provided [36]. It will first look for the k most similar training documents as test document's neighbour. It then accumulates the similarity values of these neighbouring documents belonging to the same category. The similarity value is then used as a score for each category. The test document is thus assigned to the category with the highest score. K-nearest neighbour algorithm is an instance based learner and the training examples are stored verbatim, which means a large memory is required. It uses a distance function to determine the distance between training and test sets and training set members nearest to the test set determines the predicted class of the test set [37]. The two parameters said to enhance the performance of k-NN are feature space transformation and the number (k) of nearest neighbours[38] While κ depends on the nature and type of the data, the larger k values reduce the effect of noise. It makes class boundaries less distinct[37]. Feature selection and space transformation should also be done to optimize performance because k-NN uses all features in its distance computation.

Decision tree is one of the classification techniques in data mining method that is employed for decision support systems and machine learning processes[40]. This technique plays a significant role in the process of data mining and data analysis [41]. Generally, the structure of decision tree allows the applicability and to understand the structure of trained knowledge models. An instance is classified by starting at the root node of the tree, testing the attribute specified by this node, then moving down the tree branch corresponding to the value of the attribute in the given example [42]. J48 is the java implementation of C4.5 decision tree algorithm[37]. Support vector machine is a method used for classification which bases its theory on the Structural Risk Minimization principle from computational learning[43]. The support vectors are the documents representatives closest to the decision surface [44].

Random Forest is a supervised machine learning algorithms that are adopted in practical applications of different fields [45]. Random forest is also one of the tree based ensemble algorithms that is derived from combination of random variables[46]. Considering, T-dimensional random vector $Y = (Y_1,\ Y_{2,} \dots \dots \dots Y_p)^T$ which denotes predictor variables and random variable Y which depicts real valued response. Considering,

$$F_{YK} = (W(K, r(Y))) \quad (1)$$

$$W\big(K, r(Y)\big) = I(K) \neq r(Y) = \begin{cases} 0\ if\ K = r(Y) \\ 1\ otherwise \end{cases} \quad (2)$$

Where subscripts YK represents distribution of Y and K., W denotes squared error loss. Logistic regression is one of the supervised machine learning algorithms which are used to calculate probability of binary occurrence[30] [48]. This model is treated as a linear function of a set of input variables and estimates the probability p of linear combination independent variables to determine the actual class label. The logistic regression model is illustrated in the Equation 3.

$$p = \frac{e^{\beta O + \beta 1 x 1}}{1 + e^{\beta 0 + \beta 1 x 1}} \quad (3)$$

Ensemble Methods combine two or more machine learning algorithms together into one predictive model in order to decrease variance (bagging), bias (boosting), or improve predictions (stacking). There are three main types of ensemble methods namely bagging, boosting and stacking. Stacking has the advantage of improving predictive performance of the algorithms. This research work compared the performance of stacked ensemble model with modified artificial neural network. The base models of the stack ensemble are the support vector machine (SVM), k-nearest neighbour (KNN), random forest (RF) and decision tree (DT) while the logistic regression was applied as the Meta model.

Algorithm 1: K-Nearest Algorithm Listing [36]

Training
Step 1: Build the set of training examples D.
Classification
Given a query instance x_q to be classified,
Let x_1…x_k denote the k instances from D that are nearest to *x*_q
Step 2: Return
F(x_q) = arg ⟦ max ∑_(i=1)^ kδ (v,f(*x*_i)) ⟧
Where (a, b) = 1, if a = b and – (a, b) = 0 otherwise

Algorithm 2: Decision Tree Algorithm Listing

```
DecisionTreeTrain (data, remaining features)
guess ← most frequent answer in data
Testing
Decision Tree Test (tree, test point)
If tree is of the form LEAF(guess) then
Return guess
else if tree is of the form NODE(f, left, right) then
    if f = yes in test point then
        return Decision Tree Test(left, test point)
    else
        return Decision Tree Test(right, test point)
    end if
end if
```

Algorithm 3: Support Vector Machine Algorithm Listing [42]

Let $(x^{(i)}, y^{i})$ be training data points

Step 1: Compute matrix $H = [H_{i,j}]$ where $H_{i,j=} y^{(i)} y^{(j)} (x^{(i)}. x^{(j)})$

Step 2: Select value β that controls misclassification.

Step 3: Obtain $\alpha = (\alpha_1, \alpha_2, \dots, \alpha_n)$ by solving the following quadratic optimization problem

Maximize $(\sum_i \alpha_i + \frac{1}{2} \alpha^T H\alpha)$ subject to the constraints $\sum_i \alpha_i y^i = 0, 0 \leq \alpha_i \leq \beta$

Step 4: Calculate $\alpha = \sum_i \alpha_i y^{(i)} x^{(i)}$

Step 5: Identify the supporting vectors. These are all the points for which $0 < \alpha_i \leq \beta$

Step 6: Compute $b = \frac{1}{n_s} \sum_{s'} (y^s - \sum_s a_i\, y^{(i)} x^{(i)}. x^{(s)})$

Step 7: Compute $sign(\alpha^T x' + b)$for the classification of the given point x'.

Algorithm 4: Algorithm Listing for Random Forest [47]

Training Phase:

T: Training set with *x* instances, k features and target variable

F: number of classes in target variable

W: number of classifiers in random forest

Procedure:

For w = 1 to W

1. Generate bootstrapped sample T_w^* from the training set W
2. Grow a tree using a random feature subset from bootstrapped sample T_w^*
   For a given node I.
   (i) Randomly select $m \approx \sqrt{x}$ or $m \approx x/3$ feature
   (ii) Find the best split features and cut points using the random feature subset
   (iii) Send down the data using the best split features and cut points
   Repeat (i) - (iii) stopping rules
3. Construct the trained classifiers C_w
   Testing Phase:
   Aggregate the T trained classifiers with simple majority vote. For a test instance *k*, the predicted class label from classifiers C_b as illustrated below:
   $C_T(k) = argmax_j \sum_{w=1}^{D} I(C_w(k) = j)$ *or* $j = 1, \dots \dots \dots F$

Algorithm 5: Algorithm Listing for Logistic Regression [30]

Training Data
Step 1: For $i \leftarrow 1$ to n
Each instance d_i of training data
Make the target value for the regression to be:
$K_i \leftarrow \frac{y_i - p(1|d_i)}{[p(1|d_i).(1-p(1|d_i))]}$
Initialize the weight of instance d_i to p $(1|d_i).(1 - p(1|d_i)$
Initialize a $1(j)$ to the data with class value (k_i) and weights w_j
Classification Label Decision
Assign (class Label: 1) if p $(1|d_i)$> 0.5, Otherwise (class label: 2)

Algorithm 6: Listing for Stacking Ensemble

Input: Training Data $D = \{x_i, y_i\}_{i=1}^{m} (X_i \epsilon \mathbb{R}^n, y_i \epsilon \Upsilon$
Output: An ensemble classifier H
Step 1: Learn First level classifiers
For $t \leftarrow 1$ *to* K do
Learn a base classifier h_t based on D
end for
Step 2: Construct new data sets from D
For $i \leftarrow 1$ to m **do**
Construct a new data set that contains $\{x_i^1, y_i\}$,
Where $x_i^1 = \{h_1(X_i), h_2(X_i), \ldots \ldots \ldots \ldots \ldots h_T(X_i)\}$
End for
Step 3: Learn a second level classifier
Learn a new classifier h^1 based on the newly constructed data set
Return $\boldsymbol{H(x) = h^1(h_1(X), h_2(X), \ldots \ldots h_T(X))}$

2.3 Artificial Neural Network

Artificial neural networks (ANN) is a computational network that simulate the structure and functionality of biological neural networks[49]. It consists of input, hidden and output layers with connected neurons to simulate the human brain. The input layer of the artificial neural network receives data from the outside world to which the artificial neural network needs to analyse [50,55]. The output layer provides the response to the input parameters analysed by the artificial neural network (ANN) which are interconnected from one layer to another [3, 57]. The input, hidden and output layers. Artificial neural network model was modified using parameter tuning and represented as indicated in the Table 2. Percentage split method was employed to split the dataset into 70:30 training and testing respectively.

Table 2: Parameter settings of the modified artificial neural network

Parameters	Model Values
Training	70%
Testing	30%
Activation Function	Relu
Batch size	4
Optimizer	Adam
Loss Function	Binary_cross entropy
Epochs	200

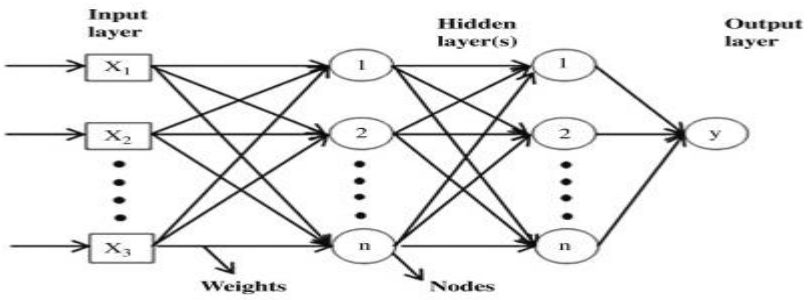

Figure 4: General Structure of Artificial Neural Networks [51]

Mathematical model for the development of multilayer artificial neural network. Considering the output layer given in the equation 5.

$$d_{2,t} = (\vec{d}_{xt,}\overrightarrow{X_{2,t}}) \quad (4)$$

$$\vec{d}_{xt} = \sum_{m=1}^{K_2} \vec{d}\, xt_m \hat{e}_m = \sum_{k=1}^{K_2} (\vec{s}, \vec{x}_{1,k})\hat{t_k}$$

Where $\vec{s}$ is the network input signal, by product rule, we have

$$d_{2,t} = \sum_{k=1}^{K_2} ((\vec{s}, \vec{x}1, m)\hat{t_k}, \overrightarrow{x_{2,t}}) = \sum_{m=1}^{K_2} (\vec{s}, \overrightarrow{x_1}, k)(\hat{t_k}, \overrightarrow{x_{2t}})$$

$$d_{2,t} = \sum_{k=1}^{K_2} ((\vec{s}, \vec{x}1, m)\, \overrightarrow{x_{2,t}}, k) = \sum_{m=1}^{K_2} (\vec{s}, \overrightarrow{x_{2,t,m}}, \overrightarrow{x_{1,m}}) \quad (5)$$

Equation 5 indicates the input and output layers of the two and one layered network.

2.4 Model Evaluation

The novel model was assessed with accuracy, precision, f1-score and recall evaluation metrics as illustrated in Equations 6, 7, 8 and 9 respectively. The mathematical equations for those metrics are given as follows. Accuracy is the ratio of the currently predicted instances to the total number of instances evaluated and it is expressed in the Equation 6. Precision is the measures the ratio of positive instance that are correctly predicted to the total positive instances in a positive class. Recall is the approximation of the positive instance that is correctly classified as positive instance. F1 score is evaluation metrics that determine the accuracy of a given dataset and it is calculated with the Equation 9.

$$\text{Accuracy} = \frac{T_P + T_N}{T_P + T_N + F_P + F_N} \times 100\% \quad (6)$$

$$\text{Precision} = \frac{T_P}{T_P + F_P} \times 100\% \quad (7)$$

$$\text{Recall} = \frac{T_p}{T_p + T_N} \times 100\% \quad (8).$$

$$\text{F1} - \text{Score} = \frac{2\times (\text{Recall} \times \text{Precision})}{\text{Precision} + \text{Recall}} \quad (9)$$

3. RESULTS AND DISCUSSIONS

Comparative analysis of the results singled classifiers and stacked ensemble were represented with Table 2. The developed model was assessed with accuracy, precision; recall and F1 score evaluation metrics. The results stacked ensemble models were then compared with the results of the optimized artificial neural networks.

Table 2: Results obtained from single and stack ensemble classifiers

Classifiers	TP	FN	FP	TN	Accuracy (%)	Precision (%)	F1-score (%)	Recall (%)
RF	6404	112	78	847	97.45	98.80	98.28	98.54
DT	6394	122	80	845	97.29	98.76	98.12	98.45
KNN	6380	136	111	814	96.68	98.29	97.91	98.10
SVM	6416	100	212	713	95.81	96.80	98.46	97.63
Ensemble	6446	70	102	823	97.69	98.44	98.93	98.68

3.1 Results of Single and Stacked Ensemble Models

The results obtained from the single classifiers and ensemble techniques were showing in the Table 2. The models were assessed with accuracy, precision, f1-score and recall evaluation metrics. The single classifiers were random forest, decision tree, k-nearest neighbor. The results showed that ensemble (stack) of the machine learning algorithms on lumpy skin dataset performed better than singled classifiers (decision tree, k-nearest neighbor, support vector machine and random forest) with an accuracy, recall and f1-score of 97.69%, 98.68% and 98.93% respectively. The predictive

performance of the stacked ensemble model was later compared with the optimized ANN. The relationship of the metrics was also represented diagrammatically in the Figure 5.

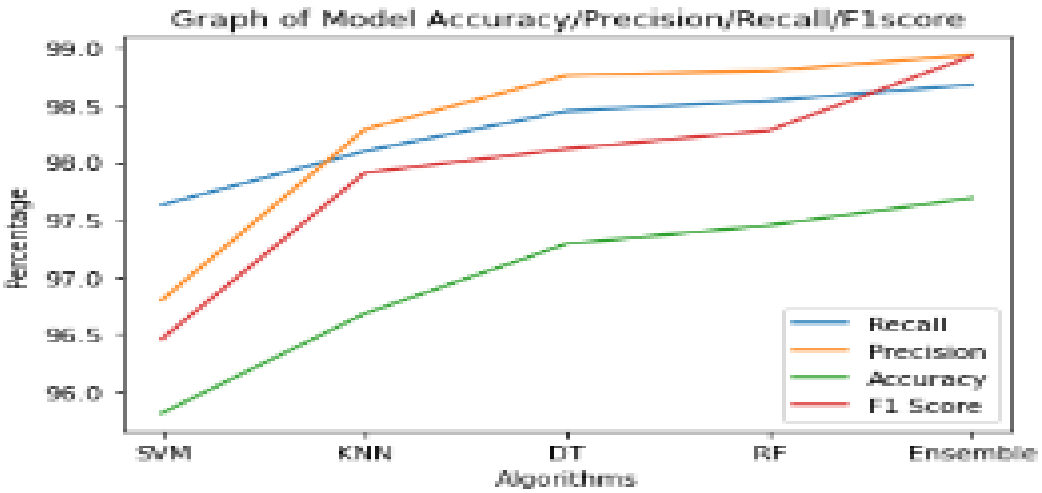

Figure 5: Representation of evaluation metrics of the algorithms

3.2 Results of the Optimized Artificial Neural Network Model

Researchers have adopted artificial neural network (ANN) for the prediction of different diseases. Here, artificial neural network model was improved by appropriate parameters tuning after application of sequential forward feature selection on the lumpy skin diseases dataset. Preceding this technique is the training and validation of model. Table 3 and Table 4 represent accuracy / loss of model training and validation respectively. Records of 200 epochs were taken at an interval of 20 epochs. Records were taken at the interval of 20 epochs and it was observed that, greatest training accuracy was achieved at the 200 epoch with 98.89%. Also, the lowest and greatest training losses were achieved at 200 epochs and 20 epochs (when compared with the records on the Table 3) which correspond to 0.0636 and 0.0880 training losses respectively. Also, when compared with validation results as illustrated in the Table 4. The greatest and smallest validation accuracies were recorded at 200 epochs and 20 epochs which correspond to 98.66% and 96.33% respectively. Also, considering loss measurement the lowest and greatest validation loss were 0.0565 and 0.0934 respectively. Graphical representations of training/validation accuracies were plotted against the corresponding epochs in the Figure 6. Also, Figure 7 depicts the graphical representation of the training/ validation loss against the corresponding epochs.

Table 3: Results of model training (Accuracy and Loss)

Epochs	Training Accuracy	Training Loss
20	0.9666	0.0880
40	0.9696	0.0813
60	0.9720	0.0760
80	0.9724	0.0731
100	0.9741	0.0701
120	0.9743	0.0680
140	0.9779	0.0670
160	0.9791	0.0648
180	0.9805	0.0649
200	0.9889	0.0636

Table 4: Accuracy and loss results for model validation

Epochs	Validation Accuracy	Validation Loss
20	0.9633	0.0934
40	0.9685	0.0815
60	0.9718	0.0729
80	0.9726	0.0669
100	0.9754	0.0625
120	0.9753	0.0606
140	0.9769	0.0583
160	0.9772	0.0598
180	0.9789	0.0598
200	0.9866	0.0565

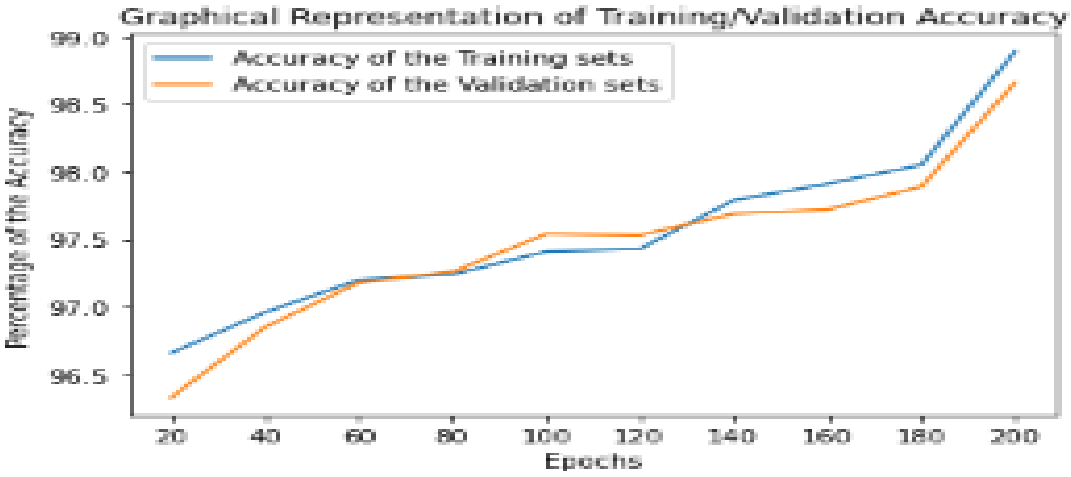

Figure 6: Training/Validation accuracy against epochs

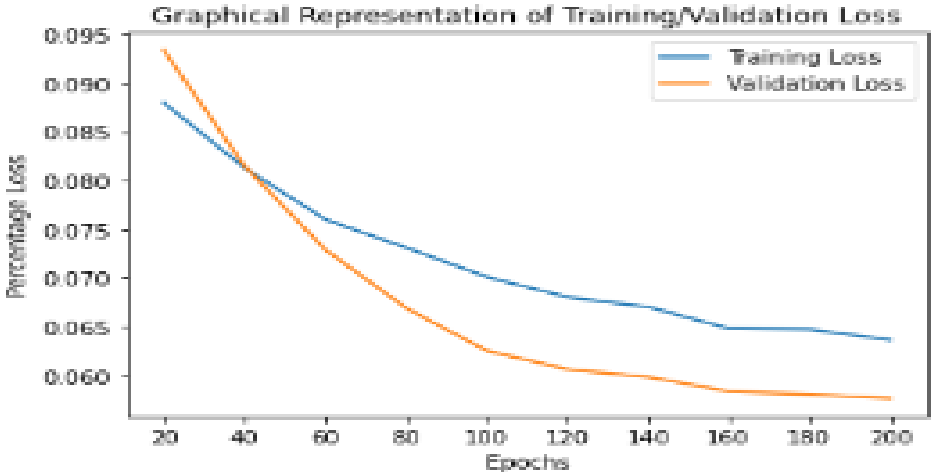

Figure 7: Training/Validation loss percentage against Epochs

3.3 Comparison of the Developed Model with Existing Model

Features of the lumpy skin diseases were selected with feature wiz feature selection technique before classification. Both stacked ensemble model and optimized artificial neural network (ANN) performed better than the work of [19]. The existing model [19] gives optimum accuracy, precision and f1 score of 97% , 88% and 94% respectively. Stacked

ensemble of the singled classifiers gives accuracy, precision and f1 score of 97.69%, 98.44% and 98.93% respectively. Optimized artificial neural network gives 98.66% accuracy. Table 5 depicts the comparison of the existing model with respect to the developed model.

Table 5: Comparison of the existing model and developed model

Author	Machine Learning	Result
[19]	ANN	97% accuracy
Developed Model	Stacked Ensemble	97.69% accuracy
	Optimized ANN	98.66% accuracy

4. CONCLUSION AND RECOMMENDATION

It has been clearly shown that the developed model outperformed the existing model. The developed model compared the predictive performance of the stacked ensemble singled classifiers model with respect to optimized artificial neural network. Features of the employed dataset were selected by feature wiz selection approach coupled with single and stacked ensemble for classification. The assessment of the developed model indicated that both the stacked ensemble and the optimized artificial neural networks performed better than the existing model. Both the ensemble model and deep learning approaches can be adopted in order to improve the predictive performance of the existing model. These techniques can be adopted in improve the predictive performance of different diseases and natural occurrences. Therefore, further studies can adopt the predictive capacities of both ensemble techniques and deep learning approach.

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