https://doi.org/ 10.48047/AFJBS.6.5.2024. 8901-8912

African Journal of Biological Sciences

Pneumonia Variant Detection from CXR Images using Meta-Learning in Machine Learning

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Article History
Volume 6, Issue 5, 2024
Received: 15 May 2024
Accepted: 02 Jun 2024
doi: *10.48047/AFJBS.6.5.2024. 8901-8912*

Abstract.

Purpose: Pneumonia is a common and possibly fatal illness among children hence prompt and precise diagnosis is essential for the proper course of therapy. X-Ray pneumonia diagnosis is impacted by cross-diagnosis, perplexing benign abnormalities, hazy images, exploding deeper network parameters, time complexity and higher accuracy. Diagnosing pneumonia in children might be difficult because of the weak clinical signs and low sensitivity of microbiological investigations. Hence, the objective of this research is to build a meta-learning model in Machine Learning that can precisely analyze the image features and build generalized model to identify the presence and diagnose the type of pneumonia in child chest radiographs.

Methods: The suggested meta-model makes use of three supervised classifiers, including decision tree, nearest neighbor's classifier and support vector classification as well as three ensemble classifier such as adaptive boosting, random forest and gradient boosting classifier. These classifiers are trained on pixel intensity features extracted from a sizable Karmany dataset of radiology images and make preliminary predictions.

Results:A robust hard voting meta-model classifier is built to diagnose pneumonia variant with bacterial or viral infection with an accuracy score of 94.54% and F1-Score of 94.34%.

Conclusion: The suggested research shows a resilient machine learning meta-model that overcomes the overfitting issue that is typically seen in traditional machine learning models like SMO, MP, LDA, Xgboost and ERBM for pneumonia diagnosis. Proposed classifier has greater generalized prediction performance over 64*64 trainable size input. The findings demonstrate that prediction accuracy, resource usage, and temporal complexity all rise together with the size of the preprocessed radiograph, potentially resulting in resource depletion. Additionally, with the increase in size of the radiograph, less preprocessing wall time and CPU time are needed.

This research endeavor is being assisted by Radiologist, Sun Lab Diagnostic, Virar, and Cardinal Gracious Memorial Hospital, Vasai, for clinical conduct and validation of outcomes.

Keywords: Pneumonia, CXR, Chest X-Ray Diagnosis, Radiology Images, Viral Pneumonia

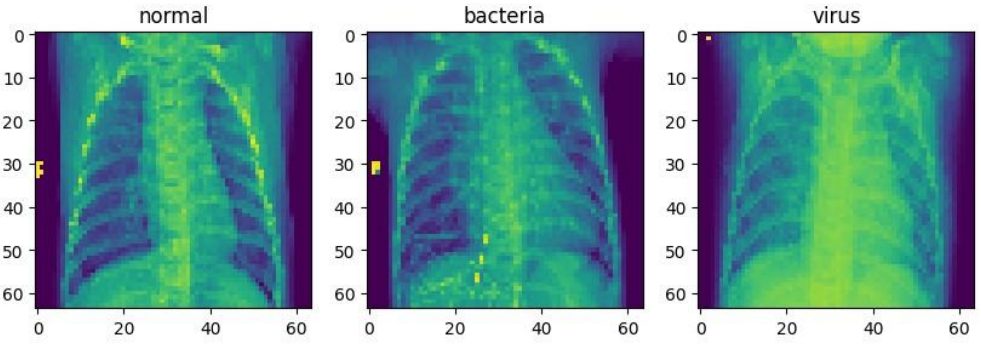
1. Introduction

One of the most serious infectious diseases that endangers human health is pneumonia. Microscopically, the air sacs are negatively impacted by the inflammation that viruses and bacteria generate [1]. Every year, pneumonia affects around 7% of the ecosphere's population, and 4 million of these individuals are at risk of dying [2]. Early diagnosis is therefore crucial for many disorders. Chest pain, breathlessness, a cough, are common pneumonia symptoms. [3]. As a result, the chest X-ray has gained significance in the diagnosis of pediatric pneumonia. Chest X-rays and sputum culture are two diagnostic methods especially for infant pneumonia diagnosis [4]. Examining and detecting chest X-rays by doctors is a laborious process in the medical field [5]. Utilizing current technology tools and software to diagnose is a very beneficial development in terms of time and cost.

Pneumonia in adults is also a dangerous condition that increases hospitalization and mortality rates [6]. In the emergency room or with severely ill patients, the diagnosis of pneumonia can be hard and difficult. Numerous frequently employed radiological indicators lack specificity [7].
Pattern analysis typically calls for a pre-processing phase with the purpose of extracting or choosing characteristics that will aid the discriminator in the classification, prediction, or clustering stage in better representing the data.

This prerequisite is important since processing raw data without first extracting or selecting the appropriate features would be difficult.

By inflaming the air sacs and causing the lung to fill with fluid, bacteria, fungi or viruses can cause pneumonia, an acute pulmonary infection. It is responsible for more than 15% of mortality in infants below the age of five. In order to save the disease from being fatal, early detection and treatment are crucial. In existing literature, various Deep Learning Models [1-5], including VGG16, DenseNet, ResNet and InceptionNet, as well as machine learning techniques such as, Support Vector Machines (SVM), LDA, Random Forest, Decision Tree, etc., [6] [8-9] [18] are used to diagnose pneumonia. It is diagnosed using medical imaging techniques like chest X-Ray (CXR), MRI, CT Scan or lung ultrasound [10-14] [39] [46-51]. Fig. 1 represents major pneumonia variants radiograph images such as bacterial and viral pneumonia which are deliberated in this research [23] [45].



(a) (b) (c)

Fig 1: Dataset images of pneumonia variant and Normal CXR images (a) Healthy Lung (b) Bacterial Pneumonia infection (c) Viral Pneumonia Chest X-Ray images

2. Literature Review

Tej Bahadur Chandra et al suggested five benchmark classifiers like sequential minimal optimization, multilayer perceptron, random forest, logistic regression, and classification through regression. Model trained on custom 412 chest X-Ray images received 95.63 percent accuracy with the logistic regression classifier and 95.39 percent accuracy with the multilayer perceptron, which is a much greater accuracy [44] after segmenting lung region from input images.

M. To˘gaçar selected 300 image features from trained deep network models like VGG-19, VGG-16 and AlexNet to classify pneumonia. These features are then provided to Support vector machine learning models, k-nearest neighbours, linear discriminant analysis, decision tree and linear regression to get best final accuracy of 99.41% from LDA model [42].

RabiaEmhamed et al. [53] compared performances of CNN with Xgboost, KNN model, Random forest, Decision Tree, Adaboost, Gradient Boost and found decision tree performs worst with accuracy of 86.64% whereas CNN gives highest classification accuracy of 98.45% on three different datasets.

Fazli Wahid et al. suggested Enhanced Restricted Boltzmann Machine, KNN, decision tree and SVM [54] to detect pneumonia disease and achieved 97.53%, 92.62%, 91.64%, and 88.77% accuracy.

2.1 Limitations.

Research gap in Machine learning model [6] [8] [9] [18] used for pneumonia disease detection are as follows.

Limited availability of labelled data. Pneumonia detection models often demand a significant amount of labelled X-Ray data for training, which is difficult for annotated pneumonia X-Ray images. There is a need for larger, diverse, and well-curated datasets to train more robust models [21].

Class imbalance and bias. Imbalanced datasets, where the number of pneumonia cases i.e. viral and bacterial pneumonia is significantly smaller than negative cases i.e. normal healthy lung which affects the effectiveness of computer learning models. Additionally, the presence of biases in the data, such as gender or racial bias, can influence the model's predictions [25].

Explainability and interpretability. Many machine learning models, such as deep learning models [19-20], [32-38] [41] are frequently seen as "black boxes," understanding them can be difficult for reasoning behind its predictions. Interpretability of the models is crucial, especially in medical applications, to gain trust from healthcare professionals and ensure transparency in decision-making [26].

Generalization to different populations and settings.ML models developed using a single population's data or healthcare system may not generalize well to other populations or settings with different demographics, imaging protocols, or disease patterns. A need for research exists. on developing models that can generalize across diverse populations and can be adapted to different healthcare settings [24].

Integration with clinical workflows. For machine learning models to have practical utility in clinical settings, they need to be seamlessly integrated into existing healthcare workflows. Research is needed to explore how to effectively deploy and integrate these models into healthcare systems, ensuring usability, scalability, and compatibility with existing electronic health record systems [27].

Table 1: Literature survey on Machine Learning model used for pneumonia disease prediction using CXR images.

Literature Reference	ML Model	Accuracy [%]	Precision[%]
Rajpurkar et al. (2017)	CheXNet (CNN)	92.7	88.0
Liang et al. (2020)	DenseNet (CNN)	94.3	91.2
Islam et al. (2018)	Inception-v3 (CNN)	89.2	85.4
Rahimzadeh et al. (2019)	SVM	87.5	83.6
Das & Santosh et al.(2020)	RF	91.8	88.5
Tej Bahadur Chandra et al. (2018)	SMO, MP, LR And RF	LR: 95.63 MP: 95.39	LR: 97.46 MP: 97.47
M. Togaçar et al. (2020)	SVM, DT, KNN, LDA, and LR	LDA: 99.41	LDA: 99.22
RabiaEmhamed et al. (2020)	Xgboost,KNN, RF, DT, GB,Adaboost, and CNN	DT: 86.64 CNN: 98.45	DT:93.49 CNN: 98.95
Fazli Wahid et al. (2022)	ERBM, KNN, DT and SVM	ERBM: 97.53 KNN: 92.62 DT: 91.64 SVM: 88.77	ERBM: 97.53 KNN: 92.62 DT: 91.64 SVM: 88.77

SMO: Sequential Minimal Optimization **KNN:** k-nearest neighbours

Literature Reference	ML Model	Accuracy [%]	Precision[%]

MP: Multilayer Perceptron **LDA:** linear discriminant analysis
LR: Logistic Regression **RF:** Random forest
SVM: Support vector machine **ERBM:** Enhanced Restricted Boltzmann Machine
DT: decision tree **GB:** Gradient Boost

Prospective validation and clinical impact. While many studies have reported promising results in retrospective settings, there is a need for prospective validation studies to assess the real-world clinical impact of ML models for pneumonia disease detection. Evaluating the models' performance in prospective studies, including their impact on clinical decision-making, patient outcomes, and cost-effectiveness, is essential for wider adoption and acceptance in clinical practice [30].Literature survey represents machine learning model used for pneumonia disease prediction using CXR images is shown in Table 1.

Several approaches can be used to fill up research gaps in machine learning models for pneumonia detection systems. The training dataset can be further increased by using data augmentation and synthesis techniques including flipping, rotating, scaling, and adding noise to already-existing images. Additionally, realistic synthetic data can be produced using generative adversarial networks (GANs). By integrating a big amount of unlabeled data with a smaller set of labeled data and carefully annotating the most informative examples, active learning and semi-supervised learning can make the most out of the limited amount of labeled data. Techniques like oversampling minorities, under sampling majorities, and hybrid sampling approaches can assist address class imbalance and bias. To reduce demographic biases, meticulous data collecting, pre-processing, and evaluation procedures are required. To increase confidenceSaliency maps, attention mechanisms, and model-independent interpretability strategies should be used in the development of explainable and interpretable models in order to improve confidence and transparency. By using knowledge from extensive datasets such as ImageNet, transfer learning and domain adaptation might enhance model performance on data relevant to pneumonia and aid in the generalization of models to other populations or healthcare environments [55]. To collect more diversified and large-scale datasets, validate models prospectively, and evaluate models' clinical impact, cooperation among researchers, medical professionals, and institutions is crucial. Working together with IT specialists and healthcare professionals, machine learning models must be integrated with clinical workflows in a way that ensures user-friendly interfaces and compatibility with electronic health record systems for efficient deployment and utilization.

By employing these strategies, significant progress in overcoming the research gaps and advancing the field of pneumonia detection using machine learning models can be done. In this study active learning method is implemented in order to realize labelled dataset also meta model which is strong classifier is developed over existing base classifiers.

3. Proposed methodology

The Voting Classifier technique for ensemble learning that pools the predictions of various distinct classifiers to provide a pneumonia detection. The Voting Classifier algorithm allows for combining the strengths of multiple classifiers and can lead to improved predictive performance compared to using a single classifier as shown in algorithm 1.

Algorithm 1: *Voting classifier Algorithm*

Input: $C_i \leftarrow$ Weak Classifiers; i=1,,n
Suppervised classifier: (Decision Tree, Support Vector, KNN)
Ensemble classifier:(Gradient Boosting, Adaboost,Random Forest)
D← Dataset
$X_i \leftarrow$ Dataset Sample

Operation:
1. Input $X_i \epsilon D$
2. P← Predict (X_i,C_i) #Every classifier Predicts output class
3. C ← MajorityVotes(P) # Majority votes decides output class minority votes are supressed

4. Return Label

The concept of using meta-models, such as stacking or ensemble techniques, are applied to pneumonia classification tasks to overcome the problem of generalization, explain ability and interpretability in existing models.

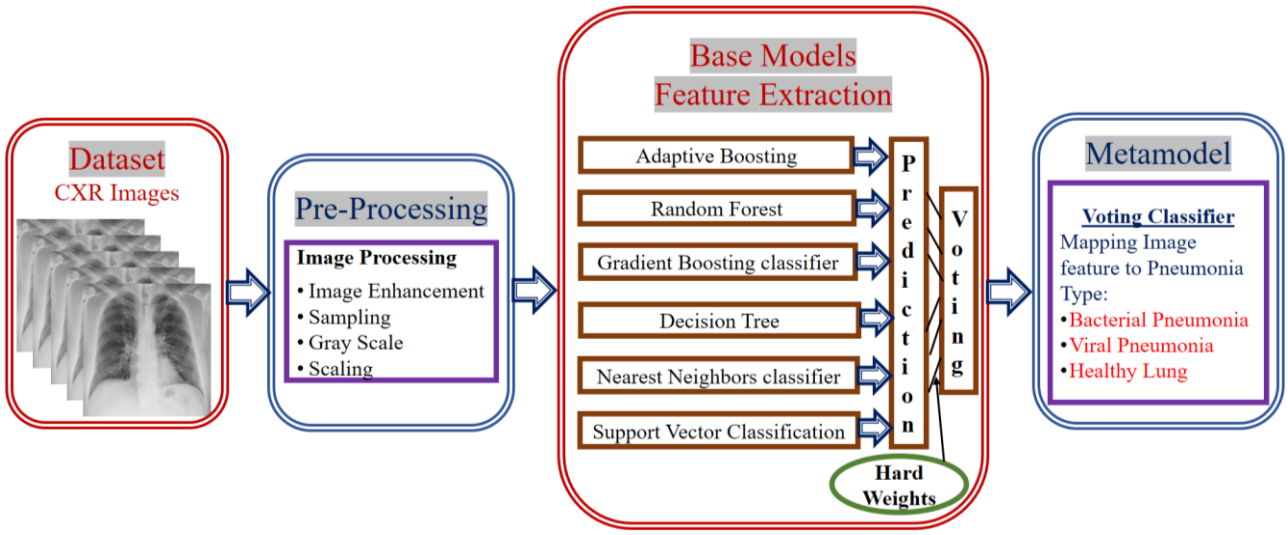


Figure 2: Proposed machine learning meta-model workflow to predict pneumonia disease

Fig. 2 shows a meta-model for pneumonia classification by fusing the forecasts of various base models trained on different features or using different machine learning algorithms.

Dataset Collection: Proposed methodology is divided into four phases in the initial phase radiograph images are acquired from kermany dataset in the split of train, test and validation.

Pre-Processing: In the second phase, pre-processing of CXR images will be performed based on various image-preprocessing techniques like sampling, gray scale conversion and resizing. The different image sizes that are used for feature analysis are 16x16, 32x32, and 64x64. The pixel intensity values of these preprocessed images, having feature count of 256, 1024, and 4096 respectively are further used as trainable dataset features by the proposed classifier for bacterial and viral pneumonia variant prediction.

Feature Extraction: In third phase,the processed X-Ray pixel values are used in the feature analysis for prediction of pneumonia using three supervised learning algorithm like DT, KNN and SVC as well as three ensemble classifiers such as Adaptive Boosting, Random Forest and gradient boosting classifier.The important information hidden in the input data must be extracted using a different module as part of the pattern analysis pre-processing stage. This helpful information can improve the data representation or class discrimination, which will improve the model's performance. Adaptive Boosting (AdaBoost), Random Forest, Decision Tree, Gradient Boosting Classifier, Support Vector Classification (SVC), and k-Nearest Neighbors (k-NN) are significant machine learning algorithms for predicting bacterial and viral pneumonia. AdaBoost improves diagnostic accuracy by focusing on difficult-to-classify cases, combining multiple weak classifiers to create a robust model. Random Forest enhances generalization by aggregating predictions from multiple decision trees built on random subsets of data, reducing overfitting and providing stable predictions. Decision Trees offer clear, interpretable decision paths, crucial for understanding medical diagnoses. Gradient Boosting Classifier incrementally corrects errors, achieving high predictive accuracy and adapting to complex data patterns. SVC maximizes the margin between classes, providing precise classifications and handling non-linear data through kernel functions. Lastly, k-NN captures local data patterns, classifying samples based on the majority label of nearest neighbors, making it simple and effective. Together, these algorithms enhance the

reliability, accuracy, and interpretability of pneumonia predictions, aiding in timely and appropriate treatment decisions.

Meta Model Building: In the last phase, meta-model is built on these predictions using hard voting classifier who strongly relies on best performing model. Final prediction is two major types of pneumonia prediction.

4. MetaModel-Hard Voting classifier

The meta-model can then learn to make the final forecast based on the outputs of the base models. A high-level example of a meta-model to be constructed for pneumonia classification is as follows:

Base Models: Train multiple base models using different algorithms or feature representations. For example, model can train a CNN on chest X-ray images and a SVM on extracted radiology features.

Predictions: Utilising the learned foundation models to obtain predictions for the pneumonia classification task. Each base model independently predicts whether a person has pneumonia or not, given input sample.

Meta-model: Train a meta-model, such as a random forest or a logistic regression, on the predictions generated by the base models. The meta-model learns to incorporate the input features from the base model predictions to get the final pneumonia classification.

Ensemble Prediction: Use the trained meta-model to forecast presence of pneumonia in a new, unseen samples. The basis models' predictions are combined in the meta-model. According to its learned weights or rules.

Meta-models are higher-level models that utilize the predictions or outputs of underlying base models to provide additional functionalities or insights as shown in Figure 2. A few common types of meta-models are possible like stacking, bagging, boosting, meta learnings [40] [52].

Stacking. A method of ensemble learning called stacking combines many base models by training a meta-model using the basic models' predictions as input. By utilizing the advantages of several base models, this method may be able to enhance overall prediction performance.

Bagging. Bagging, also known as bootstrap aggregating is an ensemble method in which numerous Base models are separately trained using distinct bootstrap samples of training dataset. After that, the combined final prediction is made using the base models' projections, frequently through voting or averaging. Bagging can aid in improving model stability and lowering overfitting.

Boosting. Another ensemble technique that sequentially mixes various base models is boosting. With an emphasis on the samples that were incorrectly classified, each base model is trained to fix the errors of the prior models. Weighted voting or weighted averaging is employed to pool the predictions of the fundamental models. By creating a strong ensemble model iteratively, boosting can enhance the performance of weak base models.

Meta-learning. The technique of training a meta-model is to learn from the experiences of several base models. Meta-learning, commonly referred to as learning to learn. The meta-model gains the ability to modify or apply the base models' expertise to fresh tasks or datasets. In the absence of labelled data or when models must swiftly adjust to changing circumstances, meta-learning might be helpful.

Meta-models offer improved prediction accuracy, generalization, robustness, interpretability, and insights into base models. Their effectiveness depends on model quality, diversity, problem domain, and dataset characteristics. Hence this study uses a stacking meta-model voting classifier for pneumonia prediction.

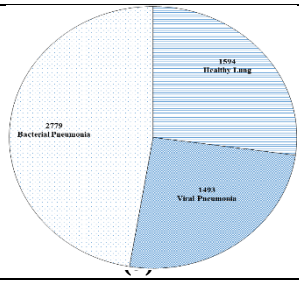
5. Results and Discussion

Proposed meta-model integrate week machine learning classifiers to build a strong classifier. The algorithm begins by splitting dataset into viral, bacterial and healthy images based on CXR image annotation. The dataset of size 5866 chest X-Ray images is split as shown in Table 2 depictsin pie chart presence of 1594 Healthy Lung CXR images, 1493 Viral Pneumonia CXR images, 2779 Bacterial CXR images.

In first phase all CXR images undergo preprocessing [7] [15] [22] [28] [29] where radiographs are transformed into gray scale pictures and further transformed into required image size for training. Kermanydataset[56][57] is further divided into training and testing by the split ration of 80:20.

Table 2: Number of CXR images in dataset for Training and Testing,(a) Kermany dataset split into training samples of Bacterial, Viral and healthy lung images.

Dataset Images	Healthy Lung	Viral Pneumonia	Bacterial Pneumonia	Total Images
Training	1275	1194	2223	4692
Testing	319	299	556	1174
Total Images	1594	1493	2779	5866



The next phase is the identification and categorization of images using conventional machine learning, which takes normalized reshaped pixel values as features from the images, interprets them, and assigns them to different categories.

5.1. Effect of input chest radiograph size on prediction. In order to scrutinize the performance of model in various different environments various input image sizes of 16*16, 32*32 and 64*64 were analyzed. A robust model is created that can precisely predict pneumonia by training a set of powerful hard voting classifiers on a sizable dataset. Data are repeatedly trained to learn the feature of the data during each epoch. Utilizing classification accuracy and cross-validation, the model's performance is estimated and displayed the outcomes as mean and standard deviation (SD). Table 3 displays the results of six machine learning classification models using. in terms of respective accuracy and volatility in performance by measure of standard deviation for specified classifier. The evaluation clearly shows that as the number of input feature values goes on increasing, the prediction performance also goes on increasing with more robust, generalized and stable performance. However, the input radiograph size cannot be increased more as processing feature size increases exponentially and system crashes due to heavy uses of RAM, GPU, TPU and other resources.

Table 3: Performance of Meta-model and associated weak classifiers on specific input size radiograph features.

Input Radiograph Size	16*16		32*32		64*64	
Feature Count	256		1024		4096	
ML Classifiers	**Mean Acc.**	**Std. Dev.**	**Mean Acc.**	**Std. Dev.**	**Mean Acc.**	**Std. Dev.**
Random Forest]	0.75	± 0.01	0.77	± 0.02	0.82	± 0.03
Adaptive Boosting	0.69	± 0.05	0.71	± 0.03	1.00	± 0.00
Gradient Boosting	0.70	± 0.02	0.71	± 0.02	1.00	± 0.00
Decision Tree	0.61	± 0.04	0.62	± 0.02	1.00	± 0.00
K-Nearest Neighbor	0.67	± 0.04	0.69	± 0.01	0.74	± 0.03
Support Vector Machine	0.76	± 0.02	0.79	± 0.02	0.77	± 0.03
Ensemble Voting Meta-model (Proposed)	**0.75**	**± 0.03**	**0.78**	**± 0.01**	**0.94**	**± 0.01**

Table 4 shows the proposed models performance on given input size chest radiograph based on different evaluation criteria's. The evaluation parameters value clearly shows that performance of model becomes more robust and generalized over increase in input radiograph size. According to

investigation, most classifiers perform much better with higher resolution pictures (64x64), especially boosting approaches and ensemble. The optimal technique, which strikes a balance between high accuracy and stability across a range of image sizes, is the ensemble voting meta-model.

It is critical to realize that when image size rises, resource usage and temporal complexity rise along with it, potentially resulting in resource bursting.It is also important to note that as radiograph size rises, the wall time needed to preprocess the required size images continues to decrease. Instruction count, CPI (clock cycles per instruction), and clock cycle time are the three main determinants of CPU performance. Additionally, when image size increases, this CPU time keeps lowering.

Table 4: Results of ML hard voting meta-classifier on different size input size radiographs.

Parameters	Precision [%]	Recall [%]	F1-Score [%]	Accuracy [%]	CPU Time	Wall Time [µs]
16*16	76.90	77.49	76.65	75.30	4	24.10
32*32	78.47	78.52	77.12	77.95	3	9.06
64*64	**94.97**	**94.54**	**94.34**	**94.54**	**2**	**8.34**

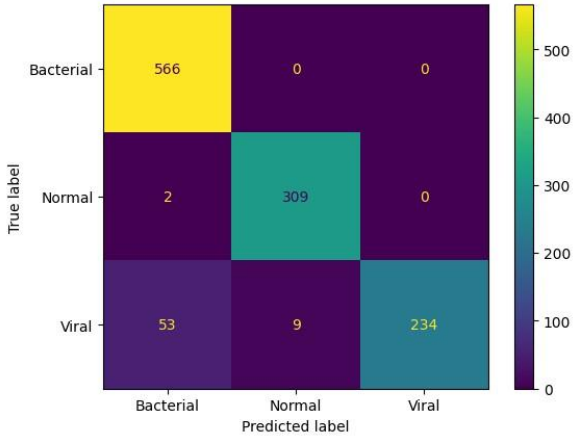


Figure 4: Confusion Matrix obtained over prediction on test dataset.

The confusion matrix received after prediction over 20% test dataset is shown in Fig. 4 reveals that the generalized accuracy reached on 64*64 radiograph by the model is 94.54%, precision is 94.97%, recall achieved is 94.54% and f1-Score is 94.34%.

6. Conclusion

The use of ML based innovative technology for pneumonia detection like SMO, MP, LDA, XGboost, ERBM has issues of model overfitting, poor generalization and interpretability. These issues can be resolved by designing ML meta-model voting classifier which is built on three ensemble classifiers like RE, AB, GBC and three supervised learning classifiers like DT, KNN, SVC. The hard voting classifier is built on these weak classifiers in order to have generalized model performance on unseen data. It is observed that GBC, DT and AB models are being over fitted by depicting 100% accuracy. Hence, ensemble voting classifier provides more generalized performance on unseen radiograph of resolution 64*64 providing 94.54%, accuracy is 94.54%, precision is 94.97%, and the F1-Score is 94.34%. Models performance on unseen validation data can be more improved by providing feature analysis at preprocessing stage to determine which extracted features contribute high in accurate model prediction. Hence, the proposed ensemble voting meta-model is the best method since it achieves a balance between high accuracy and stability over a variety of image sizes.

Declarations:

Conflict of interest: The authors declare that they have no conflict of interest.

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors.

Consent of publication: Not applicable.

Availability of data and materials: Data sharing is not applicable to this article as no datasets were generated or analyzed during the current study.

Competing interests: The authors declare that they have no competing interests

Funding: This work has no funding resource.

Author's contributions: All authors contributed to the study conception and design. Material preparation, data collection and analysis were performed by [*1]Kanchan Dabre, [2]Satishkumar L. Varma and [3]Pankaj Patil. The manuscript was written and revised by all authors on previous versions of the manuscript.

All authors read and approved the final manuscript.

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